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December 29, 2003, 16:03:18 ; Search time 13.2661 Seconds (without alignments) 927.898 Million cell updates/sec Run on:

1 MARILLLFLPGLVAVCAVHG......RVYQEATKEVPTTDIDFFCE 128 US-10-019-455A-6 676 Title: Perfect score: Sequence:

283308 segs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

283308

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES	Description	melanoma-derived	transforming prote		VAV2 pr		cell division cycl	myosin-IA - Acanth	hypothetical prote	asparagine synthas	fructose-bisphosph	Balbiani ring 1 ch	ATP-dependent RNA	hypothetical prote	AAA family ATPas	probable lipoprote	phosphoribosylamin	- 1	recG helicase [imp		hypothetical prote					polyprotein (1A,				
SOM		I38019	TVHUVV	TVMSVV	151940	RGBYCS	F90113	T32734	T48525	C64439	C69621	A23516	G96965	G86746	C90186	AG0693	A64417	D72278	C97114	D86758	C64427	T47442	E86714	139521	867383	852919	T29340	F234	824550	п
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	Length	131	839	844	878	1589	295	1215	308	541	671	383	585	722	769	84	444	699	678	209	259	1199	328	392	670	2193	2541	461	505	
۵	ery	38.1		12.6	12.1	11.6	11.3		10.9	10.6	10.6	10.5	10.5	10.5	10.5	10.4	10.4	10.4	10.4	10.4	10.4	10.3	10.2		10.2	٥.		10.1		
	Score	257.5	86.	85.5	81.5	78.5	76.5	74.5		71.5	71.5	71	71	71	71	70.5	70.5	70.5	70.5	70	70	69.5	69	69	69	69	69	68.5	68.5	
	Result No.		10	m	4	ហ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	

Transforming protein vav - human (fragments)
NyAlternate names: finger protein vav
Species: Homo sapiens (man)
C;Date: 31-Mar-1991 #sequence_revision 03-May-1996 #text_change 18-Jun-1999
C;Date: 31-Mar-1991 #sequence_revision 03-May-1996 #text_change 18-Jun-1999
C;Date: 31-Mar-1991 #sequence_revision 03-May-1996 #text_change 18-Jun-1999
R;Katzav, S; Cleveland, J.L; Heslop, H.E.; Pulido, D.
Mol. Cell. Biol. 11, 1912-1920, 1991
A;Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene
A;Reference number: A39576; MUID:91172176; PMID:2005887

A;Molecule type: mRNA A;Residues: 1-61 «KAI» A;Cross-references: GB:MS9834; NID:g340189; PIDN:AAA63267.1; PID:g340190 A;Note: the authors translated the codon CAA for residue 6 as Glu, CAG for residue 13

Balbiani ring 2 ch	hypotherical proce	nypornerical proce	Balbiani ring 2 cn	probable cytochrom	probable cytochrom	formate dehydrogen	glycosyltransferas	probable chromomet	SNF2-type helicase	methylmalonyl-CoA	VHS domain contain	polygalacturonase	glutamyl-tRNA synt	L2 protein - human	L2 protein - human
B29662	AE3482	T04200	B29960	G90951	C85800	B83966	B97258	G96719	AD1280	C75325	T39655	S24156	G82104	P2WL8	536483
7	01	N	N	N	~	~	7	7	N	7	~	N	~	н	7
162	234	332	359	366	366	782	374	839	1072	142	373	383	509	518	524
10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.0	10.0	10.0	6.6	6.6	9.9	6.6	6.6	6.6
68	9	68	89	68	68	68	67.5	67.5	67.5	67	67	29	67	67	67
30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 138019 melanoma-derived growth regulatory protein MIA - human C;Species: Homo eapleins (man) C;Species: Homo eapleins (man) C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 04-Mar-2000 A;Files: Cloning of a novel malignant melanoma-derived growth-regulatory protein, MIA. A;Resious: 138019 A;Resious: preliminary; translated from GB/EMBL/DDBJ A;Resious: preliminary; di.2%; pred No. 4.7e-19; Best Local Similarity di.2%; pred N
eri - Mao - Ma

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C. Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding C, Superfamily: vav transforming protein; zinc finger
C, Keywords: phosphoprotein; transforming protein; zinc finger
F, 32-107, Region: leucine-rich
F, 32-107, Region: acidic
F, 194-458/ Domain: CDC24 homology <CD24>
F, 386-340/ Region: muclear location signal
F, 386-340/ Region: muclear location signal
F, 518-563/ Domain: protein kinase C zinc-binding repeat homology <KZ1>
F, 528-548/ Region: zinc finger CCC motif
F, 558-56/ Region: zinc finger HCCH motif
F, 558-56/ Region: zinc finger HCCH motif
F, 558-56/ Region: muclear location signal
F, 504-659/ Region: proline-rich
F, 504-659/ Region: proline-rich
F, 506-609/ Region: signal
F, 506-609/ Region: proline-rich
A;Cross-references: EMBL;X64361; NID:955220; PIDN:CAA45713.1; PID:955221
R;Adams, J.M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.
Oncogene 7, 611-618, 1992
A;Titler: The hematopoietically expressed vav proto-oncogene shares homology with the d A;Feference number: S23669; MUID:92228488; PMID:1565462
A;Contents: annotation; the authors note the frameshift difference with sequence in A6 A;Note: the complete sequence was submitted to Genbank; see S36941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: 151940
R;Henske, E.P.; Short, M.P.; Jozwiak, S.; Bovey, C.M.; Ramlakhan, S.; Haines, J.L.; Krann. Hum. Genet. 59, 25-37, 1995
A;Title: Identification of VAV2 on 9q34 and its exclusion as the tuberous sclerosis ge A;Feference number: 151940; MUID:95283235; PMID:7762982
A;Accession: I51940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Map position: 9q34-9q34
C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding F;198-462/Domain: CDC24 homology <CD24>
F;198-462/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F;673-764/Domain: SH2 homology <SH2>
F;623-872/Domain: SH3 homology <SH3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 ASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 VYT---ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEM 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Indels 13; Gaps
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A;Residues: 1-878 <RES>
A;Cross-references: GB:S76992; NID:g913345; PIDN:AAB34377.1; PID:g913346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.6%; Score 85.5; DB 1; Length 844; 31.4%; Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
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Best Local S
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A;Molecule type: mRNA
A;Molecule type: mNNA
A;Molecule type: mNNA
A;Molecule type: mNNA
A;Molecule type: mNNA
Mol. Call. Biol. 11, 1912-1920, 1991
A;Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene action mnDer: A39576; MUID:91172176; PMID:2005887
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A; Residues: 1-323, 'DLLMVPWQRVLKYHLLLQELVK', 346-347, 'QDAT', 352, 'K', 354, 'N', 355-453, 'R', 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; voc. in the sequence from mouse the authors find three additional nucleotides that procoursed in the published human sequences
C; Comment: In comparing these sequences with the mouse (see PIR:TVMSVV), there appear to
                                                                      EMBO J. 8, 2283-2290, 1989
A,Title: vav, a novel human oncogene derived from a locus ubiquitously expressed in hema
A,Reference number: S05382; MUID:90005432; PMID:2477241
                                                                                                                                                                                                                                                                                                                                                               R,Adams, J.M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R. Oncogene 7, 611-618, 1992
A,Title: The hematopoietically expressed vav proto-oncogene shares homology with the dbl. A,Reference number: $23669; MUID:92228488; PMID:1565462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F,126-170/Region: acidic
F,126-170/Region: acidic
F,188-452/Domain: CDC24 homology <CD24>
F,509-557/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F,522-542/Region: zinc finger CCC motif
F,522-542/Region: zinc finger HCCH motif
F,547-560/Region: zinc finger HCCH motif
F,588-648/Domain: SH3 homology <SH3A>
F,664-756/Domain: SH3 homology <SH3B>
F,483-831/Domain: SH3 homology <SH3B>
F,433/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GDB:127112; OMIM:164875
A;Map position: 19p13.3-19p13.3
C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding
C;Keywords: phosphoprotein; transforming protein; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transforming protein vav - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Bate: 03-May-1994 #sequence_revision 16-Peb-1996 #text_change 18-Jun-1999
C;Accession: A61187; A39576; Z38941; S23669
R;Coppola, J; Bryant, S; Koda, T; Conway, D; Barbacid, M.
Call Growth Differ. 2, 95-105, 1991
A;Title: Mechanism of activation of the vav protooncogene.
A;Reference number: A61187; MUID:91299578; PMID:2069873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.8%; Score 86.5; DB 1; Length 839;
Best Local Similarity 32.9%; Pred. No. 1;
Matches 23; Conservative 13; Mismatches 21; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-28,'E',30-93 <KAT>
A;Cross-references: GB:M59833; NID:g202343; PIDN:AAA63402,1; PID:g202344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 839;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.8%; Score 86.5; 32.9%; Pred. No. 1;
                       R;Katzav, S.; Martin-Zanca, D.; Barbacid, M.
                                                                                                                                                                                                                                              A, Molecule type: mRNA
A, Residues: 62-839 < KAT2>
A, Cross-references: EMBL:X16316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S36941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: GDB: VAV1; VAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S36941
                                                                                                                                                                                                         A;Accession: S05382
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C;Accession: T48525
K;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, B.; Brandt, A.; Duesterhoeft, A.; Bancrof
submitted to the Protein Sequence Database, April 2000
A;Reference number: 224490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Introns: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 296/1; 340/3; 390/3; 447/3; 50
C,Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homo
                  R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
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                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-295 <DOU>
A;Cross-references: GB:AJ010592; NID:g12580757; PIDN:CAC27075.1; GSPDB:GN00151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 GIVKICDFGMGTF---LCSKKICLSDKIV-TLW-----YRAPE----ILLGQHFYDY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AF085185; NID:g3599477; PID:g3599478; PIDN:AAC35357.1
A;Experimental source: strain Neff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 VYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypochetical protein T22P22.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr_2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Acanthamoeba castellanii
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 08-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Reywords: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 GLVAVCAV-HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 SKLVKENGA--GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 SVDMWSFGCVIGELITGEILFQGKSELDQL------NKIFQ--TIGTPTTEI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Indels 13; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
11.3%; Score 76.5; DB 2; Length 295;
Best Local Similarity 28.4%; Pred. No. 3.5;
Matches 33; Conservative 16; Mismatches 36; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1215 <LEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;14-674/Domain: myosin motor domain homology <MMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.0%; Score 74.5; D: 28.6%; Pred. No. 25; tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myosin-IA - Acanthamoeba castellanii
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1205 GVFPANYVED 1214
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nes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Genome: nucleomorph
                                                                                                                                                                                                       A; Status: preliminary
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C, Accession: F90113
                                                                                                                                                                          A; Accession: F90113
                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 2
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A; Residues: 1-1589 < PAUJ
A; Residues: 1-1589 < PAUJ
A; Cross-references: BMEL:U17247; NID:9577216; PIDN:AAB67360.1; PID:9577222; GSPDB:GN0001
B; Camonis, J.H.; Kalekine, M.; Gondre, B.; Garreau, H.; Boy-Marcotte, E.; Jacquet, M.
EMBO J. 5, 375-380, 1986
A; Pittle: Characterization, cloning and sequence analysis of the CDC25 gene which control
A; Reference number: A23444; MUID:86220116; PMID:3011405
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-496, YY, 498-953, LSVIMNLSR', 964-1589 < CAM>
A; Cross-references: EMEL:X03579; NID:93483; PIDN:CAA27259.1; PID:93484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Curr. Genet. 10, 879-885, 1986
A;Title: The CDC25 "Start" gene of Saccharomyces cerevisiae: sequencing of the active C-A;Reference number: S43051; WUID:88194639; PMID:3329037
A;Accession: S43051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Description: positive control of level of cellular cAMP at the stage at which the cell C;Superfamily: budding yeast CDC25, CDC25.type guanine nucleotide exchange activator how C;Keywords: cell cycle control; transmembrane protein P;65-123/Domain: SH3 homology <SH3>.
                                                                                                                                                                                            cell division control protein CDC25 - yeast (Saccharomyces cerevisiae)
N.Alternate names: protein L2142.6; protein YLR310c
C;Specises: Saccharomyces cerevisiae
C;Specises: Saccharomyces cerevisiae
C;Accesion: A26596; S51442; A23444; S43051; S47990
R;Brock, D.; Tody, T.; Michaeli, T.; Levin, L.; Birchmeier, C.; Zoller, M.; Powers, S.; Cell 48, 739-799, 1987
A;Title: The S. cerevisiae CDC25 gene product regulates the RAS/adenylate cyclase pathwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fil301-1542/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 LSSSPSTSELTSIRPIGIVVAAYDFNYPIKKDSSSQLLSVQQGETIYILNK----NSSG-99
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A,Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C,Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A;Residues: 1-1589 <BRO>
A;Residues: 1-1589 <BRO>
A;Cross-references: EMBL:M15458; NID:g171184; PIDN:AAA34478.1; PID:g171185
R;Pauley, A.
submitted to the EMBL Data Library, November 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
11.6%; Score 78.5; DB 1; Length 1589;
Best Local Similarity 25.8%; Pred. No. 13;
Matches 23; Conservative 21; Mismatches 34; Indels 11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Description: The sequence of S. cerevisiae cosmid L2142. A, Reference number: S51437 A, Accession: S51442
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A, Residues: 877-1589 < DAN>
C, Gross-references: EMBL: X03579
A, Genetics:
A, Gene: SGD: CDC25; CTN1; MIPS: YLR310C
A, Cross-references: SGD: S0004301; MIPS: YLR310C
C, Function: 12R
       | :|:|| |:|: 862 GRIGWFPSTYVEEEGI 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: A26596
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Kieger, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlo A, Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekweska, A.; Ser ateuchi, M.; Tamakoshi, A.; Terpstra, P.; Pognoni, A.; Tosato, V.; Ser ateuchi, M.; Panakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyam T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A, Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A.; Reference number: A69580; MulD:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Residues: 1.671 «KUN»
A,Cross-references: GB:299124; GB:AL009126; NID:g2636442; PIDN:CAB16056.1; PID:g263656
A,Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Pathway: gluconeogenesis
A;Note: requires manganese ion for stability and phosphoenolpyruvate for activation
C;Superfamily: Bacillus subtilis fructose-bisphosphatase; phosphoesterase core homolog
C;Reywords: carbohydrate metabolism; gluconeogenesis; metalloprotein; phosphoric monoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cydcession: A23516
Richog, C.; Engberg, C.; Wieslander, L.
Nucleic Acids Res. 14, 703-719, 1986
A;Title: A BR 1 gene in Chironomus tentans has a composite structure: a large repetiti
A;Reference number: A23516; MUID:86120366; PMID:3003693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-383 <HOO>
A; Cross-references: GB:XO3490; NID:97043; PIDN:CAA27206.1; PID:9769785
A; Note: the authors translated the codon GAA for residue 118 as Gly and TTC for residu C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Description: catalyzes the hydrolysis of fructose-1, 6-bisphosphate to fructose-6-pho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-dependent RNA helicase, superfamily II [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Balbiani ring 1 chain - midge (Chironomus tentans) (fragment)
C,Species: Chironomus tentans
C,Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 DRLASKKI.CADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 LRNGSGRVXEKIRDIFSGVIYDREIDBLAALVYYPEDKLKLIKHDFDAKEALNE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 KENGAG-----EFWAGSVYGDGQDEMGVVGYFPRN---LVKEQRVYQEATKE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
10.6%; Score 71.5; DB 1; Length 671;
Best Local Similarity 22.8%; Pred. No. 27;
Matches 26; Conservative 21; Mismatches 38; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.5%; Score 71; DB 2; Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 GSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 GSVEVDGKK-----LSPEKKEKFGKALQDAVK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 28.0%; Pred. No. 17; nes 26; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 273/1
C;Superfamily: unassigned Balbiani ring proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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Cipacoles: Bacillus subtilis

Cipace: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 03-Jun-2002

Cipace: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 03-Jun-2002

Cipacoles: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 03-Jun-2002

Cipacoles: Cipacoles: Cipacoles: Cipacoles: Cipacoles: Cipacoles: Cipacoles: Cipacoles: N.W.; Cho

A; Britch, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, S.

Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, Cipacoles: Cipacol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G.A.Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschil A;Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) [similarity] - Methanococcus ja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Nolecule type: DNA
A;Residues: 'MRD',1-541 <BUL>
A;Cross-references: GB:U67554; GB:L77117; NID:g2826365; PIDN:AAB99117.1; PID:g1591755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Superfamily: asparagine synthase (glutamine-hydrolyzing)
C;Keywords: asparagine biosynthesis; ligase
F;2-541/product: asparagine synthase (glutamine-hydrolyzing) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 IFMDRLAS------KKLCADDEC-VYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Species: Methanococcus jannaschii
C, Date: 13.Sep-1996 #sequence_revision 09-Jun-2000 #text_change 19-Jul-2002
C, Accession: C64439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: C64439
A;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
10.9%; Score 74; DB 2; Length 308;
Best Local Similarity 37.2%; Pred. No. 6.6;
Matches 16; Conservative 8; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 KGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNL 104
                                A;Accession: T48525
A;Status: preliminary
A;Molecule type: DABA
A;Residues: 1-308 <BBA>
A;Eross_references: EMBL:AL163814
A;Experimental source: cultivar Columbia; BAC clone T22P22
C;Genetics:
C;Genetics: 5
A;Introns: 63/3; 117/3; 135/3; 180/3
A;Note: T22P22.50
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Matches 27; Conservative
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Gaps

DB 2; Length 769;

A; Accession: C90186

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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-769 «KUR»
A;Cross-references: GB:AE006641; NID:g13813572; PIDN:AAK40746.1; GSPDB:GN00155
C;Genetics:
A;Gene: SSO0421
C;Superfamily: transitional endoplasmic reticulum ATPase; FtsH/SEC18/CDC48-type ATP-bi
                                                                                                                                                                                                                                                                                                                             67 YVYSKLVKENG------VKE 107
                                                                                                                                                                                                                                                                                                                                                                Query Match
10.5%; Score 71; DB
Best Local Similarity 35.0%; Pred. No. 35;
Matches 28; Conservative 10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 AQV-ODATKVVLAPTOPISF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 26.8%
Matches 22; Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-84 < PAR>
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OB6746

Disperies and protein nrdE [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

Disperies: Lactococcus lactis subsp. lactis

C;Species: Larctococcus lactis subsp. lactis

C;Species: Larctococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C;Accession: G86746

R;Bolotin, A.; Mincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli

A;Tille: The complete genome sequence of the lactic acid bacterium Lactococcus lactis sa

A;Tille: The complete genome sequence of the lactic acid bacterium Lactococcus lactis sa

A;Status: preliminary
C;Accession: G96995
K;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, S.; Nolling, J.; Breton, G.; Omelchenko, B.V.; Smith, D.R.
j. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
j. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A9690; MUID:21359325; PMID:21359325
A;Reference number: A9690; MUID:21359325; PMID:21359325
A;Status: preliminary
A;Kocssion: G96995
A;Status: Dreliminary
A;Residues: 1-585 «KUR»
A;Residues: 1-585 «KUR»
A;Residues: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0778
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Cispecies: Sulfolobus solfataricus
Cispecies: Sulfolobus solfataricus
Cispecies: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
Cidecession: C90186
Cifacession: C90186
Rishe, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A; Deference number: Appil39
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A;Experimental source: strain IL1403
C;Genetics:
A;Gene: nrdb
C;Superfamily: Salmonella typhimurium ribonucleoside-diphosphate reductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 GLVAVCAVHGIFMDRLASKKLCADDEC-VYTISLASAQEDYNAPDCRFINVKKGQQIYVY 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 KLCADD----ECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSK----LVKBNGAGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | | : : | : | | : | | : | | EPYFVEKYYGKPFAEVDITAEYDKMVANPBIRKTSINARELBQELSK 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 SKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 10.5%; Score 71; DB 2; Length 722; 1 Similarity 26.2%; Pred. No. 33; 28; Conservative 21; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 FWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                           / Match 10.5%; Score 71; DB Local Similarity 29.4%; Pred. No. 26; nes 30; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-722 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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C90186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Cispecies: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AG0633
C;Accession: AG0634
C;Accession: AG0634
C; Accession: AG0634
C; Accession: AG0634
C; Moule, S; O'Gaora, P.
A; Moule, S; O'Gaora, P.
A; Moule, S; O'Gaora, P.
A; Moule, S; O'Gaora, P.
A;Authors: Parry, C:; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica ser
subsp. enterica serovar Typ
                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AL513382; PIDN:CAD01920.1; PID:g16502762; GSPDB:GN00176
C;Genetics:
A;Gene: ydhA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 84;
     probable lipoprotein ydha [imported] - Salmonella enterica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.4%; Score 70.5; D
26.8%; Pred. No. 3.8;
ive 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::|:|
LLTLKQGISASGARYTDGIYVF 82
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                     Copyright
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protein search, using sw model . protein

December 29, 2003, 16:03:18 ; Search time 5.01961 Seconds (without alignments) 1199,181 Million cell updates/sec Run on:

US-10-019-455A-6

1 MARILLEFIPGLVAVCAVHG......RVYQEATKEVPTTDIDFFCE 128 Title: Perfect score: Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched: 127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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SUMMARIES	4	ID	OTOR_HUMAN	OTOR_MOUSE	OTOR_CHICK		MIA_HUMAN	MIA_BOVIN	MIA_RAT	MIA_MOUSE	VAV3_MOUSE	VAV_HUMAN	VAV3 HUMAN	VAV_RAT	VAV MOUSE	VAVZ MOUSE	VAV2_HUMAN	CC25 YEAST	TR11_MOUSE	ITINI_HUMAN	SHK1_HUMAN	ITN1_RAT	ASNH_METJA	ITN1 MOUSE	SHK1_RAT	PUR2 METJA	ZO3 MOUSE					SHK3 RAT			POLG_EC09H
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	* Query	Match	0.0	9.1	1.0		8.1			4.8	3.1		2.8		5.6		ς.	4	1.5	1.1	6.0	8.0	9.0	0.5	0.5	0.4	0.4	0.4	0.4	4.0	0.4	0.4	10.2	0.2	0.5
	* Š	Σ	7						'n		Т	-	-	Н	Н	н	-	7																	
		Score		602	480	390	ß	256.5	254	235.5	88.5	86.5	86.5	85.5	85.5	82.5	81.5	78.5	78	75	74	73	71.5	71	71	70.5	70.5	70	70	70	70	70	69	69	69
	Result	No.		7	m	4	ស	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q66577 e genome po P42686 spongilla 1 P42690 spongilla 1 P08725 chironomus P58161 escherichia Q80905 human papil Q12554 aspergillus Q1153 vibrio chol P06419 human papil P19919 oligotropha Q8y668 listeria mo
POLG EC09B SRK1_SPOLA SRK4_SPOLA BAR2_GHIPA TORY_ECO57 TORY_ECO57 PGL3_ASPNG SYE_VIBCH VL2_HPV17 DCMI_OLICA PYRE_LISMO
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2203 5005 162 162 366 534 474 518 524 800
001111000000000000000000000000000000000
68 68.5 68.5 68 68 67 67 67 67 67
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### ALIGNMENTS

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MEDLINE=21638749; PubMed=11780052;

MEDLINE=21638749; PubMed=11780052;

MEDLINE=21638749; PubMed=11780052;

MEDLINE=21638749; PubMed=11780052;

MEDLINE=21638749; PubMed=11780052;

MEDLINE=21638749; MEDLINE MEDLINE, Beard D.M.,

Basaley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

Buck D., Burrill W.D., Buller A.P., Carder C., Carter N.P.,

Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

Colley V.E., Collier R.E., Connor R.E., Corby N.R.,

Coulson A., Cobiely V.E., Collier R.E.,

Ralingron A.G., Frankland J.A., Fraser A., French L., Garner P.,

Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R.E.,

Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson D.,

Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUB-Brain, and Cochlea;
TISSUB-Brain, and Cochlea;
MEDLINE-211000875; PubMed=11161796;
Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;
Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;
"Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation.";
Genomics 71:40-52(2001).
                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Otoroplin precursor (Fibrocyte-derived protein) (Melanoma inhibitory activity like protein).
OTOR OR FDP OR MIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=20568254; PubMed=10998416;
Cohen-Salmon M., Frenz D., Liu W., Verpy E., Voegeling S., Petit C.;
Cohen a new fibrocyte-derived protein related to MIA/CD-RAP, has an irRpp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Cochlea;

PEDLINE-201346.19; PubMed-10873378;

Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,

Boens C.S., Bell A.M., Hudspeth A.J., Morton C.C.;

Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;

An novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping.";

Genomics 66:242-248(2000).
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                  128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 275:40036-40041(2000)
                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                           HUMAN
OTOR HUMAN
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                                               RAPARA RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KKGQQIYVYSKLVKENGAGEFWAGSVYGBGQDEMGVVGYFPRNLVKEQRVYQEATKEVPT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MARILLEFERGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60
Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Trocay A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Mhitched S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Rogers J., Mray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                        'The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9BB52C7F5D4FB700 CRC64;
                                                                                                                                                                                                                                         ; Score 676; DB 1;
; Pred. No. 5.4e-63;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
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OTORAPLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF233281, AAF82078.1; ---
EMBL, AZ533281, AAG42356.1; --
EMBL, AUZ42552, CAC2443.1; --
EMBL, AJ252324, CAC28085.1; --
EMBL, AJ25328; CAC28085.1; JOINED.
EMBL, AJ252327; CAC28085.1; JOINED.
EMBL, AJ252327; CAC28085.1; JOINED.
EMBL, AJ34284; CAC16848.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00126; SH3; 1.
PROSITE; PS50002; SH3; FALSE_NEG.
Signal; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 60500/; -.
GO; GO:0007605; P:hearing; TAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; Q16674; 111J.
Genew; HGNC:8517; OTOR.
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DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KKGQQIYVYSKIVTENGAGEFWAGSVYGDHQDEMGIVGYFPSNLVKEQRVYQEAIKEIPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KKGQQIYVYSKIVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MARILLLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60
                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21100875; PubMed-11161796; Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.; Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.; "Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent Golymorphism that abolishes translation."; Genomics 71:40-52(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                        MEDINE=20334619; PubMed=10873378; Resendes B.L., Weremowicz S., Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S., Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.; Conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping."; Genomics 66:242-248(2000).
                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Otoraplin precursor (Melanoma inhibitory activity-like protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.1%; Score 602; DB 1; Length 128; 86.7%; Pred. No. 2.4e-55; Live 9; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3DD47D4C77C4A7FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLURAR LOCATION: Secreted (Potential).
-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
-1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-1- SIMILARITY: CONDAINS 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; Q16674; 111J.
MGD; MGI:1888678; Otor.
GO; GO:0001502; P:cartilage condensation; IMP.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 128 OT
39 110 SH
32 37 BY
55 127 BY
128 AA; 14328 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF23333; AAF82079.1; -.
EMBL; AJ243939; CAC27444.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                        OTOR OR MIAL.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal; SH3 domain.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                TISSUE=Fetal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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RESULT 3

128 AA.

PRT;

OTOR MOUSE STANDARD; EQUIE3; 16-OCT-2001 (Rel. 40, Created)

OTOR MOUSE

RESULT 2

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SEQUENCE FROM N.A.
MEDLINE=20334619; PubMed=10873378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein, MIA.";
Cancer Res. 54:5695-5701(1994)
                                                                                                                                                                                                                                                                                        EMBL; AF233519; AAF82728.1; -.
HSSP; Q16674; 111J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66; Conservative
                                                                                                                                                                                                                                                                                                              InterPro; IPR01452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
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133
115
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Q16674;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 QQIYVYSKLVKENGAGEFWAGSVYGDG-QDEMGVVGYFPRNLVKEQRVYQEATKEVPTTD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ILLLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKG
                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=20334619; PubMed=10873378;
Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
"A novel conserved cochlear gene, OTOR: identification, expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.0%; Score 480; DB 1; Length 132; 73.8%; Pred. No. 1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 1e-42;
11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
9D1CB07FD353CE1C CRC64;
                                                                                                                                                                                                                             OTOR RANCA STANDARD; PRT; 133 AA. 0918B5; 16-0CT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                          (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
OTORAPLIN.
SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF233518; AAF82727.1; -. HSSP; Q16674; 111J. InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15177 MW;
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                                                                                                      Gallus gallus (Chicken).
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132
114
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                     STANDARD;
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42 1
35 1
58 1
132 AA;
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                                                                                  Otoraplin precursor.
                                                                                                                                                     NCBI_TaxID=9031;
                                             16-OCT-2001
                                                                    28-FEB-2003
                     OTOR CHICK
Q918P6;
                                                          16-0CT-2001
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DISULFID
SEQUENCE
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Best Local $
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OTOR RANCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 YGVYMQKLSDKKT.CADDECIYAISFGRAEDDYNAPDCRFVNLKKGELVXIYTKLVKENDD
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                                                                                                                                                                                                                              78 AGEWAGSVYGDG-ODEMGVVGYFPRNLVKEQRVYQBATKEVPTTDIDFFCE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 AGEFWSGSVYSDQXRDQQGLVGYFPSSLVTELTVYKDELQELPTTAVDFYCD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        noumo sapiens (numan).
Bukaryota: Metazos Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.7%; Score 390; DB 1; Length 133; 58.9%; Pred. No. 2.1e-33; Live 26; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 40 BY SIMILARITY.
58 132 BY SIMILARITY.
133 AA; 15243 MW; 25440CIA3CF911AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 AA
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                                                                                                                                                                                                             MEDILINE=22388257; PubMed=12477932;
A Krausberg R.L., Faingold E.A., Grouse L.H., Derge J.G.,
A Krausberg R.L., Faingold E.A., Grouse L.H., Derge J.G.,
A Krausberg R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Battow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
A Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Frhey J., Helton E., Ketteman M., Madan A., Schrifted G.G.,
Whithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Chenerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Human and mouse cDNA sequences.";
Rodeneration and initial analysis of more than 15,000 full-length
L. Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AS WELL AS SOME OTHER NEUROBCTODERMAL TUMORS, INCLUDING GLIOMAS.
-: SUBCELLULAR LOCATION: Secreted.
-: TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND INFREQUENTLY IN GLIOMA CELL LINES.
-: PTM: MAY POSSESS TWO INTRAMOLECULAR DISULPIDE BONDS.
-: SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-: SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bosserhoff A.-K., Hein R., Bogdahn U., Buettner R., structure and promoter analysis of the gene encoding the human melanoma-inhibiting protein MIA."; J. Biol. Chem. 271:490-495(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00018; SH3; 1.
SMART; SM0326; SH3; 1.
PROSITE; PS50002; SH3; 1.
Growth factor; Signal; SH3 domain; 3D-structure.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005615; C:extracellular space; TAS. GO; GO:0008283; P:cell proliferation; TAS. InterPro; IPR001452; SH3.
                                      TISSUE=Placenta;
MEDLINE=96132947; PubMed=8550608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC005910; AAH05910.1; -. PIR; 138019; 138019. PDB; 111J; 16 MAX-01. PDB; 114J; 29-JAN-02. PDB; 1KOX; 24-JUL-02. Genew; HGNC:7076; MIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X75450; CAA53203.1; -. EMBL; X84707; CAA59195.1; -.
[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                 SECUENCE FROM N.A.
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55 CRFINVKKGQQIYVYSKLVKENGAGE-FWAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQ 112
                                                                                                                                                                                                                                                                                    1 MARILLLFLFGLVAVCA-----VHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-96216414; PubMed=8621736;
Dietz U.H., Sandell L.J.;
"Cloning of a retinoic acid sensitive mRNA expressed in cartilage and during chondrogenesis.";
                                                                                                                                                                                                                                                        13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIA OR CDRAP.

Bos taurus (Bovine).

Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;

Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinoic acid-sensitive protein) (CD-RAP).
MELANOMA DERIVED GROWTH REGULATORY PROTEIN.
SH3.
                                                                                                                                                                                                                                     38.1%; Score 257.5; DB 1; Length 131; 41.2%; Pred. No. 1.1e-19; Live 26; Mismatches 41; Indels 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 271:3311-3316(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.
-1- INDUCTION: RESPERSES by retinoic acid.
-1- PIDM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
-1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
                                                                                                                                                                                                                     14509 MW; 4D3BB30BD6008BDC CRC64;
                                                                                                                                                                                                                                                                                                                                                 113 EATKEVPTTDIDFFCE 128
                                                                                                                                                                                                                                                                                                                                                                  116 PGKVDVKTDKWDFYCQ 131
                                                                                                                                                                                                                                                         56; Conservative
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                             131 AA;
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                     MIA BOVIN
Q28038;
                              DISULFID
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                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QOIYVYSKLVKENGAGE-FWAGSV----YGDGQDEMGVVGYFPRNLVKEQRVYQEATKEV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 VILSAFPGPSA----GGRPMPKLADRKMCADEECSHPISVAVALQDYVAPDCRFLTIHQG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ILLLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dietz U.H., Sandell L.J.; "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.9%; Score 256.5; DB 1; Length 130;
43.1%; Pred. No. 1.3e-19;
tive 23; Mismatches 36; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinoic acid-sensitive protein) (CD-RAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Gene expression changes associated with chemically-induced rat
                                                                                                                                                                                                                                                                                                                                                                             MELANOMA DERIVED GROWTH REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             during chondrogenesis.";
J. Biol. Chem. 271:3311-3316(1996).
-!- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mammary carcinogenesis.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.

BY SIMILARITY.

95D153161C78E02A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley; TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 AA.
                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Cartilage;
MEDLINE=96216414; PubMed=8621736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14353 MW;
                                                                                                                                                                                                            EMBL; U51437; AAC48523.1; -.
HSSP; Q16674; 111J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 34-124 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 PITDIDFFCE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 KIDIWDFYCQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                            112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                            35
58
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Q62<u>9</u>46; P97591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OR CDRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 QOIYVYSKLVKENGAGE-FWAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LLGIVILSVPSGLSRADRAMPKLADRKLCADEECSHPISMAVALQDYVAPDCRFLTIYRG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 LPGLVAVCAVHGI-----FMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hessdoerfer B., Schmitt A., Jachimczak P., Lottspeich F., Buettner R., Bogdahn U.; "Cloning of a novel malignant melanoma-derived growth-regulatory protein, MIA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE STANDED (19745).

Q61865, 009086, P97455,

Q1-NOV-1997 (Rel. 35, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinoic acid-sensitive rotein) (CD-RAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MELANOMA DERIVED GROWTH REGULATORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.6%; Score 254; DB 1; Length 130; 40.9%; Pred. No. 2.4e-19; tive 26; Mismatches 39; Indels 1
MAINTENANCE.

-1- SUBCELLULAR LOCATION: Secreted.

-1- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.

-1- INDUCTION: Repressed by retinoic acid.

-1- PTM: NAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.

-1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.

-1- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5F99149AECF74501 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
MA -> VT (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50002; SH3; FALSE_NEG.
Growth factor; Signal; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/c;
MEDLINE=95007612; PubMed=7923218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 AA; 14536 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; US1438; AACS2481.1; -. EMBL; U67884; AAB40659.1; -. HSSP; Q16674; IIIJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : ||:|:
124 EWDFYCQ 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF067816; AAF09171.1; -. HSSP; P29355; 1SEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00233; PH; 1.
SM00325; RhoGEF; 1.
SM00252; SH2; 1.
SM00326; SH3; 2.
                                                                                                                                               ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probom; PD000093; SH2; 1
Probom; PD000066; SH3; 1
SMART; SM0109; CI; 1.
SMART; SM00033; CH; 1.
SMART; SM00333; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1888518; Vav3.
                                                                                                                                                                                               Name=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART:
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                                             STRAIN=129/Sv;

MEDLINE=97251341; PubMed=9097023;

MEDLINE=97251341; PubMed=9097023;

MEDLINE=97251341; PubMed=9097023;

Bosserhoff A.K., Kondo S., Moser M., Dietz U., Copeland N.G.,

Gilbert D.J., Jenkins N.A., Buetner R., Sandell L.J.;

Mouse CD-RAP/MIA gene: structure, chromosomal localization, and

expression in cartilage and chondrosarcoma.";

expression in cartilage and chondrosarcoma.";

per Dyn. 208:516-525(1997).

ILL PUNCTION: ELICITS GROWTH INHIBITION ON MELANOWA CELLS IN VITRO AS

SIMILARITY: CATION: Secreted.

INTREQUENTLY IN GLIOWA CELL LINES TESTED AND

INTREQUENTLY IN GLIOWA CELL LINES.

INTREQUENTLY IN GLIOWA CELL LINES.

INTREQUENTLY SHOUNGS TO THE MIA / OTOR FAMILY.

C -- SIMILARITY: CONTAINS 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 MPKLADWKLCADEECSHPISMAVALQDYVAPDCRFLTIYRGQVVYVFSKL---KGRGRLF 82
                                                                                                                                                                                                                                                                                                                                                                          HSSP; Q16674; 111J.
MGD; MGI:109615; Mia.
MGD; MGI:009615; Mia.
MGD; G0:0007160; P:cell-matrix adhesion; IMP.
GO; G0:0030198; P:extracellular matrix organization and bioge. . .; IMP.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. MELANOMA DERIVED GROWTH REGULATORY
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.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
34.8%; Score 235.5; DB 1; Length 130;
Best Local Similarity 43.5%; Pred. No. 2e-17;
Matches 47; Conservative 21; Mismatches 35; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 WAGSVYGDGODEMGV-VGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN.
SH3.
BY SIMILARITY.
BY SIMILARITY.
TL -> NS (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0cT-2001 (Rel. 40, Created)
16-0cT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE, PS50002; SH3; FALSE NEG.
Growth factor; Signal; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 T.
14593 MW;
               Cancer Res. 54:5695-5701(1994).
                                                                                                                                                                                                                                                                                                                                             EMBL; X94322; CAA63983.1; -. EMBL; U85612; AAB42082.1; -. EMBL; X97965; CAA66608.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00018; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 J
                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vav-3 protein.
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Q9R0C8;
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DISULFID
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAV3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAV3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
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                                                                                                                                                                                                                     quantum nucleotide exchange factors";
gene 245:139-149(2000)
-!- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,
-!- TO A LESSER EXTENT, RACTOR FOR SPINSICALLY TO THE NUCLEOTIDE-FREE STATES OF THOSE GTPASES (BY SIMILARITY).
SEQUENCE FROM N.A. MEDDMed=10713454; Melsh J.; Melsh J.; Trenkle T., McClelland M., Adlkofer K., Welsh J.; McClelland M., Adlkofer K., Welsh J., McClelland M., Adlkofer K., McClelland M., McClelland M., Adlkofer K., McClelland M., McClelland M., Adlkofer K., McClelland M., McC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Contains 1 DBL-homology (CH) domain.
-!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
-!- SIMILARITY: Contains 1 PH domain.
-!- SIMILARITY: Contains 1 Zinc-dependent phorbol-ester and DAG binding domain.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 2 SH3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50002; SH3; 2.
Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=09R0C8-2; Sequence=Not described;
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PROSITE; PS00479; DAG PE BIND DOM 1; 1.
PROSITE; PSS0081; DAG PE BIND DOM 2; 1.
PROSITE; PSS0010; DH 2; 1.
PROSITE; PSS00741; DH 1; 1.
PROSITE; PSS00001; SH 1: 1.
PROSITE; PSS00001; SH 2: 1.
PROSITE; PSS00001; SH 2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isold=Q9R0C8-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IRR001715; Calponin-like.
InterPro; IRR002247; CH type.
InterPro; IRR002219; DAG PE-bind.
InterPro; IRR001319; DAG PE-bind.
InterPro; IRR001319; PH.
InterPro; IRR0010849; PH.
InterPro; IRR000209; SH2.
InterPro; IRR0010805; SH2.
InterPro; IRR0010805; SH2.
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Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
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PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00888; SM2ZCALPONIN.
ProDom; PD001527; CH type; 1.
ProDom; PD000093; SH2; 1.
ProDom; PD000066; SH3; 1.
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41 ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 299-334 FROM N.A.

MEDLINE=96038895; PubMed=7478592;

Ramos-Morales F., Romero F., Schweighoffer F., Bismuth G., Camonis J.,

Tortolero M., Fischer S.;

"The proline-rich region of Vav binds to Grb2 and Grb3-3.";

Oncogene 11:1665-1669(1995).
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MEDLINE=91172176; PubMed=2005887;

Katzav S., Cleveland J.L., Heaslop H.E., Pulido D.;

"Loss of the amino-terminal helix-loop-helix domain of the vav proto-
oncogene activates its transforming potential.";

Mol. Cell. Biol. 11:1912-1920(1991).
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY TO CDC24 FAMILY.
MEDLINE-92228488; PubMed=1565462;
Adams J.M., Fouston H., Allen J., Lints T., Harvey R.;
"The hematopoietically expressed vav proto-oncogene shares homology with the dbl GDP-GTP exchange factor, the bcr gene and a yeast gene (CDC24) involved in cytoskeletal organization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                              21; Indels 11;
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MEDLINE=90005432; PubMed=2477241;
Katzav S., Martin-Zanca D., Barbacid M.;
"vav, a novel human oncogene derived from a locus ubiquitously
expressed in hematopoietic cells.";
EMBO J. 8:2283-2290(1989).
                                                                                                                                                                                                                                                                                                    13.1%; Score 88.5; DB 1; Length 847; 31.3%; Pred. No. 0.24;
                                                                                                                      PHORBOL-ESTER AND DAG BINDING
Guanine-nucleotide releasing factor; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                          97946 MW; 9A6B63F0D9E60F8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAV HUMAN STANDARD; PRT; 845 AA. P15498; Q15860; 01-AP99 (Rel. 14, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                 14; Mismatches
                                                                                                                                                       SH3 1
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                                                                                                                                                                                                                                                                                                                                    Local Similarity 31.3%
nes 21; Conservative
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VAV1 OR VAV.
Homo sapiens (Human)
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847 AA;
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VAV HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWEM outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                              alphabet.
-!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
-!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
-!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
-!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG binding domain.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 2 SH3 domains.
-!- CAUTION: Ref. 2 sequence differs from that shown due to frameshifts in position 322 and 355.
           FUNCTION: Couples tyrosine kinase signals with the activation of
the Rho/Rac GTPases, thus leading to cell differentiation and/or
proliferation.
                                                     -!- SUBUNIT: Interacts with SLA (By similarity). Interacts with Grb2
                                                                           -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT NOT IN OTHER CELL TYPES.
                                                                                                           -!- PTM: Phosphorylated on tyrosine residues.
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GO; GO:0003700; F:transcription factor activity; TAS.
GO; GO:0007048; P:oncogenesis; TAS.
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InterPro; IPR001219; CAL type.
InterPro; IPR001219; DAG PE-bind.
InterPro; IPR001849; PH.
InterPro; IPR001849; PH.
InterPro; IPR000129; RhGEF.
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EMBL; M5984; AAA63267.1; -.
EMBL; X83931; CAA58783.1; -.
PIR; B39576; TVHUVV.
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EMBL, AF030224, AAC25011.1, JOINED.
EMBL, AF030225, AAC25011.1, JOINED.
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EMBL, AF030202, AAC25011.1, JOINED.
EMBL, AF030203, AAC25011.1, JOINED.
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AAC25011.1;
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Oncogene 7:611-618(1992)
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EMBL; AF030219;
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EMBL; AF030213;
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Guanine-nucleotide releasing factor, Repeat, Phosphorylation.
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MOVILLE $99455043; PubMed=10523675;
Movilla N., Bustelo X.R.;
"Biological and regulatory properties of Vav-3, a new member of the Vav family of oncoproteins.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PHORBOL-ESTER AND DAG BINDING.
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AC3BC9736FD2F138 CRC64;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
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PROSITE; PS50010; DH 2; 1.

R PROSITE; PS50010; DH 2; 1.

R PROSITE; PS50003; PH DOWAIN; 1.

PROSITE; PS50001; SH3; 1.

PROSITE; PS50002; SH3; 1.
       InterPro; IPR001452; SH3.
InterPro; IPR003096; SM22_calponin.
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SMART; SM00033; CH; 1.
SMART; SM000323; PH; 1.
SMART; SM00223; RhoGEF; 1.
SMART; SM00252; SH2; 1.
SMART; SM00252; SH2; 1.
PROSITE; PSS0021; CH; 1.
PROSITE; PSS00479; DAG_PE_BIN
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RE MOI. Cell. Biol. 19:7870-7885 [1999).

RESURCES FROM N. N. 1820 [12]

RESURCES FROM N. N. 1820 [13]

RESURCES FROM N. N. 1820 [13]

RESURCES FROM THE SET FROM THE SET FROM THE NUCLEOTIDE-FREE COMPLIANCE FROM THE NUCLEOTION THE NUCLEOTIDE-FREE COMPLIANCE FROM THE NUCLEOTIDE FREE COMPLIANCE FROM THE NUCLEOTION THE NUCLEOTIDE FREE COMPLIANCE FROM THE NUCLEOTIDE FROM THE NUCLEOTION THE NUCLEOTION THE NUCLEOTIDE FROM THE NUCLEOTION THE NUCLEOTION THE NUCLEOTIDE FROM THE NUCLEOTION THE NUCLEOT
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              845 AA
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(Rel. 23, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50021; CH; 1.
PS00479; DAG_PE_BIND_DOM_1;
PS50081; DAG_PE_BIND_DOM_2;
PS50010; DH_2; 1.
                                                                                                                       InterPro; IPR001715; Calponin-like.
InterPro; IPR002175; CH type.
InterPro; IPR001314; GB E-bind.
InterPro; IPR001311; GBS_CDC24.
InterPro; IPR001649; PH.
InterPro; IPR000219; RhoGEF.
                                                                                                                                                                                                                                    InterPro; IPR001452; SH3.
InterPro; IPR003096; SM22_calponin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DH_1; 1.
PH_DOMAIN; 1.
SHZ; 1.
                                                                                                                                                                                                                                                               Pfam; PF001307; CH; 1.
Pfam; PF001307; CH; 1.
Pfam; PF00130; DAG PB-bind; 1.
Pfam; PF00161; RhoGEF; 1.
Pfam; PF001017; SH2; 1.
Pfam; PF001018; SH3; 2.
PRINTS; PR00451; SH3; 2.
PRINTS; PR00451; SH3DOWAIN.
PRINTS; PR00888; SM22CALPONIN.
PF0DOm; PD000093; SH2; 1.
ProDom; PD000093; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97953 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Probom, PD000666; SH3; 1. SWART; SM00109; C1; 1. SWART; SM0013; CH; 1. SWART; SM0033; PH; 1. SWART; SM00325; RAGSEF; 1. SWART; SM00325; SH2; 31. SWART; SM00326; SH3; 2.
                                                                                                EMBL; U39476; AAA98606.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50003;
PROSITE; PS50001;
PROSITE; PS50002;
                                                                                                                 HSSP; P29354; 1GRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50021;
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P27870;
01-AUG-1992
01-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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VAV MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                    41 ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEPWKQCAQWLIHCKVLPTNHRVTWDSAQVFDLAQTLRDGV
LLCQLLNNLRAHSINLKBINLRPQMSQFLCLKNIRTFLTAC
CETFGMRKSELFEAFDLFDVRDFGK -> MQLPDCPCRAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJINE-99233974; PubMed=10395673; Song J.S., Haleem-Smith H., Arudchandran R., Gomez J., Scott P.M., Song J.S., Haleem-Smith H., Arudchandran R., Gomez J., Scott P.M., Mill J.F., Tan T.-H., Rivera J.; Arudchandran E. of production in mast cells by a Rac/c-Jun N-terminal kinase-dependent pathway."; J. Immunol. 163:802-810(1999).

-1. FUNCTION: Couples tyrosine kinase signals with the activation of the Rho/Rac GTPases, thus leading to cell differentiation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proliferation.
-- Subuntr: Interacts with SLA (By similarity).
-- SUMUNTR: Interacts with SLA (By similarity).
-- PTM: Phosphorylated on tyrosine residues.
-- SIMILARITY: Contains 1 calponin-homology (CH) domain.
-- SIMILARITY: Contains 1 DH. domain.
-- SIMILARITY: Contains 1 pH domain.
-- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG binding domain.
-- SIMILARITY: Contains 2 SH3 domains.
                                                                                                                                                                                                                                                                                                                                                                          ch 12.8%; Score 86.5; DB 1; Length 847; 1 Similarity 31.3%; Pred. No. 0.39; 21; Conservative 14; Mismatches 21; Indels 11;
                                                                                                                                                                                                                                                     P (in isoform Beta).
/FTId=VSP 001820.
K -> E (IN REF. 2).
Y -> H (IN REF. 1; AAD20348).
T -> S (IN REF. 2).
V -> A (IN REF. 1; AAD20348).
W; CIE29F0B094CB721 CRC64;
                                                                        SH2 domain; SH3 domain; Repeat; factor; Alternative splicing.
                                                                                                                      DH.
PH.
PHORBOL-ESTER AND DAG BINDING.
SH3 1.
SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
               PROSITE; PS00741; DH 1; 1.
PROSITE; PS50003; PH DOWAIN; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 2.
Phorbol-ester binding; Zinc; SH2
Guanine-nucleotide releasing fact
                                                                                                                                                                                                                                                                                                                                                    97775 MW;
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VAVI OR VAV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
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217
298
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                                                                                                                                                                                                                                                                                                                                     429
847 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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CONFLICT
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Proto-oncogene; Phorbol-ester binding; Zinc; Sh2 domain; Sh3 domain; Sh2 domain; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHORBOL-ESTER AND DAG BINDING.
SH3 1.
SH2.
SH3 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C4A5CACD45FCB80E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.6%; Score 85.5; DB 1;
31.4%; Pred. No. 0.49;
rative 14; Mismatches 21;
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                                                                                                                                                                                                                                                         SEQUENCE OF 1-93 FROM N.A.
MEDLINE=91172176; PubMed=2005887;
Katzav S., Cleveland J.L., Heaslop H.E., Pulido D.;
"Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene activates its transforming potential.";
Mol. Cell. Biol. 11:1912-1920(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Exp. Med. 191:463-474 (2000).
-!- FUNCTION: Couples tyrosine kinase signals with the activation of the Rho/Rac GTPases, thus leading to cell differentiation and/or proliferation.
                                                                                                                                                      Adams J.A., Houston H., Allen J., Lints T., Harvey R.;
"The hematopoietically expressed vav proto-oncogene shares homology
with the dbl GDP-GTP exchange factor, the bcr gene and a yeast gene
(CDC24) involved in cytoskeletal organization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBDATT: Interacts with SLA.
-!- TISSUE SPECIFICITY: Widely expressed in hematopoietic cells but
                                                                                                                                                                                                                                                                                                                                                           [3]
INTERACTION WITH SLA.
MEDLINE=20130290; PubMed=10662792;
Sosinowski T., Pandey A., Dixit V.M., Weiss A.;
"Sosinowski T., Pandey A., Dixit V.M., Weiss A.;
"Src-like adaptor protein (SLAP) is a negative regulator of T cell
"Src-like adaptor protein (SLAP)
                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD, MGI:98923, Vavi.
InterPro; IRR00115; Calponin-like.
InterPro; IRR00124; CH type.
InterPro; IRR001219; DAG PE-bind.
InterPro; IRR00131; GDS_CDC24.
InterPro; IRR00131; PH.
InterPro; IRR00131; PH.
InterPro; IRR00139; RhGEF.
InterPro; IRR000199; RhGEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001452; SH3.
InterPro; IPR003066; SM22_calponin.
Pfam; PF001307; CH; 1.
Pfam; PF00130; DAG PE-bind; 1.
Pfam; PF00169; PH; 1.
                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=92228488; PubMed=1565462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X64361; CAA45713.1; -. EMBL; M59833; AAA63402.1; -. PIR; A61187; TVMSVV.
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PDB; 1GCP; 28-JAN-03.
PDB; 1GCQ; 28-JAN-03.
PDB; 1XIZ; 18-DEC-02.
TRANSFAC; T01230; --
                                               Mus musculus (Mouse)
                   Vav proto-oncogene.
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44 ASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  787 AXARYDFCARDRSELSLKEGDII----KILNKKGQQGWWRGEIYGR-----IGWFPSN 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.4%; Pred. No. 0.49;
tive 14; Mismatches 21; Indels 13; Gaps
                                                                                                                                                                                                                                                                                        Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
Guanine-nucleotide releasing factor; Repeat; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6;
MEDLINE=96313271; PubMed=8710375;
MEDLINE=96313271; PubMed=8710375;
Schuebel K.E., Bustelo X.R., Nielsen D.A., Song B.J., Barbacid M.,
Goldman D., Lee I.J.;
"Isolation and characterization of murine wav2, a member of the vav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%; Score 85.5; DB 1; Length 845;
                                                                                                                                                                                                                                                                                                                           CH.
DH.
PH.
PHORBOL-ESTER AND DAG BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                 Q -> E (IN REF. 2).
3666DCCD1C5229DA CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 868 AA.
                                                                                                          SWART; SW00109; CI; I.
SWART; SW00033; CI; I.
SWART; SW00235; RhGGEF; I.
SWART; SW00225; RhGGEF; I.
SWART; SW00225; SH2; I.
PROSITE; PS50021; CH; I.
PROSITE; PS50021; CH; I.
PROSITE; PS50011; DAG PE BIND DOM I; I.
PROSITE; PS50010; DH Z; I.
                                                                                                                                                                                                                                                                                                                                                                               SH3 1.
                                                                                                                                                                                                                                                                                                                                                                                          SH2.
SH3 2.
                              PRINTS; PRO0401; SH2DOWAIN.
PRINTS; PRO0452; SH3DOWAIN.
PRINTS; PRO0488; SM22CALPONIN.
ProDom; PD001527; CH type; 1.
ProDom; PD000093; SH2; 1.
ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                             PROSITE; PS50003; PH DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                845 AA; 98136 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Conservative
RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   836 YVEED--YSE 843
                                                                                                                                                                                                                                         PROSITE; PS00741; DH 1;
          Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 PROSITE; PS50001;
PROSITE; PS50002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /av-2 protein.
                                                                                                                                                                                                                                                                                                                    3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                        802 VFTPRVIGTAVARYNFAARDWRELSLREGDVVKIYSRIGGDQG---WWKG-----ETN 851
38 VYT---ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEM 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=9528328315; PubMed=7762982; Henske E.P., Short M.P., Jozwiak S., Bovey C.M., Ramlakhan S., Haines J.L., Kwiatkowski D.J.; Haines J.L., Kwiatkowski D.J.; Haines J.L., Kwiatkowski D.J.; Ann. Hoentification of VAV2 on 9q34 and its exclusion as the tuberous sclerosis gene TSC1."; Ann. Hum. Genet. 59:25-37(1995).
                                                                                                                                                                                                                                                                                                                                                                          Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Ras-related GTPases.
--- TISSUE SPECIFICITY: Widely expressed.
--- SIMILARITY: Contains 1 calponin-homology (CH) domain.
--- SIMILARITY: Contains 1 PBL-homology (DH) domain.
--- SIMILARITY: Contains 1 PH domain.
--- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG binding domain.
--- SIMILARITY: Contains 1 SH2 domain.
--- SIMILARITY: Contains 2 SH3 domains.
                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                           878 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001715; Calponin-like.
InterPro; IPR003247; CH type.
InterPro; IPR002219; DAG PE-bind.
InterPro; IPR001311; GDS_CDC24.
                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00307; CH; 1.
Pfam; PF00130; DAG PE-bind; 1.
                                                                                                            | :|:|| |:|: |
852 GRIGWFPSTYVEEEGV 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; S76992; AAB34377.1; -. PIR; I51940; I51940.
                                                                                      95 GVVGYFPRNLVKEORV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000219; RhoGEF.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P08631; 1BU1.
Genew; HGNC:12658; VAV2.
                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              600428; -
                                                                                                                                                                                                                                                                                                                               Vav-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
                                                                                                                                                                                                                               VAV2 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                 P52735;
                                                                                                                                                                                          RESULT 15
VAV2_HUMAN
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                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                      -:- SIMILARITY: Contains 1 calponin-homology (CH) domain.
-: SIMILARITY: Contains 1 DBL-homology (DH) domain.
-: SIMILARITY: Contains 1 PH domain.
-: SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG binding domain.
-: SIMILARITY: Contains 1 SH2 domain.
-: SIMILARITY: Contains 2 SH3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
12.2%; Score 82.5; DB 1; Length 868;
Best Local Similarity 27.6%; Pred. No. 1;
Matches 21; Conservative 20; Mismatches 22; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHORBOL-ESTER AND DAG BINDING.
SH3 1.
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              calponin-homology (CH) domain.
DBL-homology (DH) domain.
PH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (BY EGFR)
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PHOSPHORYLATION (BY EGFR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
D18581E7EEB2DBC2 CRC64;
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PROSITE; PSS00479; DAG PE BIND DOM 1; 1.
PROSITE; PSS00810; DAG PE BIND_DOM_2; 1.
PROSITE; PSS00010; DH 2; 1.
PROSITE; PSS00011; DH 1; 1.
PROSITE; PSS00013; PH DOMAIN; 1.
PROSITE; PSS00001; SH2; 1.
PROSITE; PSS00001; SH2; 1.
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                                                                                                                                                                                                                                                                                                                   ENBL, U37017, AACGZ761.1; --
HSSP, Q60631; 1GB0.
MGJ, MGJ:102718; Vav2.
InterPro; IPR001715; Calponin-like.
InterPro; IPR001715; Calponin-like.
InterPro; IPR001219; DAG_PE-bind.
InterPro; IPR001219; DAG_PE-bind.
InterPro; IPR001219; PH-
InterPro; IPR00121; PH-
InterPro; IPR00131; PH-

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     868 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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DOMAIN
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12.1%; Score 81.5; DB 1; Length 878;
Best Local Similarity 26.3%; Pred. No. 1.3;
Matches 20; Conservative 21; Mismatches 22; Indels 13; Gaps
                                                                                                                                                                                                         R SWART; SM00109; C1; 1.

R SWART; SM00109; C1; 1.

R SWART; SM00109; C1; 1.

SWART; SM00109; C1; 1.

SWART; SM00123; PH; 1.

SWART; SM00125; PH; 1.

SWART; SW00125; PH; 1.

SWART; SWO0125; PH; 1.

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PHOSPHORYLATION (BY EGFR).
PHOSPHORYLATION (BY EGFR).
PHOSPHORYLATION (BY EGFR).
MW; C8FF7681032146B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 376 DH.
405 512 PH.
524 652 SH3
586 652 SH3
673 767 SH2.
814 H2 SH2
142 142 PHOS
1159 159 PHOS
172 PHOS
818 AA, 101256 MW; C
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF; 1.
Pfam; PF00011; SH2; 1.
Pfam; PF000118; SH3; 2.
PRINTS; PR00401; SH2DOMAIN.
PRODOM; PD001527; CH type; 1.
ProDom; PD000093; SH3; 1.
ProDom; PD000066; SH3; 2.
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| 862 GRIGWFPSTYVEEEGI 877
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MOD_RES
MOD_RES
SEQUENCE
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Search completed: December 29, 2003, 16:04:12 Job time: 7.01961 secs

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December 29, 2003, 16:03:18; Search time 19.7199 Seconds (without alignments) 1674.996 Million cell updates/sec
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676
1 MARILLIFLPGLVAVCAVHG......RVYQEATKEVPTTDIDFFCE 128
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing Eirst 45 summaries
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1: sp_archea:*

3: sp_bacteria:*

3: sp_fungi:*

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5: sp_mamman:*

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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

)	Description	Q9ji09 mesocricetu	Ospjes mns mnscnin	Q8bi84 mus musculu	Ogepcs nomo sapien	Q921x3 mus musculu	Q91zv0 mus musculu	Q90xf1 tetraodon n	O8c899 mus musculu	Q9vma8 drosophila	Q9vma7 drosophila	Q8r076 mus musculu	Q8uux6 gallus gall	Q9h0h2 homo sapien	Q8n157 homo sapien	Q96d37 homo sapien	O08526 mus musculu
27777777777	8	Q9J109	Q8BJE9	Q8B184	Q96PC5	Q921X3	0912V0	Q90XF1	Q8C899	Q9VMA8	Q9VMA7	Q8R076	Q8UUX6	09нон2	Q8N157	Q96D37	008526
	80	17	11	7	4	11	11	13	11	Ŋ	'n	11	13	4	4	4	11
	% Query Match Length DB	96	268	1239	119	137	119	88	68	1257	1430	287	846	1196	1196	719	166
	% Query Match	33.5	31.8	31.8	27.4	26.8	26.0	24.9	22.9	13.2	13.2	13.1	13.1	13.1	13.1	12.8	12.6
	Score	226.5	215	215	185.5	181	176	168.5	155	89	8	88.5	88.5	88.5	88.5	86.5	85.5
	Result No.		7	m	4	ហ	v	7	00	0	10		12	113	14	15	16

O8vdu4 mus musculu	Q8btv7 mus musculu	Q8uux5 gallus gall	Q9h803 homo sapien	Q8ti46 methanosarc	Q8uwe6 tetraodon n	Q8mvs1 ciona intes	Q8jhv0 litoria inf	093jt7 pseudomonas	Ogavze guillardia	Q28616 oryctolagus	O9hjf2 thermoplasm	O8k3e4 mus musculu	Q8k3e5 mus musculu	077202 acanthamoeb	O9lyg4 arabidopsis	Q9hdz9 schizosacch	Q9ftz8 oryza sativ	Q9fu04 oryza sativ	Q8s631 oryza sativ					_	Q8jft4 brachydanio		Q94f88 arabidopsis	Q23770 chironomus
11 Q8VDU4	11 O8BTV7	13 Q8UUX5	4 Q9H803	17	13	'n	13	7	10	9	17 Q9HJF2	11	11	Ŋ	10	٣	10	10	10	10	10	10 Q94E30	10	13	13	16	10 Q94F88	5 Q23770
12.6 806	12.6 845	4	12.2 498				11.7 192				11.1 407											10.7 615			10.7 1721			10.5 383
85.5	יי	200	20.00		. C	5 6	6.6	77	76.5	76	75	74.5	74.5	74.5	74	73.5	73	7.3	73	7.3	7.2	72	72	72	72	71.5		71
17	. a	3 5	20	3 6	100	, ,	40		26	27	28	29	30	31	32	33	) (c	, v.	9 6	3.7	. 8	6 6	4	41	4.2	4 4	4 4	45

### ALIGNMENTS

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Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Ran K.H., Doyle C., Baxker B.G., Helt G., Nelson C.R., Miklos G.L.G., Ran A. Anti-V., Andrews-Pfannkoon C., Baldwin D., Ral Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley B.M., Beeson K.Y., Barnos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkeran D., Botchar A., Challer B.D., Brother D., Botchar A., Challer B.D., Brother D., Botchar A., Challer B.D., Brother D., Botchar J., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Backer J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Racher D., Botchar J., Brother H., Cadieu E., Center A., Chandra I., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Borbin K.J., Evangelista C.C., Ferrierz C., Ferrierz S., Fleistchmann W., Roller M., Gorder P., Gorrell J.H., Gu Z., Chan P., Harris M., Alush P., Karpen G.H., Mez M., Huller B., Kalush P., Karpen G.H., Nealen T.J., Hermann T.J., Hermannez J.R., Howland C.J., Kraft C., Kravlitz S., Kulb D., Lai Z., Liang Y., Lin X., Alasko P., Lei Y., Levitsky A.A., Liu Z., Liang Y., Lin X., Alush P., Marlishina N.V., Mobarry C., Morles G., Moshrefi A., Moly M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Alus S., Pollar D., Puri V., Reese M.G., Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shaih T., RA Shier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., RA Shier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O., RA Shier E., Spradling A.C., Turner R., Vanner B., Wang S., Yao Q. A., RA Walliams S.M., Woodage T., Worley K., Wang S., Yao Q., Zheng L., The Genome Sequence of Drosophila melanogaster.";

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Redniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Revans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H. Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Reriters S., Frise E., Galle R.F., Garge N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Lbegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

Rollntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

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Pacleb J., Paragas V., Fithman G.S., Puri V., Richards S., Scheeler F.,

Ry Stapleron M., Strong R., Svirskas R., Tector C., Tyler D.,

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Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.B., Kronmiller B., Marshall B., Millburn G., Richter J., Harris N., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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5843F0540EEA9511 CRC64;

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AE003614, AAF52413.2; -. FlyBase; FBgn0051635; CG31635. SEQUENCE 1257 AA; 139136 MW; 5843F0540EEA9511 CRC64;

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RG STRANH=Bergeley;

RAMENN=Bergeley;

RAMENN=Bergeley;

RAMEDLINE_20196006;

PUBBERGE S.B., Holt R.A., Evans C.A., Gocayne J.D.,

RAMENTELENE_20196006;

RAMENTELENE_20196006;

RAMENTELENE_20196006;

RAMENTELENE_20196006;

RAMENTELENE_C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RAMENTELENE_C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RAMENTI J.E., Agosyani A., An H.-J., Andrews-Fennoncoh C.R., Miklos G.L.G.,

RAMENTI J.E., Agosyani A., Barandale J., Bayzakazoglu L., Basaley E.M.,

RAMENT J.R., Bernos P.V., Berman B.P., Bhandari D., Boltahakov S.,

RAMENTS R.C., Busann D.A., Butler H., Cadleu E., Center P.,

RAMENTS R.C., Busann D.A., Buller H., Cadleu E., Center A., Chandra I.,

RAMENTS J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.C.,

RAMENTY J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.C.,

RAMENTY J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.C.,

RAMENTY J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.C.,

RAMENT J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.C.,

RAMENT J.M., Cawley D., Halman T.J., Herrandez J.R., Fleischmann W.,

RAMENT J.M., Harvey D., Halman T.J., Herrandez J.R., Fleischman W.,

RAMENT D.L., Harvey D., Halman T.J., Herrandez J.R., Rouck J.,

RAMENT D.L., Harvey D., Halman T.J., Wei M.-H., IDegen D.L.,

RAMENT D.L., Harvey D., Halman T.J., Wei M.-H., IDegen D.L.,

RAMENT D.L., Harvey D., Murphy B., Murphy L., Morrison J.A., Retci B., Molliams S.M., Molecol M.P., Morleon D.L.,

RAMENT D.R., Nation R., Murphy B., Murphy L., Marzny D.M., Nelson D.L.,

RAMENT S.M., Noy M., Murphy B., Murphy L., Marzny D.M., Nelson D.L.,

RAMENT S.M., Noy M., Murphy B., Murphy L., Warzny D.M., Wang X.,

RAMENT S.M., Reinert R., Remington R.A., Worley R.C., Wu D., Yang S., Zhon B.,

RAMENT S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhon S.,
                                                                   3,
                                                                                                                                      6 ILFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQ 65
                                                                                                                                                                                                         17 LALVLGLLICCLPTLTWAATLSDKRLCADPKCEQIISMGIAKITYAIGGEGLISFKINSP 76
                                                                                                                                                                                                                                                                                66 IYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVY---QEATKEVP 119
                                                                                                                                                                                                                                                                                                                             77 IRVLSKSAGSN--MQLW-----GVDINGRRGYANKDFIMEKKILVRDKDLLYEVP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
Length 1257;
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                              55;
   DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1430 AA
           13.2%; Score 89; DB 527.4%; Pred. No. 1.2; ive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 287:2185-2195(2000).
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                      Query Match
Best Local Similarity 27.49
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG11098 protein.
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ProDom; PD000066; SH3; 1.
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Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Reriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Diegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapleron M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
"Sequencing of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 IYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVY---QEATKEVP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Gaps
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Mistra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K..
Mistra S., Crosby M.A., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
"Annotation of Drosophila melanogaster genome.",
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
13.2%; Score 89; DB 5; Length 1430;
Best Local Similarity 27.4%; Pred. No. 1.4;
Matches 32; Conservative 18; Mismatches 55; Indels
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01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 32.7 kDa protein.
VAV3.
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QBR076
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                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11805146;
Inabe K., Ishlai M., Scharenberg A.M., Freshney N., Downward J.,
Kurosaki T.;
                                                                                                                                                                                                                                             11;
                                                                                                                                                                                   Query Match
13.1%; Score 88.5; DB 11; Length 287;
Best Local Similarity 31.3%; Pred. No. 0.22;
Matches 21; Conservative 14; Mismatches 21; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Vav3 Modulates B Cell Receptor Responses by Regulating
SWART; SM00252; SH2; 1.
SWART; SM00326; SH3; 2.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 2.
Hypothetical protein.
SEQUENCE 287 AA; 32662 MW; BF2850B8F921F048 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
GDP/GTP exchange factor VAV3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphoinositide 3-Kinase Activation, 1, 8xp. Med. 195:189-200 (2002).

J. BXD. Med. 195:189-200 (2002).

- SIMILARITY: CONTAINS 1 SH3 DOWAINS.
- SIMILARITY: CONTAINS 1 PH DOMAINS.
REBL; AY046915, AAL06249.1; -
INTERPO; IPR001715, Calponin-like.
INTERPO; IPR001715, Calponin-like.
INTERPO; IPR001331; GDS_CDC24.
INTERPO; IPR001331; GDS_CDC24.
INTERPO; IPR001899; PH.
INTERPO; IPR001999; RhGEF.
INTERPO; IPR001452; SH3.
INTERPO; IPR001452; SH3.
INTERPO; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00307; CH; 1.
Pfam; PF00130; DAG PR-bind; 1.
Pfam; PF00169; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00888; SM22CALPONIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD001527; CH type; 1.
PD000093; SHZ; 1.
PD000066; SH3; 1.
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SWART; SW0023; CH; 1.
SWART; SW0023; PH; 1.
SWART; SW00225; RhoGEF; 1.
SWART; SW00252; SH2; 1.
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Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
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1050 VDTAPTVVALYDYTANRSDELTIHRGDIIRVF---FKDN--EDWWYGSI-GKGQE---- 1098
                                                                                                                                                                                                                                                                                                                                                                                            41 ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYF 100
                                                                                                                                                                                                                                                                                                                                                                                                                     38 VYŢISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVV 97
                                                                                                                                                                                                                                                                                  / Match
Local Similarity 32.8%; Pred. No. 0.84;
les 22; Conservative 13; Mismatches 21; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Indels 11; Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.1%; Score 88.5; DB 4; Length 1196; 33.3%; Pred. No. 1.3;
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PROSITE; PS50002; SH3; 1.
PROSITE; PS50084; WD_REPEATS_2; 4.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
PYPOCHELICAL DEFOCE THE REPEATS_REGION AND REPEATS_REGION TO REPEATS REPEATS SEQUENCE THOSE AND TABLE THE TABLE THE TABLE THOSE THE TABLE TABLE THE TABLE T
                                                                                                                                                                                                                                     846 AA; 97815 MW; C47EE949D873821B CRC64;
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Last annotation update)
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Best Local Similarity 33.3%; Pred. No. 1.3;
PROSITE, PS50021, CH; 1.
PROSITE, PS00479; DAG PE BIND DOM 1; 1.
PROSITE; PS50081; DAG PE BIND DOM 2; 1.
PROSITE; PS50081; DH 1; 1.
PROSITE; PS50010; DH 2; 1.
PROSITE; PS50001; PH DOMAIN; 1.
PROSITE; PS50001; SH3; 1.
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InterPro; IPR001680; WD40.
Pfam; PP000400; WH40.
Pfam; PF00400; WD40.
ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel, 16, 01-MAR-2001 (TrEMBLrel, 16, 01-MAR-2003 (TrEMBLrel, 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00326; SH3; 1.
SMART; SM00320; WD40; 5.
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DKFZP434N031.
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                                                                                                                                                                                                                       SH3 domain.
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1050 UDTAPTVVALYDYTANRSDELTIHRGDIRVF---FKDN--EDWWYGSI-GKGQE---- 1098
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Close J.P., Game I.G., Clark B., Thein S.L.;

Close J.P., Game I.G., Clark B., Thein S.L.;

a quantitative trait loci for foetal haemaglobin expression.";

Thesis (2002), Department of Clinical medicine, University of Oxford,

Oxford, United Kingdom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sudiyama T., Irie R., Otsuki T., Sato H., Makamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human cDN sequencing project.";
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12; Mismatches 31; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PSS0002, SH3; 1.
PROSITE; PSS0084; WD_REPEATS_IRGGION; 1.
Hypothetical protein; Repeat, SH3 domain; WD repeat.
SEQUENCE 1196 AA; 137114 MW; 16A237C915DABF0F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                  01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ34943.
Homo sapiens (Human).
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                                                                                                                                                                                                                                              PRT; 1196 AA.
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EMBL; AK092262; BAC03840.1; -.
EMBL; AJ459824; CAD30871.1; -.
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                                     1099 GYFPANHVASETLYQELPPEI 1119
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98 GYFPRNLVKEQRVYQEATKEV 118
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ProDom; PD000066; SH3; 1.
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InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 5.
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Q96D37
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us-10-019-455a-6.rspt

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12.8%; Score 86.5; DB 4; Length 719; ilarity 32.9%; Pred. No. 1.1; Conservative 13; Mismatches 21; Indels 13; Gaps
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini; Hominidae; Homo.
1918 TaxID=5606;
                                                                                                                                    A Strausberg R.;
Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: CONTAINS 2 SH3 DOWAINS.
--- SIMILARITY: CONTAINS 1 PH DOWAIN.
--- SIMILARITY: CONTAINS 1 PH DOWAIN.
--- SIMILARITY: CONTAINS 1 PH DOWAIN.
--- SIMILARITY: CONTAINS 2 SH3 DOWAIN.
--- SIMILARITY: CONTAINS 2 SH3 DOWAIN.
--- SIMILARITY: CONTAINS 2 SH3 DAG-PE-bind.
--- R InterPro; IPR001849; PH.
--- R InterPro; IPR001849; PH.
--- R InterPro; IPR001849; PH.
--- R InterPro; IPR001852; SH3.
--- R Pfam; PF00163; DAG-PE-bind; 1.
--- R Pfam; PF00169; PH; 1.
--- R Pfam; PF00169; PH; 1.
--- R Pfam; PF0018; SH3; 2.
--- R PRINTS; PR00401; SH3ZDOWAIN.
--- R PRINTS; PR00402; SH3; 2.
--- R PRODOW; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS=0VCz; S=1; d.
Hypothetical protein; SH3 domain.
SEQUENCE 719 AA; B3727 MW; A51B757DA543BA6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWART; SW00109; CI; I. SWART; SW00109; CI; I. SWART; SW00235; RhoGEF; I. SWART; SW00225; RhoGEF; I. SWART; SW00226; SH2; I. SWART; SW00326; SH3; 2. PROSITE; PS00419; DAG PE BIND_DOM_1; I. PROSITE; PS50019; DH_1; I. PROSITE; PS50010; DH_2; I. PROSITE; PS50010; SH2; I. PROSITE; PS50001; SH3; I. PROSITE; PS50001; SH3; I. PROSITE; PS50001; SH3; I.
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SEQUENCE FROM N.A.
TISSUE=Placenta;
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104 LVKEQRVYQE 113 710 YVEED--YSE 717 ద  $\dot{\delta}$ 

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44 ASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRN 103

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Search completed: December 29, 2003, 16:06:24 Job time : 22.7199 secs

Human protein sequ Human TANGO 130 MI Human TANGO 130 pr Human TANGO 130 po Human PRO POLYPEPT Human PRO POLYPEPT Human secreted/tra

Human MIA protein Recombinant human Melanoma inhibitin

Rat MLP protein se Rat MLP protein se Melanoma inhibitin

Human growth regul Mouse MLP protein

PRO polypept PRO polypept secreted/tra PRO polypept

Human Human

human secret secreted/tra

Human Novel Human Human

secreted/tra TANGO 130 MI PRO polypept PRO19670. H

Human Human Mouse Human Human Human Human Human Human Human Novel Human Human Novel

angiogenesis PRO19670 pro PRO19670 pro

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secreted/tra

human secret PRO polypept secreted/tra

human secret secreted/tra

Perfect score:

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Sequence:

Minimum DB s Maximum DB s

Database

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Result

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Searched:

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Growth regulatory-like polypeptide; human; cartilage; melanoma;
neuroectodermal tumour; glioma; cancer; therapy; diagnosis.
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/label= Signal_peptide
4..128
/label= Mature_protein
/note= "separately claimed in Claim 10"
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AAU29304
AAB87608
AAB87608
ABB95600
ABB4994
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ABU72034
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ABU67701
ABU65559
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ABB82118
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ABU71407
ABU65864
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ABU10805
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AAM25834
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02-MAY-2000; 2000US-0563786.
(first entry)
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WO200155332-A2
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    B X H X X B X X B X L L L L L L L X B X X B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C 
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Human PRO9673 prot
Human PRO protein,
Novel human secret
Mouse MLP protein
Rat MLP protein se
Human MLP protein se
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                                                                                                                                                           ; Search time 25.098 Seconds (without alignments) 809.506 Million cell updates/sec
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| SIDSI/gcgdata/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqp-embl/AA1981.DAT:*
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| SIDSI/gcgdata/gene
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1 MARILLLFLPGLVAVCAVHG.....RVYQEATKEVPTTDIDFFCE 128
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                                GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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AAB69123
ABB95602
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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                                                                                                                                                                       December 29,
                                                       Copyright
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61 KKGQQIYVYSKIVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPT 120
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                                                                                                                           Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system
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          Liu C;
            Tang YT,
              Ford JE, Arterburn MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human MLP protein sequence SEQ ID NO:6.
                                                                                                                                                                                                                                       Claim 10; Page 116-117; 119pp; English.
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arthritis and inflammation.
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                 Boyle BJ,
                                                                            2001-483233/52
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N-PSDB; AAH26343
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                                    Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                       The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant extivities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing to rreating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                       Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                                                                                                                                                  Noguchi Y, Yoshimura K;
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; Pred. No. 7.9e-80;
0; Mismatches 0;
                                                                                                                                                                                     Nishi K, Ogi K, Ohkubo S, Mogi S,
                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 91-92; 111pp; Japanese.
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                                                                                                                              99JP-0186718.
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Best Local Similarity 100.
Matches 128; Conservative
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               Homo sapiens.
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PRO proteins. These are useful for treating or diagnosing a cardiavascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophiebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.
                                                                                                                                                                                                                                                                                              KKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; angiogenesis, cardiant, cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; hymphangitis; tumour angiogenesis; breast carcinoma; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
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2000US-0664610.
2000US-0665350.
2000US-242922P.
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2000US-222695P.
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2000US-0747259
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                                                                                                                                  128 AA;
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02-AUG-2000;
17-AUG-2000;
23-AUG-2000;
24-AUG-2000;
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18-SEP-2000;
18-SEP-2000;
24-OCT-2000;
08-NOV-2000;
10-NOV-2000;
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20-DEC-2000;
20-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marsters SA, Pan J, Paoni NF, 4, Wood WI, Ye W;
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J, Hillan KJ, Marsters S.
IK, Williams PM, Wood WI
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                                                              20-JUL-2000; 2000US-219556P.
25-JUL-2000; 2000US-220664P.
28-JUL-2000; 2000US-220664P.
28-JUL-2000; 2000US-220664P.
28-JUL-2000; 2000US-220664P.
28-JUL-2000; 2000US-222695P.
17-AUG-2000; 2000US-222695P.
15-SEP-2000; 2000US-053328.
16-SEP-2000; 2000US-066350.
18-SEP-2000; 2000US-066350.
18-SEP-2000; 2000US-066350.
18-SEP-2000; 2000US-066350.
28-PEB-2000; 2000US-05698.
20-DEC-2000; 2000US-05698.
20-DEC-2000; 2000US-05698.
21-JAN-2001; 2001US-076668.
22-JAN-2001; 2001US-076668.
22-JAN-2001; 2001US-076668.
23-JAN-2001; 2001US-076668.
24-MAR-2001; 2001US-086689.
25-MAR-2001; 2001US-086621.
26-MAY-2001; 2001US-0866034.
26-MAY-2001; 2001US-0866034.
26-MAY-2001; 2001US-0866034.
26-UUN-2001; 2001US-0870574.
                                      09-JUL-2001; 2001WO-US21735
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GERRITSEN M E.
GODDARD A.
GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAN J.
PAONI N F.
STEPHAN J F.
WATANABE C K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-171999/22.
N-PSDB; ABL95740.
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FERRARA N.
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      31-JAN-2002
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(BAKE/)
(FERK/)
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(GODD/)
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PRO protein, Seq ID No 72.
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           Human
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                                                                                                                                                                                                                                                                                                                                                 ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABL885003. The PRO proteins and polymucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polymucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular theumatoid arthritis, angina, myceardial infarctions, thrombophhebitis, theumatoid arthritis, angina, myceardial infarctions, thrombophhebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polymucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPT 120
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KJ, Marsters SA, Pan J, Paoni NF;
... wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MARILLLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV
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                                                                                                                                                                                                                                                                                    One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                   Hillan KJ, Mar
Williams PM,
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                                                                                                                                                                                                           Gerber H,
                                         2001US-0802706.
2001US-0808689.
2001US-0816744.
2001US-0828366.
                                                                                                                               25-WAY-2001; 2001WO-US17092.
30-WAY-2001; 2001US-0870574.
30-WAY-2001; 2001WO-US17443.
01-JUN-2001; 2001WO-US17800.
                    2001WO-US06520.
2001WO-US06666.
                                                                                                         2001US-0866028.
2001US-0866034.
                                                                                     2001US-0854208
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                                                                                                                                                                                                                    PJ, Gurney AL,
JF, Watanabe CK,
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N-PSDB; ABL88251.
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                                         09-MAR-2001; 2
14-MAR-2001; 2
22-MAR-2001; 2
05-APR-2001; 2
                                                                                                         25-MAY-2001;
25-MAY-2001;
                                                                                              10-MAY-2001;
                     28-FEB-2001;
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AAU83627
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One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO protein sequences of the invention.
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sphan JF, Watanabe CK, Wood WI;
Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerritsen ME, Goddard /
Smith V, Stephan JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Figure 72; 359pp; English.
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2000US-220624P.
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2000US-220664P.
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2001US-0854280.
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Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour or liver tumour
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24-AUG-2000;
15-SEP-2000;
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28-NOV-2000;
                                                                                                                                                             Homo sapiens
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28-FEB-2001;
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100.0%; Score 676; DB 23; Length 128;

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Length 128;

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The invention relates to an isolated novel secreted polypeptide (I) and polynucleotide (II). (I) and (II) are useful for treating cancer, discorders, inclaimed diseases, wound healing disorder, infections, hematopoietic disorders, inclaimentory disorders, infertility, neurological and psychiatric diseases, cardiovascular diseases, respiratory diseases, renal diseases, or gastrointestinal diseases. These may also be used to treat diseases, abnormalities and disorders caused by abnormal expression, production, function and/or metabolism of the genes, as vaccines for inducing immunological response in a marmal, and in production of mRNA and polypeptide in cells. The polypeptides can be used as immunogens to produce antibodies immunospecific for the polypeptides,
                                      ö
                                                                                                                                                                                                                                                                                              61 XKGQQIYVYSKI.VKENGAGEFWAGSYYGDGQDEMGVVGYFPRNI.VKEQRVYQEATKEVFT 120
                                                                                                                                                                                                                                                       KKGQQIXVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPT 120
                                                                                                        1 MARILLLFLFGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60
                                                                                                                                                                              1 MARILLLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and to identify membrane-bound or soluble receptors. The polynucleotides may be used as diagnostic reagents, in chromosome localisation studies, and in tissue expression studies. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiinflammatory; neuroprotective; nephrotropic; cardiovascular; human; cancer; autoimmune disease; wound healing disorder; infection; haematopoietic disorder; inflammatory disorder; infertility; neurological disease; psychiatric disease; cardiovascular disease; respiratory disease; renal; gastrointestinal.
                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein; cytostatic; immunosuppressive; vulnerary; vaccine;
                                  0; Indels
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100.0%; Pred. No. 7.9e-80; ive 0; Mismatches 0;
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24-APR-2000; 2000US-199417P.
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                                      128; Conservative
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       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                              121
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       Best Local
                                              Matches
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61 KKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPT 120
                                                                                                                                                                                                        61 KKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
                                                                                                                                                                       1 MARILLLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
                                                                                                                                    1 MARILLLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 128;
amino acid sequence of novel human secreted protein #12
                                                                  Score 676; DB 23;
Pred. No. 7.9e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in the exemplification of the present invention.
                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse MLP protein sequence SEQ ID NO:12.
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                                                                                                                                                                                                                                                                                                                                                                                                    AAB69125 standard; Protein; 128 AA.
                                                              100.0%;
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                                                                                  Best Local Similarity 100.
Matches 128; Conservative
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                                  128 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF59068.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tanaka H;
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB69125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yoshimura K;
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                                                                                                   MARILLLFLPGLVAVCAVHGI FMDRLASKKLCADDECVYTI SLASAQEDYNAPDCRFINV
                                         Gaps
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                                       Indels
3.66-70;
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                                       Mismatches
                   No.
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                                                                                                                                                                                                                                                                                                                                                                                           AAB69130 standard; Protein; 128 AA
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                   Pred.
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                 86.78;
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                                    Conservative
                                                                                                                                                                                                                                                                                       128
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                   Similarity
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Tanaka H;
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                   Best Local
                                       Matches
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                       KKGQQIYVYSKIVTENGAGAFWAGSVYGDHQDEMGIVGYFPSNLVREQRVYQEATKEIPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant estivities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   joint
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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100.0%; Pred. No. 1.1e-68;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                            Human MLP protein sequence SEQ ID NO:24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 97-98; 111pp; Japanese.
                                                                                                                                                                                                                                        AAB69126 standard; Protein; 110 AA
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                                                                                     TDIDFFCE 128
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                                                                                                                            TDIDFFCE
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N-PSDB; AAF59079.
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Tanaka H;
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                                                                                                                                                                                               RESULT
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Gaps

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Length 128;

88.8%; Score 600; DB 22; Length 1 86.7%; Pred. No. 6.6e-70; ive 9; Mismatches 8; Indels

Matches 111; Conservative

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Query Match Best Local Similarity

1 MARILLLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV

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Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of a novel human growth regulatory-like polypeptide (GRLP) mature protein. The sequence is predicted from a novel assembled CDNA (see AAH26343) based on Hyseq clone number 16372272. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP belongs to the same protein family as growth regulatory proteins, procurs, human melanoma derived growth regulatory proteins precursor (64% similarity and 45% identity over 11 amino acids)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or melanoma inhibitory activity, cattle cartilage-derived retinoic acid sensitive protein (CD-RAP, 44 identity and 64% similarity over 126 amino acids) and other retinoic acid-sensitive proteins. GRLP polypeptides and polynuclectides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                        Growth regulatory-like polypeptide; human; cartilage; melanoma; neuroectodermal tumour; glioma; cancer; therapy; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ford JE, Arterburn MC, Tang YT, Liu C;
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                                                                                                                                                                                                                                                                                                                           Human growth regulatory-like polypeptide (mature protein).
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                                                                            AAB82672 standard; Protein; 105 AA.
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02-MAY-2000; 2000US-0563786.
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                                                                                                                                                                                                                                                   02-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                  AAB82672;
RESULT 10
                                    AAB82672
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0; Gaps

Indels

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                  1 DRIASKKICADDECYYIISIASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
24 DRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                            MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEFWAGSVYGDHQDEMGIVGYFPSNLVKEQRVYQEATKEIPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKBVPTTDIDFFCE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.9%; Score 547; DB 22; Length 110; 90.0%; Pred. No. 4.5e-63; ive 7; Mismatches 4; Indels (
                                                                                 84 GSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 128
                                                                                                                                                                                                                                                                                               Mouse MLP protein sequence SEQ ID NO:26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 98-99; 111pp; Japanese.
                                                                                                                                                                                         AAB69127 standard; Protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-2000; 2000WO-JP04278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-0186718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-159271/16.
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Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Itoh Y, Nishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF59080
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200102564-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                              23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fanaka H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                            AAB69127;
                                                                                                                                                        RESULT 11
                                                                                                                                                                         AAB69127
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30-JUN-1999;
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                                                                                                     11-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
26-OCT-1995
                                                             Rattus sp.
                                                                                                                                                                                      Itoh Y, N
Tanaka H;
                                        inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR69811;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  atches
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                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes novel MLP proteins and their encoding MAAS. The MLP proteins and DNAs have antinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing to treating bone and joint diseases as well as pathologic angiogenesis. AAF55063 to AAF55099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint diseases
                                                                                                                                                                                                                                                                               Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA
                                                                                                 MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%; Score 541; DB 22; Length 110; llarity 89.1%; Pred. No. 2.7e-62; Conservative 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                              Noguchi Y,
                                                                                                                                                                                                                                                                              Mogi S,
                                                                               Rat MLP protein sequence SEQ ID NO:49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat MLP protein sequence SEQ ID NO:39.
                                                                                                                                                                                                                                                                              Ohkubo S,
                   AAB69131 standard; Protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 107; 111pp; Japanese
                                                                                                                                                                                                                  29-JUN-2000; 2000WO-JP04278
                                                                                                                                                                                                                                       99JP-0186718
                                                                                                                                                                                                                                                          (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB69129 standard; Protein;
                                                          (first entry)
                                                                                                                                                                                                                                                                             Ogi K,
                                                                                                                                                                                                                                                                                                            WPI; 2001-159271/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
tes 98; Conserv
                                                                                                                                                                                                                                                                              Nishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 AA;
                                                                                                                                                                                                                                                                                                                       N-PSDB; AAF59099
                                                                                                                                                                         WO200102564-A1
                                                                                                                                                                                                                                      30-JUN-1999;
                                                          23-APR-2001
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                                                                                                                                                                                              11-JAN-2001
                                                                                                                                 inhibitor.
                                                                                                                                                      Rattus sp.
                                                                                                                                                                                                                                                                                        Tanaka H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                       AAB69131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB69129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                             Itoh Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
AAB69129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
        AAB69131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint diseases
                                                                                                                                                                                                                                                                                                                                                                                                    Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 DRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma; small cell lung cancer; neuroectodermal tumours; immunosuppressant; phytohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection; probe; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                    Noguchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                  Mogi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSVYGDGQDEMGVVGYFPRNLVKEQRV 110
                                                                                                                                                                                                                                                                                                                                                                                                  s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 9; Page 103; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSVYGDHQDEMGIVGYFPSNLVREQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Melanoma inhibiting protein (human).
                                                                                                                                                                                                                                                                                                                                                                                                  Ohkubo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR69811 standard; Protein; 131
                                                                                                                                                                                                                                                           29-JUN-2000; 2000WO-JP04278.
                                                                                                                                                                                                                                                                                                                                                  (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  Ogi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-159271/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                               Nishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 AA;
                                                                                                                                                              WO200102564-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9503328-A2.
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Use of melanoma inhibiting activity protein or its derivatives as immune modulatory agents for the treatment of inflammatory diseases, specifically rheumatoid arthritis

Verheijden GFM;

Nelissen RLH,

WPI; 2001-611446/70.

N-PSDB; AAH47783

23-MAR-2000; 2000EP-0201063

(ALKU ) AKZO NOBEL NV

Example 4; Page 34; 41pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRFINVKKGQQIYVYSKLVKENGAGE-FWAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                     58
                                                                                                                                                                                                                                                                  peripheral blood lymphocytes). Antibodies raised against the protein can be used to detect cell producing the protein and also for protein purification. Probes derived from DNA encoding the protein (AAQ84050, AAQ84051) can be used to detect sequences encoding the protein (AAQ84050, AAQ84051). The protein may be expressed as a fusion protein (conjugated with dihydrofolate reductase (DHFR)).
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MARILLLFLPGLVAVCA-----VHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIA; melanoma inhibiting activity protein; antiinflammatory; human; antiarthritic; antirheumatic; antithyroid; osteopathic; nephrotropic; immunosuppressive; ophthalmological; dermatological; antidiabetic; neuroprotective; immune tolerance; T-cell tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                         13; Gaps
                                                                                                                                                                                                                       This protein has melanoma-inhibiting activity and can be used to treat cancer (melanoma, glioblastoma, nuroblastoma, small cell lung cancer, neuroectodermal tumours) or as an immunosuppressant (it inhibits IL-2 or phytohaemagglutinin induced proliferation of
                                                                                                                                                      New melanoma inhibiting protein and related nucleic acid - vectors, transformed cells, antibodies etc., useful for treating tumours and as immunosuppressant e.g. by gene therapy
                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 131;
                                                                                                                                                                                                                                                                                                                                                                               38.1%; Score 257.5; DB 16; Length 41.2%; Pred. No. 3.6e-25; ive 26; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG65614 standard; Protein; 131 AA.
                                                                            (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                   Kaluza
                                                                                                                                                                                                  Claim 1; Page 54; 85pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 EATKEVPTTDIDFFCE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-EP02369.
                                                                                                                      WPI; 1995-075191/10.
N-PSDB; AAQ84050, AAQ84051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2001; 2001WO-EP02991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human MIA protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 41.2
Matches 56; Conservative
                                                                                                  Bogdahn U, Buettner R,
                                                                                                                                                                                                                                                                                                                                                           131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200170253-A1
                               19-JUL-1994;
                                                       20-JUL-1993;
           02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                            Seguence
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The invention relates to the use of melanoma inhibiting activity (MIA)

protein and/or its fragments that have anti-inflammatory effects and
induce systemic immune tolerance or specific T-cell tolerance to MIA
antidem, for manufacturing a preparation against inflammatory diseases
and for induction of systemic immune tolerance or specific T-cell
colerance in patients suffering from or susceptible to inflammatory
diseases. A fragment of MIA is useful as a therapeutic substance and is
useful for manufacture of pharmacoutical preparations against
inflammatory diseases such as an immune-cell mediated cartilage
destruction disease, specifically rheumatoid arthritis, autoimmune
diseases like Graves' disease, juvenile arthritis, primary
glomerulonephritis, polyarthritis, osteoarthritis, siogren's syndrome,
myasthenia gravis, Addison's disease, primary biliary sclerosis,
myasthenia gravis, Addison's disease, primary biliary sclerosis,
uveitis, systemic lupus erythematosis, inflammatory bowel disease,
multiple sclerosis or diabetes. The MIA polypeptides have specific
the immune systemi intact as compared to the non-specific suppressive
fiften or the autoreactive T-cells thus leaving the other components of
the immune system intact as compared to the non-specific suppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MARILLELPGEVAVCA-----VHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MARSLVCL--GVIILLSAFSGPGVRGGPMPKLADRKLCADQECSHPISMAVALODYMAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 CRFINVKKGQQIYVYSKLVKENGAGE-FWAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressive drugs. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.1%; Score 257.5; DB 2
41.2%; Pred. No. 3.6e-25;
ive 26; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: December 29, 2003, 16:09:02 Job time: 27.098 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 PGKVDVKTDKWĎFYCQ 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human MIA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 AA;
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December 29, 2003, 16:09:08; Search time 17.5686 Seconds (without alignments) 1449.984 Million cell updates/sec
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1: (cgn2_6/prodate/2/pubpaa/PCT_NEW_PUBCOMB.pep:*

2: (cgn2_6/prodate/2/pubpaa/PCT_NEW_PUB.pep:*

3: (cgn2_6/prodate/2/pubpaa/USG_NEW_PUB.pep:*

4: (cgn2_6/prodate/2/pubpaa/USG_NEW_PUB.pep:*

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17: (cgn2_6/prodate/2/pubpaa/USG_PUBCOMB.pep:*

18: (cgn2_6/prodate/2/pubpaa/USG_PUBCOMB.pep:*

18: (cgn2_6/prodate/2/pubpaa/USG_NEW_PUB.pep:*

18: (cgn2_6/prodate/2/pubpaa/USG_NEW_PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence:
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                                                                                                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Sequence 72,		Sequence 72,		Seguence 72,					Seguence 72,			Sequence 72,	
SUMMARIES	US-10-216-163-72	US-10-218-765-72	US-10-219-063-72	US-10-219-066-72	US-10-219-067-72	US-10-219-068-72	US-10-219-069-72	US-10-219-073-72	US-10-219-475-72	US-10-219-480-72	US-10-219-483-72	US-10-219-525-72	US-10-219-526-72	US-10-219-530-72	US-10-219-531-72
DB	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12
% Query Watch Length DB	128	128	128	128	128	128	128	128	128	128	128	128	128	128	128
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	929	. 676	676	676	676	929	929	919	929	919	929	919	919	919	9/9
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Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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122	12	12	12	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15
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676 676 676	676	676	676	919	9/9	919	9/9	676	9/9	919	929	676	9/9	919	919	919	929	676	929	9/9	929	676	676	919	919
16 17 18	19	225	7 7 7 7 3 7 7	24	25	26	27	28	29	30	31		33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

Sequence 72, Application US/10216163
Sequence 72, Application US/10216163
Sequence 72, Application US/10216163
Sequence 72, Application US/10216163
Sequence 72, Application No. US20030149239A1
SENERAL INFORMATION:
APPLICANT: Beare, Kevin P.
APPLICANT: Gedvaki, Paul J.
APPLICANT: Gedvaki, Paul J.
APPLICANT: Gedvaki, Paul J.
APPLICANT: Germaldi, J. Christopher
APPLICANT: Girmaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Girmaldi, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
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APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
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APPLICANT: Watanabe, Colin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANTON NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/07891
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079296

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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
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US-10-216-163-72
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LENGTH: 128
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PRIOR APPLICATION NUMBER: 60/08232
PRIOR FILING DATE: 1998-06-06
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PRIOR PRINCATION NUMBER: 60/100390
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PRIOR PAPELCATION NUMBER: 60/10648

PRIOR PAPELCATION NUMBER: 60/10646

PRIOR PAPELCATION NUMBER: 60/10695

PRIOR PAPELCATION NUMBER: 60/10695

PRIOR PAPELCATION NUMBER: 60/10695

PRIOR PAPELCATION NUMBER: 60/10891

PRIOR APPLICATION NUMBER: 60/10891

PRIOR APPLICATION NUMBER: 60/10891

PRIOR APPLICATION NUMBER: 60/10894

PRIOR APPLICATION NUMBER: 60/11326

PRIOR APPLICATION NUMBER: 60/11326

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PRIOR PLILING DATE: 1998-12-23

PRIOR PLILING DATE: 1999-11-12

PRIOR PLILING DATE: 1999-11-12

PRIOR PLILING DATE: 1999-01-12

PRIOR PLILING D
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APPLICANT: Goddard, Marry
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrin J. Christopher
APPLICANT: Grimalid, J. Christopher
APPLICANT: Grimalid, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: APPLICANTON WATER: US/10/19, 480
PRIOR APPLICANTON WATER: 60/062387
PRIOR FILING DATE: 1997-10-13
PRIOR FILING DATE: 1997-10-21
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PRIOR APPLICANTON WATER: 60/063913
PRIOR FILING DATE: 1999-10-21
PRIOR APPLICANTON WATER: 60/063910
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-03-26
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100.0%; Score 676; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 7.8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0
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PRIOR FILING DATE: 1999-08-11
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
PRIOR PILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/16361
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TDIDFFCE 128
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ATTLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFREENCE: P3530PLC31
CURRENT APPLICATION NUMBER: US/10/219,067
CURRENT PILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US/119,480
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PELICATION NUMBER: 60/06287
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/063873
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-21
PRIOR PELICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR PILING DATE: 1998-03-26
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PDAME PILING DATE: 1998-03-27
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                                                                 1 MARILLEFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60
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  Gaps
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NUMBER OF SEQ ID NOS: 246
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100.0%; Pred. No. 7.8e-74;
tive 0; Mismatches 0;
  0; Mismatches
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Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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Publication No. US20030187204A1
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
  Matches 128; Conservative
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Matches 128, Conservative
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                                                                                                                                                Gaps
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                                                                                                   Query Match 100.0%; Score 676; DB 12; Length 128; Best Local Similarity 100.0%; Pred. No. 7.8e-74; Matches 128; Conservative 0; Mismatches 0; Indels 0
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Pred. No. 7.8e-74;
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US-10-219-066-72
US-10-219-066-72
Sequence 72, Application US/10219066
Publication No. US20030187203A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                  ; TYPE: PRT
; ORGANISM: Homo Sapien
US-1.0-219-063-72
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ORGANISM: Homo Sapien
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Best Local Similarity
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; Sequence 72, Application US/10219073; Publication No. US2030187207A1 GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
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APPLICANT: Baker, Kevin P.

APPLICANT: Geritsen, Mary

APPLICANT: Godowski, Paul J.

APPLICANT: Matanabe, Colin L.

APPLICANT: Matanabe, Colin L.

APPLICANT: Mood, William I.

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: PS53 OPH C31

CURRENT APPLICATION NUMBER: 10/119, 480

PRIOR FILING DATE: 2002-09-1

PRIOR PELING DATE: 1997-09-1

PRIOR PELING DATE: 1997-09-1

PRIOR APPLICATION NUMBER: 60/06349

PRIOR APPLICATION NUMBER: 60/06349

PRIOR PELING DATE: 1997-10-28

PRIOR PLING DATE: 1997-10-28

PRIOR PLING DATE: 1997-10-31

PRIOR PLING DATE: 1997-10-31

PRIOR PLING DATE: 1997-10-31

PRIOR PLING DATE: 1997-10-31

PRIOR PLING DATE: 1997-10-32

PRIOR PLING DATE: 1998-03-26

PRIOR PLING DATE: 1998-03-27

REMAINS PRIOR PLING DATE: 1998-03-27

PRIOR PLING DATE: 1998-03-27

REMAINS PRIOR PLING DATE: 1998-03-27

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61 KKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVFT 120
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                                                                                                                                                                                                                                                                                                                          Sequence 72, Application US/10219068 Publication No. US20030187205A1 GENERAL INFORMATION:
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US-10-219-068-72
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Matanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: WATANAWARENERANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: PASSOPTICAT
CURRENT APPLICATION NUMBER: 10/119,480
PRIOR PELING DATE: 2002-04-03
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/063549
PRIOR RILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06340
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06349
PRIOR PELING DATE: 1997-10-28
PRIOR PELING DATE: 1997-10-31
PRIOR PELING DATE: 1997-10-31
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PRIOR PELING DATE: 1998-03-20
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                             Sequence 72, Application US/10219069; Publication No. US20030187206A1; GENERAL INFORMATION:
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Gerritsen, Mary
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                                                                                                                                                     APPLICANT: Baker, Kevin P.
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US-10-219-069-72
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Best Local Similarity
JS-10-219-069-72
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                                            APPLICANT: Goddwarki, Audiesy
APPLICANT: Goddwarki, Audiesy
APPLICANT: Goddwarki, Audiesy
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stath, Victoria
FAPLICANT: Stath, Victoria
APPLICANT: Matanabe, Colin L.
APPLICANT: Wood, William I.
APPLICANT: ON WOMBER: 10/10/219,073
CURRENT FILING DATE: 2002-04-09
FRIOR FILING DATE: 1007-04-09
FRIOR FILING DATE: 1997-10-17
FRIOR APPLICATION NUMBER: 60/06287
FRIOR APPLICATION NUMBER: 60/06287
FRIOR APPLICATION NUMBER: 60/063549
FRIOR FILING DATE: 1997-10-28
FRIOR FILING DATE: 1997-10-29
FRIOR FILING DATE: 1997-10-29
FRIOR FILING DATE: 1997-10-37
FRIOR FILING DATE: 1997-10-37
FRIOR FILING DATE: 1997-10-37
FRIOR FILING DATE: 1998-03-20
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Publication No. US20030187208A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaddi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
Gerritsen, Mary
Goddard, Audrey
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US-10-219-073-72
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APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE SEPREBACE: 2002-08-13
CURRENT APPLICATION NUMBER: US/10/19,480
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-06-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-18
PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
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APPLICANT: Desnoyers, Luc.
APPLICANT: Gedard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Shith, Victoria
APPLICANT: Shith, Victoria
APPLICANT: Matanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF LARRENCE: P3530PLC3B
CURRENT APPLICATION NUMBER: US/10/219,480
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ORGANISM: Homo Sapien
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US-10-219-480-72
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PRIOR PEDICACTION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR PEDICATION NUMBER: 10/020-04-09
PRIOR PELING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-28
PRIOR PELING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/06913
PRIOR APPLICATION NUMBER: 60/069873
PRIOR PILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR PILING DATE: 1997-10-31
PRIOR PLING DATE: 1999-03-20
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
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PRIOR PLING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07956
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 
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Publication No. US20030187210A1
GENERAL INFORMATION:
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ORGANISM: Homo Sapien
US-10-219-480-72
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Godwski, Paul J.
APPLICANT: Grimaldi, J. Cristopher
APPLICANT: Grimaldi, J. Cristopher
APPLICANT: Smith, Victoria
APPLICANT: Stephan. Jean-Philippe F.
APPLICANT: Stephan. Jean-Philippe F.
APPLICANT: Stephan. Jean-Philippe F.
APPLICANT: Stephan. Jean-Philippe F.
APPLICANT: Stephan. Jean-Philippe F.
APPLICANT: Stephan. Jean-Philippe F.
APPLICANT: Stephan. Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYFEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 19330PL029
CURRENT APPLICATION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 60/069113
PRIOR APPLICATION NUMBER: 60/069113
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06349
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06349
PRIOR APPLICATION NUMBER: 60/06349
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/069873
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                       FRIOR FILING DATE: 1997-10-28

FRIOR FILING DATE: 1997-10-28

FRIOR PEDICATION NUMBER: 60/064103

FRIOR APPLICATION NUMBER: 60/069873

FRIOR APPLICATION NUMBER: 60/078910

FRIOR APPLICATION NUMBER: 60/078910

FRIOR FILING DATE: 1998-03-20

FRIOR FILING DATE: 1998-03-25

FRIOR FILING DATE: 1998-03-25

FRIOR PILING DATE: 1998-03-25

FRIOR PILING DATE: 1998-03-25

FRIOR APPLICATION NUMBER: 60/07956

FRIOR APPLICATION NUMBER: 60/07956

FRIOR APPLICATION NUMBER: 60/07928

FRIOR APPLICATION NUMBER: 60/07928

FRIOR APPLICATION NUMBER: 60/07928

FRIOR FILING DATE: 1998-03-27

FROMAINING DATE: 1998-03-27

FROMAINING PAIOR APPLICATION NUMBER: 60/079728

FROMAINING PAIOR APPLICATION NUMBER: 60/07978
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APPLICATION NUMBER: 60/063549
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Gerritsen, Mary
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ORGANISM: Homo Sapien
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APPLICANT Goddard, Audrey
APPLICANT Goddard, Paul J.
APPLICANT Goddard, Paul J.
APPLICANT Granaldi, J. Christopher
APPLICANT Stepher
APPLICANT Stepher
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APPLICANT Stepher Jean-Philippe F.
APPLICANT Watanabe, Colin L.
APPLICANT Watanabe, Colin L.
APPLICANT Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P35300P1C41
CURRENT APPLICATION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-18
PRIOR PLING DATE: 1997-10-18
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR PLING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
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FILING DATE: 1997-12-17
APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/079294
FILING DATE: 1998-03-25
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APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
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Publication No. US20030187212A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 128; Conservative
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Gerritsen, Mary
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; ORGANISM: Homo Sapien
US-10-219-525-72
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ENGTH: 128
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PRIOR PELLING DATE: 2002-04-04

PRIOR PELLING DATE: 3002-04-04

PRIOR PELLING DATE: 3002-04-04

PRIOR PELLING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/06287

PRIOR PELLING DATE: 1997-10-17

PRIOR PELLING DATE: 1997-10-17

PRIOR PELLING DATE: 1997-10-31

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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Juctoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
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100.0%; Score 676; Dr.
Best Local Similarity 100.0%; Pred. No. 7.8%
Matches 128; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/219,530
CURRENT FILING DATE: 2002-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 72, Application US/10219530; Publication No. US20030187213A1; GENERAL INFORMATION:
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Gerritsen, Mary
Goddard, Audrey
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CRGANISM: Homo Sapien
US-10-219-530-72
                                                                                                                                                             TYPE: PRT
CORGANISM: Homo Sapien
US-10-219-526-72
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LENGTH: 128
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APPLICANT: Srephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Watenabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE SEPREMENTS: P3520PIGE
CURRENT APPLICATION NUMBER: US/10/219,531
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: (0/0591)3
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
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Query Match
Best Local Similarity 100.0%; Pred. No. 7.8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0
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Godowski, Paul J.
Grimaldi, J. Christopher
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Publication No. US20030187214A1
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Smith, Victoria
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Gerritsen, Mary
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; ORGANISM: Homo Sapien
US-10-219-531-72
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                                                                       December 29, 2003, 16:03:18; Search time 9.32213 Seconds (without alignments) 580.961 Million cell updates/sec
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Sequence 5,
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/cgn2_6/ptodata/2/iaa/RecTUS_CONB.pep:*
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-577-600-15

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US-08-245-511-48
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US-08-459-967-8
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Best Local Similarity 41.2%; Pred. No. 6.7e-26;
Matches 56; Conservative 26; Mismatches 41; Indels 13; Gaps
                                                                                                                                                                                                                                                                                              Sequence
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Sequence
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APPLICANT: Ulrich Bogdan
APPLICANT: Ulrich Buttner
APPLICANT: Brighter Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
COUNTRY: New York
COUNTRY: USA
US-08-459-871-8
US-09-024-532-2
US-09-104-6234-2
US-09-104-533-2
US-08-417-3594-2
US-08-434-255-6
US-08-459-871-6
US-08-459-967-6
US-08-459-967-4
US-08-459-967-4
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US-08-459-871-2
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | REPERENCE / DOCKET NUMBER: BOER 1035-PFF/ALT TELECOMMUNICATION INFORMATION: TELEPONNEN: 1212 | 888-9200 | TELEPAX: (212) 888-3884 | INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHRACTERISTICS: LENGTH: 131 amino acids | TYPE: amino acid | TYPE: amino acid | TOPOLOGY: linear | MOLECULE TYPE: protein US-08-578-649-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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; Patent No. 5770366
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REGISTRATION NUMBER: 31,575
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337
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Barbacid, Mariano
VENTION: Vav Proto-Oncogene Protein
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CURRENT APPLICATION NUMBER: US/09/346,510B
CURRENT FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 08/871,732
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: DC10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 921-5901
TELEFAX: (609) 921-4526
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                             VE: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Gaul, Timothy J.
REGISTRATION NUMBER: 33,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    844 amino acids
  APPLICANT: Barbacid, Mar:
TITLE OF INVENTION: Vav I
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 LVKEQRVYQE 113
                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Domain
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US-09-346-510B-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                          59 CRFLTIHRGQVVYVFSKL.---KGRGRLFWGGSVQGDYYGDLAARLGYFPSSIVREDQTLK 115
                                                  55 CRFINVKKGQQIYVYSKLVKENGAGE-FWAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 MPKIADWKLCADEBCSHPISMAVALQDYVAPDCRFLTIYRGQVVYV5SKL---KGRGRLF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 MDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGE-F 81
       1 MARSLVCL--GVIILLSAFSGPGVRGGPMPKLADRKLCADQECSHPISMAVALQDYMAPD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.2%; Score 231.5; DB 1; Length 130;
43.5%; Pred. No. 1.7e-22;
tive 21; Mismatches 35; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 128
                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08578649
; Sequence 5, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMTION:
    APPLICANT: Ulrich Bogdan
    APPLICANT: Reinhard Buttner
    APPLICANT: Reinhard Buttner
    APPLICANT: Brighter Kaluza
    ITILE OF INVENTION: MELANOWA-INHIBITING PROTEIN
    NUMBER OF SEQUENCES: 24
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Reife & Lynch
    STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATOMNET ADDRESS TATOMNET TATAMNET TO THE REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect
CURRENT APPLICATION:DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION: A35
PRIOR APPLICATION DATA:
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // Sequence 2, Application US/07646537B
// Patent No. 5348864
                                                                                                                                           113 EATKEVPTTDIDFFCE 128
                                                                                                                                                                                    116 PGKVDVKTDKWDFYCQ 131
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amino acid
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Best Local Similarity 43.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / TOPOLOGY: linear
// MOLECULE TYPE: protein
US-08-578-649-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALLALLES BUDD LESTREET: BUDD LESTREET BUDD LESTREET NEW YORK STATE: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                         RESULT 2
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44 ASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRN 103
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12.6%; Score 85.5; DB 1; Length 844;
Best Local Similarity 31.4%; Pred. No. 0.039;
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) Sequence 21, Application US/09346510B
| Patent No. 6281014
| GENERAL INFORMATION:
| APPLICANT: Worlen, Timothy J.
| APPLICANT: Wang, Yinxiang
| TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: amino acid sequence of Vav SH3 domain
                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/646,537B
ADDRESSEE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543-4000
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46 AQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLV 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 LSSSPSTSELTSIRPIGIVVAAYDFNYPIKKDSSSQLLSVQQGETIYILNK----NSGG-99
                                 GENERAL INFORMATION:
APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Boriack-Sjodin, Dafna
APPLICANT: Boriack-Sjodin, Dafna
APPLICANT: Cole, Philip
APPLICANT: Cole, Philip
APPLICANT: Kuriyan, John
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-28M
CURRENT APPLICATION NUMBER: 08/09/356,952
CURRENT FILING DATE: 1999-07-19
EARLIER APPLICATION NUMBER: 60/093,631
EARLIER FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.6%; Score 78.5; DB 3; Length 1589;
Best Local Similarity 25.8%; Pred. No. 0.81;
Matches 23; Conservative 21; Mismatches 34; Indels 11; Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft.Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
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Sequence 15, Application US/08996139

Setuence 15, Application US/08996139

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.

APPLICANT: Maraskovsky, Eugene

TITLE OF INVENTION:
TITLE OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 WWDGLVIDDSNGKVN-RGWFPQNFGRPLR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Saccharomyces cerevisiae US-09-356-952-4
                                                                                                                                                                                                                                                                Sequence 4, Application US/09356952 Patent No. 6117663
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US-09-356-952-4
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45 SAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFW----AGSVYGDGQDEMGVVGYF 100
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APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Warsakovsky, Eugene
IIILE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
11.5%; Score 78; DB 3; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
            PRIOR APPLICATION DATA:
APPLICATION MURBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION MURBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION NURBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
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; Patent No. 6242213
                                                                                                                                                                                                                                                NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 285.1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                   TELEPALONE: (206)567-0430
TELEPAL: (206)233-0644
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 i: 625 amino acids
amino acid
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MOLECULE TYPE: protein
US-08-996-139-15
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CLASSIFICATION:
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217 VLLLFISVVVVAAIIFGVYYRKGGKALTANLWNWVNDACSSLSGNKESSGDRCAGSHSAT 276
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/996,139
FILING DATE: «Unknown»
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
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APPLICATION UNMERS: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <UNKNOWN>
                                                                                    APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
APPLICATION NUMBER: USSN 08/813,509
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                                                                                                                                                                                                                                             2852-A
                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852
TELECOMMINICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                         TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                       07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                             : 625 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-995-659-15
                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
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                            FILING DATE: 0
CLASSIFICATION:
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217 VLLLFISVVVVAAIIFGVYYRKGGKALTANLWNWVNDACSSLSGNKESSGDRCAGSHSAT 276
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                                                                                                                                                                                                                                                                                                                                                            48; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
                                                                                                                                                                                                                                                                                                            11.5%; Score 78; DB 3; Length 625; 21.1%; Pred. No. 0.24; tive 26; Mismatches 48; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
           REGISTRATION WIMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 PRNLVKEQRVYQEATKEVPTTD 122
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/09577780 Patent No. 6419929 GENERAL INFORMATION:
                                                                               TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                   TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 21.18
10:20 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          45 SAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFW----AGSVYGDGQDEMGVVGYF 100
                                                                                                                                                                                                                                                                                                                                                                                                       -----LASKKLCADDECVYTISLA 44
                                                                                                                                                                                                                                      48; Indels 38; Gaps
                                                                                                                                                                                  Query Match
11.5%; Score 78; DB 4; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SUGTWARE: Microsoft Word for Power Macintosh 6.0.1
APPLICATION NUMBER: US/09/577,800
FILING DATE: 24-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09577800
Patent No. 6479635
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Anderson, Dirk M.
APPLICANT: Marskovsky, Bugene
APPLICANT: Marskovsky, Bugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ANDERSONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                               4 ILLLFLPGLVAVCAVHGIFMDR-------
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APPLICATION NUMBER: US 08/996,139
FILING DATE: 22 DECEMBER 1997
PRIOR APPLICATION NUMBER: USSN 60/064,671
APPLICATION NUMBER: USSN 60/064,671
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
TYPE: protein
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-577-780-15
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FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 PRNLVKEORVYQEATKEVPTTD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 --TLVSEVETQGDLSRKIPTED 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 285
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)233-0644
TELEFRAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       625 amino acids
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-09-577-800-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: S
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45 SAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFW----AGSVYGDGQDEMGVVGYF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 SSQQEV----CEGILLMTREE-----KMVPEDGAGVCGPVCAAGGPWABVRDSRTF--- 323
                                                                                                                                                                                                                                                                                                                                                                                                                         -----LASKKLCADDECVYTISLA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
ODERATING SYSTEM: Apple Operating System 7.5.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/466,496
FILING DATE: 17-Dec-1999
CLASSIFICATION: <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u >u <u <u >u 
                                                                                                                                                                                                                      11.5%; Score 78; DB 4; Length 625; 21.1%; Pred. No. 0.24; tive 26; Mismatches 48; Indels
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TITLE OF INVENTION: Receptor Activator of NF-kappab
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 4 OCTOBER 1997
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
PILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ILLLFLPGLVAVCAVHGIFMDR-------
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REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-466-496-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 PRNLVKEORVYOEATKEVPTTD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 --TLVSEVETQGDLSRKIPTED 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/09466496; Patent No. 6528482; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 625 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                  30; Conservative
                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98101
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-466-496-15
                                                                                                                                          US-09-577-800-15
                                                                                                                                                                                                                                                                                                                                  Matches
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SAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFW----AGSVYGDGQDEMCVVGYF 100
                                                             277 SSOGEV----CEGILLMTREE----KMVPEDGAGVCGPVCAAGGPWAEVRDSRTF---- 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFW----AGSVYGDGQDEMGVVGYF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 SSQQEV----CBGILLMTREE-----KMVPEDGAGVCGPVCAAGGPWAEVRDSRTF---- 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LASKKLCADDECVYTISLA 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 625;
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                                                                                                                                                                                                                                                                                                                                                        Marsekovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEB: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,291
FILING DATE: 30-May-2001
CLASSIFICATION: cUnknown-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: cUnknown-
APPLICATION NUMBER: USBN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USBN 08/772,330
FILING DATE: 23 DECEMBER 1996
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11.5%; Score 78; DB ABest Local Similarity 21.1%; Pred. No. 0.24
Matches 30; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-291-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ILLLFLPGLVAVCAVHGIFMDR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
                                                                                                                                 324 --TLVSEVETQGDLSRKIPTED 343
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                                                                                                                                                                                                                             US-09-871-291-15; Sequence 15, Application US/09871291; Patent No. 6562948; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
                                                                                                                                                                                                                                                                                                                   APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                         101 PRNLVKEQRVYQEATKEVPTTD
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INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
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                                                                                                           SAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFW----AGSVYGDGQDEMGVVGYF 100
                                                                                                                                                                                              LASKKLCADDECVYTISLA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 ILLLFLPGLVAVCAVHGIFMDR--------LASKKLCADDECVYTISLA 44
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                                         38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/8096,139
FILING DATE: CUNKnown>
PRIOR APPLICATION NUMBER: US/80 08/813,509
FILING DATE: 07 WARCH 1997
APPLICATION NUMBER: US/80 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
DB 4; Length 625;
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                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
                                         48;
Query Match 11.5%; Score 78; DB 4;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches
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ATTORIET 1990
ATTORIET PETKINS, PATRICIA Anne
REGIGTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INPORMATION:
TELEPHONE: (206)587-0430
TELEPAC (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-856-15
                                                                                                                                                                                                                                                   101 PRNLVKEQRVYQEATKEVPTTD 122
                                                                                                                                                                                                                                                                         Sequence 15, Application US/09871856
Patent No. 6537763
GENERAL INFORMATION:
                                                                                   4 ILLLFLPGLVAVCAVHGIFMDR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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Best Local Similarity
Matches 30; Conserva
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US-09-871-856-15
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9410 Key West Avenue
                          Rockville
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                                                                                             Sequence 84, Application US/09071035

Patent No. 6448043

CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL OF INVENTION:
CORRESPONDENCE: 496

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 82, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: 611 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 VTAHDFEYAWKKMIDEKNG---FVYSFLIVETIQNGA-EISAGKL---AFNELGVTAVDD 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 YNAPDCRF----INVKKGQQIYVYSKLVKE---NGAGEFWAGSVYGDGQDEMGVVG--- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ILLLFLPGLVAVCAVHGIF----SKKLCADDECVYTISLA----SAQED 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.2%; Score 76; DB 4; Length 526; 28.2%; Pred. No. 0.34; Live 21; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                              STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER TRADABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
ODPRATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
  --TLVSEVETQGDLSRKIPTED 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 YILKVILKEPKPYFTSLLAFPT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: A. Anders Brockes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELETAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 anthro acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 28.23
Matches 40; Conservative
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                        STREET: 9410 Ke
                                                                                  -09-071-035-84
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US-09-071-035-82
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4 ILLLFLFGLVAVCAVHGIF----MDRLA----SKKLCADDECVYTISLA----SAQED 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.2%; Score 76; DB 4; Length 546; ilarity 28.2%; Pred. No. 0.36; Conservative 21; Mismatches 49; Indels
                                               COMPUTER: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS Version 6.2 SOFTWARE: ASCII TEXT CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/071,035 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: December 29, 2003, 16:11:49 Job time: 10.3221 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 YFPRNLVKEQRVYQEATKEVPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB365
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 amino acids
                                                                                                                                                                                                                                                                    FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-09-071-035-82
                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
Maryland
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                   COUNTRY: US
ZIP: 20850
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Title:

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RESULT 1
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-MODEL=frame+ p2n.model.-DEV=xlh
-Q=/Cgn2_1/USPTO_spool/US10019455/runat_29122003_160347_240/app_query.fasta_1.1770
-Q=/Cgn2_1/USPTO_spool/US10019455/runat_29122003_160347_240/app_query.fasta_1.1770
-Q=/Cgn2_1/USPTO_spool/US10019455/runat_29122003_160347_240/app_query.fasta_1.1770
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -FRANS=buman40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -FRANS=buman40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=Dlosum62 -FRANS=buman40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=Dlosum62 -FRANS=buman40.cdi -LIST=65
-UNITS=bits -NORM=Ext -HEAPSIZE=560 -WAIT -NORM=0 -MAXLEN=200000000
-USER=US10019455_@CGN_1 1_6034_@runat_29122003_160347_240 -NCPU=6 -ICPU=3
-NO MANAP -LIARGEQUERY -NGG SCORES=0 -WAIT -DSPEDGCK=100 -LONGLOG
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                             December 29, 2003, 16:11:59; Search time 2106.98 Seconds (without alignments) 2485.278 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                      676
1 MARILLLFLPGLVAVCAVHG.....RVYQBATKEVPTTDIDFFCE 128
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                           OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext C
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext
nelop 6.0 , Delext
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1: 9b ba: *
2: 9b_ha: *
3: 9b_htg: *
5: 9b_om: *
5: 9b_om: *
6: 9b_ph: *
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Maximum DB seq length: 2000000000
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em htg hum: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 384)

Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H.
Novel polypeptide and its DNA
Patent: WO 0102564-A 3 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD,YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,
                                                                                                                                                                                                                                                                                    Homo sapiens (human)
WO 0102564-A/3
11-JAN-2001
29-JUN-2000 WO 2000JP004278
30-JUN-1999 JP 99P 186718
YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
                                                                                                                                                                                                                                                                                                                                                                  I MOGI,
I VIKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
C CLANIS/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC
A61K38/17,
C A61K39/395,A61K49/16,A61P19/02,A61P19/08,A61K31/7088//(C12P21/
                                                                                            PAT 27-AUG-2002
    301 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 lleSerLeuAlaSerAlaGluAspTyrAsnAlaProAspCysArgPhelleAsnVal 60
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Mismatches:
Indels:
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                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 384
/organism="Homo sapiens"
/wol_type="genomic DNA"
/db_xref="taxon:9606"
a 70 c 106 g 109
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                                                                                          BD093103
Novel polypeptide and its DNA.
BD093103.1
GT:22638691
WO 0102564-A/3.
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                        9.67e-77
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Homo sapiens
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Best Local Similarity:
Query Match:
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SOURCE
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ORIGIN
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JOURNAL
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AUTHORS
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BD093103
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             PAT 31-JAN-2002
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Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Patent: JP 2011069994.A 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ilePheMetAspArgLeuAlaSerLysLeuCysAlaAspAspGluCysValTyrThr
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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        384 bp
Novel polypeptide and DNA thereof.
BD010802
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                                                                                                                                                                                                                 29-JUN-2000 JP 2000195911
                                                                                                                                                                              Homo sapiens (human)
JP 2001069994-A/3
21-MAR-2001
                                         BD010802.1 GI:18639175
JP 2001069994-A/3.
Homo sapiens (human)
Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genentech, Inc. (US)
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/mol_type="genomic DNA"
/db_txef="taxon:9606"
a db_txef="taxon:9606"
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                                                                              Sequence 71 from Patent W00208288. AX362311
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  218 AAAAAAGGCAGCAGCAGTCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 277
                                                         101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                            Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0200690-A 359 03-JAN-2002,
Genentech, Inc. (US)
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Batent: WO 0208284-A 359 31-JAN-2002,

Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard, Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US); Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US); Pan, James (US); Pan, Nicholas F. (US); Stephan, Jean-Philippe F. (US); Matanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
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Sequence 359 from Patent WO0208284.
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Sequence 359 from Patent WO0200690.
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AF243505 865 bp mRNA linear PRI 26-DEC-2000
Homo sapiens fibrocyte-derived protein (FDP) mRNA, complete cds.
AF243505
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NLVKEQRVYQEATKEVPTTDIDFFCE"
1145 c 207 g 255 t
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2 (bases 2 to 865)
Cohen-Salmon,M., Frenz,D., Verpy,E., Voegeling,S. and Petit,C.
Direct Submission
Submitsed (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue du Dr. Roux, Paris 7515, France
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, in vitro effect on the early differentiation of the inner ea
                                                                                                                                                                                                                Cohen-Salmon,M., Frenz,D., Liu,W., Verpy,E., Voegeling,S.
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J. Biol. Chem. 275 (51), 40036-40041 (2000)
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/organism="Homo sapiens"
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        405 ACGGATATTGACTTCTTCTGCGAG 428
                                                                                                                     AF243505.1 GI:11991843
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                                                                                                                                                Homo sapiens (human)
Homo sapiens
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NLVKEQRVYQEATKEVPTTDDIPCE"
147 c 25 g 259 t
1 (bases 1 to 846)
Robertson, N. G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C.
A novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping Genomics 66 (3), 242-248 (2000)
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2 (bases 1 to 846)
2 (bases 1 to 846)
Robertson,N.G., Heller,S., Lin,J.S., Resendes,B.L., Weremowicz,S., Bohis,C.S., Bell,A.M., Hudspeth,A.J. and Morton,C.C.
Direct Submission
Submitted (09-FEB-2000) Pathology, Brigham and Women's Hospital, Francis Street, Boston, MA 02115, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
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Mismatches:
Indels:
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45. 431
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Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.
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30-JUN-1999 JP 99P 186718
YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
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| CI2N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00,
| A61K38/17
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Novel polypeptide and its DNA.
BD093121
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WO 0102564-A/21
11-JAN-2001
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WO 0102564-A/21.
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C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
                                                                                                                                          PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
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188 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 247
                                                                            248 TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTATTTC 307
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PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19
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PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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Novel polypeptide and DNA thereof.
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JP 2001069994-A/21.
Homo sapiens (human)
Homo sapiens
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/trānslation="marillipplpglvavcavhgipmdrlaskkilcaddbcvytisla
Saqedynapdcrfinvkkgqqiyvyskivkengagbfwagsvygdgqdbmgvvgyfpr
Nlvkeqrvyqeatkevpttdidffce"
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/gene="MIAL"
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protein id="CAC7443.1"
db_xref="GI:12619173"
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/gene="MIAL"
/number=2
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/gene="MIAL"
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/gene="MIAL"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
PheTrpalaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe
                                                                        41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal
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                                                                                                                                  154 ATTICTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (21-MAX-1999) Rendtorff N.D., Department of Medical Genetics, Institute of Medical Biochemistry and Genetics, Blegdamsvej 3, 2200 Copenhagen N, DENMARK
Revised by author 03-AUG-1999
Related sequence: AJ252324 (Mus musculus mRNA)
Related sequences: AJ252224 to AJ252327 (GS:::anic sequence).
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/gene="MIAL"
/pene="MIAL"
/product="melanoma inhibitory activity like protein"</pre>
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Homo sapiens (human)
Homo sapiens
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| Organism="Homo sapiens"
| Mol_type="mRNA"
| db xref="texon:9606"
| chromosome="20"
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/tissue type="brain and /dev stage="fetal"
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1to,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
Novel polypeptide and its DNA
Novel polypeptide and its DNA
Patent: WO 0102564-A 6 11-3NA-2001,
TAKEDA CHEMICAL INDUSTRIES LTD,YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO
OGI, SHOIGH OKUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,
HIDEYUKI TANAKA
OS Mus Sp. (mouse)
PN WO 0102564-A/6
PD 11-JAN-2001
PP 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 384)
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a 68 c 111 g 107
                                                                                                                                                                                                                                                                    Novel polypeptide and its DNA.
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                                                                                                                                             121 ThrAspIleAspPhePheCysGlu 128
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WO 0102564-A/6.
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BD093106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
                                                                                                                           PAT 31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                     OS Mus sp. (mouse)
PN JP 200106994-A/6
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02
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Location/Qualifiers
1. 384
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/db_xref="taxon:10095"
98 a 68 c 111 q '''
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                                                                                                                   Novel polypeptide and DNA thereof.
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BD010805.1 GI:18639178
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86.72$
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Mus sp.
Mus sp.
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PC C12P21/0
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DB:
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ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValBroThr 120
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Ito, Y., Mishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.

Novel polypeptide and DNA thereof
Patent: JP 2001069994, A. 22 21-WAR-2001;
PAKEDA CHEMICAL INDUSTRIES LTD
PN JP 2001069994-A/22
PN JP 2010669994-A/22
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CIZNI5/09,A6IK38/00,A6IK45/00,A6IK48/00,A6IP9/00,A6IP19/02,
                                                21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr
                                                                                                                                                                                                       41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAenVal
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                                                                                                                                                                                                                                                                                                                                                                                                            249 TITIGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC
                           MetAlaArgIleLeuLeuLeuPeleuProGlyLeuValAlaValCysAlaValHisGly
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a 158 c 221 g 289
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Location/Qualifiers
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JP 2001069994-A/22.
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SHINICHI MOGI
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G01N33/53//
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/
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121 ATTICTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 180
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                            LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu
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                                                                                     AAGAAAGGCCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG
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Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25:
du Dr. Roux, Paris 75015, France
Location/Qualifiers
1. .9cganism="Mus musculus"
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//strain="mALBA"
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in vitro effect on the early differentiation
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Mus musculus
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AF243504.1 GI:11991841
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/gene="Fdp"
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/gene="Fdp"
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ORIGIN
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JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

JOURNAL

TITLE

FEATURES

gene

Score:

REFERENCE AUTHORS

TITLE

PAT 31-JAN-2002

308

RESULT 14 AF243504

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Length:

7.47e-67

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111 9 8 0 0		AlavalCysAlavalHi	GTTCTATGTGCCGGGCA	AspAspGluCysValTy	GATGAGGAGTGTGTCTA	AspCysArgPhelleAs		TyrSerLysLeuValLysGluAsnGlyAlaGlyGlu	ACAGAAAACGGAGCTGC	Υ.		TyrGlnGluAlaThrLysGluValProThr	GCCACCAAGGAGATCCC			
Matches: Conservative: Mismatches: Indels: Gaps:	(1-947)	MetAlaargileLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHi		1lePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr	:::	lleSerLeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPhelleAsnVal		ValTyrSerLysLeuVal	AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAACGGAGCTGGAAGA	TyrGlyAspGlyGlnAspGluMetGlyValValGl	TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGATTGTAGTTTTTTTT	3lnArgValTyrGlnGlw	CCCAGCAACTIGGTGAAGGAGCAGCGTGTTTTTTTCCAGGAGGCCACCAAGGAGATCCCAACC	31u 128	394 3AA 394	
602.00 93.75% 86.72% 89.05%	28) x BD010821	rglleLeuLeuLeu		et Asp Arg Leu Ala:		euAlaSerAlaGln	  GGCAAGAGCACAGG	LysLysGlyGlnGlnIleTyrVal	GCAGCAGATCTAT	ySerVal	TGGCAGTGTTTAT	ProArgAsnLeuValLysGluGlnArgVal	CTTGGTGAAGGAG	eAspPhePheCysGlu	ACGGATATTGACTTCTTCTGTGAA	
Score: Percent Similarity: Best Local Similarity: Query Match: DB:	US-10-019-455A-6 (1-128)	1 MetAlaAz	11 ATGGCAAC	21 IlePheMe	71 GTATTTAT	41 IleSerLe	131 ATTTCTCT	61 LysLysG	191 AAGAAAGC	81 PheTrpAlagl	251 TTTTGGGC	101 ProArgAs	311 CCCAGCAA	121 ThrAspil	371 ACGGATAT	
Score: Percent Sim. Best Local Query Match	US-10-	ò	qq	ζ	QQ	ò	οg	δλ	qq	δ	QΩ	ò	QQ	ò	qq	

Search completed: December 29, 2003, 19:57:14 Job time : 2110.98 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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December 29, 2003, 16:23:14; Search time 1324.28 Seconds (without alignments) 2349.180 Million cell updates/sec
                                                                                      US-10-019-455A-6
676
1 MARILLEFLEGLVAVCAVHG.....RVYQEATKEVPTTDIDFFCE 128
 nucleic search, using frame_plus_p2n model
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Xgapop 10.0, Xgapext C
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Sequence:
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    ı
OM protein
                                Run on:
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Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

22781392 segs, 12152238056 residues

Searched:

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10019455/runat_29122003_160347_254/app_query.fasta_1.1770
-DB=EST -QFWT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MAXIX=Dlosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -NORM=ext -HEAPSIZE=560 -MINLEN=0 -NAXIEN=200000000
-USER=USIO19455_GCGN 1 1 6063_Grunat_29122003_160347_254 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NEG SCORES=0 -MATIX -DEPELOCK=100 -LONGIGG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPORT=0.5 -FGAPOP=6

Database :

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## 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

ò	cription	0570035 qi	0564607 dilabo2	0568498 qi109c	0564134 gilld0	741 gil35£	Q564944 qi27q0	0568471 gi108g0	1549 BB6115	5637 gi42g03	3768 gi06c09	5932 gi73g09	11 gi37b12	5443 144645	2622 BY2	7343 gi88d08	5179 gi32a07.	241 CH3#	783 GILL4IU 54 AT.925854	776 gi69	227 gi01a05	965 Mus m	928	24 df53	404	7 4	4 (	0 UI-E-EJO	2734	8261	1778	1561 AGENCOU	STATESTO	BG/66328 602/39U14	102 802/3941	3 2100h05	724 154861	3401 UI-H-CC	09768 UI-R	527297 nq68q01.	39750 nadi3c1	G_TIT COOOACC
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## ALIGNMENTS

RESULT 1 BQ570035	
rocns	BQ570035 398 bp mRNA linear EST 19-, HN-2002
DEFINITION	gil43bl0.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
	clone qi143b10 5', mRNA sequence.
ACCESSION	BO570035
VERSION	BQ570035.1 GI:21473352
KEYWORDS	BST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Butheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus
REFERENCE	1 (bases 1 to 398)

JOURNAL

FEATURES

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reptinentium was carefully dissected out of the modiolus.

Total RNA was extracted using the micro Pasttrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library constructions. Reverse transcription and
library constructions. Reverse transcription and
library constructions. Reverse transcription and
digapack III Gold Cloning kit (Gatalog # 237612), both
from Strategene | 137211, Stratagene) and Uni-Zap KR
Gigapack III Gold Cloning kit (Gatalog # 237612), both
from Strategene | 137211, Stratagene) and Uni-Zap KR
Gigapack III Gold Cloning kit (Gatalog # 237612), both
from Strategene | 137211, Stratagene) and Uni-Zap KR
Gigapack III Gold Cloning kit (Gatalog # 237612), both
from Strategene | 137211, Stratagene)
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid Oilgo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
Moloney mutrine leukemia virus reverse transcribed using
Moloney mutrine leukemia virus reverse transcribed with
BONA was blunt ended with Pfu DNA polymerase. Iigated with
BONA was blunt ended with Pfu DNA polymerase, ligated with
BONA was blunt ended with Pfu DNA polymerase, ligated with
BONA was blunt ended with Pfu DNA polymerase, ligated with
BONA was blunt ended with Pfu DNA scater than 400bp and 1000
orecompinates Stratagene's Spin-1000 (Clontech, Pala Alto, CA)
columns to enrich for cDNA was then directionally ligated to
the Uni-Zap KR vector, which had been predigested with
BCOR I and Xho I. The phagemid was packaged with Gigapak
III Gold and, upon titration on XLI Blue MRF' cells, the
Vield of the phage library was estimated to be 11,100,000
recombinates. Stratagene's ExAssist Interference
resistance helper phage (catalogue # 211203) was adopted
to rescue plasmid DNA from the phages. Upon plating of the
rescued library, individual cDNA was estimated endered and
purified from the phage library was planting to be
combinate Stratagene's ExAssist Interference
sel
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/dev_stage="Post natal day 5 to 13"
/dev_stage="Post natal day 5 to 13"
/clocallb="Mouse Organ of Corti cDNA pBluescript:
/note="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P3. After Xilling animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Concert96 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the CDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGAC) and 25% strength BigDye terminator sequencing chemistry (Applied Bisystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Poster
                                              gene expression in the mouse Organ of Corti at the
                                                                                                                                                                                          Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: kacharb@nidcd.nih.gov
Plate: 143 row: b column: 10
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol type="mRNA"
/strain="BALB/C"
/db xref="taxon:10090"
/clone="gi143b10"
                                              EST analysis of conset of hearing Unpublished
AUTHORS
TITLE
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BQ564607 488 bp mRNA linear EST 19-JUN-2002 gil9h02.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gil9h02 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                 City, CA). The frequency distribution of the library is so follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 488)
Kachar, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kachar,B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
                                                                                                                                                                                                                                                                                                                                                                 13 ATGGCAAGGATATTGATTCTTTTTGCTTGGGGGCCTTGTGGTTCTATGTGCCGGGCATGGT
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                                                                                                                                                                                                                                                                                                                                              1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly
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Mismatches:
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Plate: 19 row: h column: 02
Seg primer: M13RP1 reverse primer (ABI)
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Mismatches: Indels:

86.72%

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KEYWORDS
SOURCE
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BQ568498
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                                                                                                                                                                                   /dex_male an in semale / factor male day 5 to 13" / factore libe whose organ of Corti, ODN applusecript; The organ: Organ: Organ of Corti, Vector: pallusscript; The organ: Organ: Organ of Corti, Vector: pallusscript; The organ: Organ: Organ of Corti, Vector: pallusscript; The organ of Corti, IOCN was fine disascred from a total of 386 or according to manual part of the manual organial organ of Corti, OCN was fine disascred from a total organ of Corti, IOCN parages from post-natal (p) day 5; 72 from P10 or according to manual part of the cochlea was chipped away stria vascularis and spiral ligament were removed and the bony use removed and opened in Leibowitz medium. The bony large light of the cochlea was chipped away stria vascularis and spiral ligament were removed and the sensory. Total RNA was extracted using the micro Fasticrack kit (catalog # K1951-02; Invitrogen, Carlabad, CA), according to manutacturer's instructions Reverse transcription and library construction were carried out with the Unit-Zap XR Grandspare (IA Jolla, CA, MS), according to manutacturer's instructions Briefly: 1.5 ug mRNA was blunt eached with Catalog # 237211, Stratagenel and Unit-Zap XR Grandspare (IA Jolla, CA, MS), according to manutacturer's instructions Briefly: 1.5 ug mRNA was blunt ended with Pub MA polymerase and transcribed using Myoloney with XNO I The coDNA was sequentially size fractionated vore Pharmacia size Septon (Hanamacia, Upagala, Swaeden) and Clonnar to enrich for CONNA grater than 400p and 1000 hower Pharmacia and Clonnar Size Septon (Hanamacia, Upagala, Swaeden) and Clonnar to enrich for CONNA grater than 400p and 1000 hower Pharmacia upages to manutactively. The coDNA was then directionally ligated to the phage library was estimated to be 11,100,000 resident of the phage library was estimated to be 11,100,000 resident of the phage library was estimated to be 11,100,000 resident below to the combinants. Stratagene's Exaragene's Exaragene's Exaragene's Exaragene's Exaragene's Exaragene's Exaragene's Exaragene's 
                                                      organism="Mus musculus"
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                                                                                                                                                                            'sex="male and female"
         Location/Qualifiers
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Conservative:

4.3e-70 602.00 93.75%

Percent Similarity:

Alignment Scores: Pred. No.:

BASE COUNT

ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 TTTTGGGCTGGCAGTGTTATGGTGACCACCAGGATGAGATGGGGAATTGTAGGTTATTTC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
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                                                                                                                                                                                                                                                                                                                                                         99
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 514)
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Structural Cell Biology
National Institute of Deafness and other Communication Disorders
National Institute of Deafness and other Communication Disorders
101-402-159
Exa: 301-402-1765
Email: Racharbenided.nih.gov
Plate: 109 row: c column: 02
Seq primer: M13RP1 reverse primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                7 AIGGCAAGGATATTGATTCTTTTGCTTGGGGCCTTGTGGTTCTATGTGCCGGGCATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPhe1leAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu
                                                                                                                                                                                                                                                            MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                        IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr
800
                                                                                                                                                              US-10-019-455A-6 (1-128) x BQ564607 (1-488)
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Mus musculus
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EST.
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from 66, 60 from P7, 46 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P8, 10 from P
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BASE COUNT

8 8

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/sex="male and female"
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/dev stage="Post natal day 5 to 13"
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/clone lib="Mouse Organ of Corti; Vector: pBluescript: The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fastrack kit (catalog # K1533-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR digapack III Gold Cloning kit (catalog # 237612), both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQD64134 514 bp mRNA linear BST 19-JUN-2002 gilld01.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gilld01 5', mRNA sequence.
                                                                                                                                                                                                                   81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
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                                                                                                                                                                                                                                                                                                                                                         305 CCCAGCAACTIGGTGAAGGAGCAGCGTGTAIACCAGGAGGCCACCAAGGAGATCCCAACC 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 534)
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Structural Cell Biology
Artional Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
                            245 TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC
                                                                                                            61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu
                                                                                                                                                               185 AAGAAAGGCAGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG
IleSerLeuAlaSerAlaGinGluAspTyrAsnAlaProAspCysArgPheIleAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: kacharb@nidcd.nih.gov
Plate: 11 row: d colum: 01
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ThrAspileAspPhePheCysGlu 128
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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  41
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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COMMENT
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from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mENA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an XAD 1 site. First strand synthesis was primed with the linker- primer and transcribed using Moloney mutrine leukemia virus reverse transcriptese (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase, and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with ECOR I adapters in the presence of ligase and digested with ECOR I adapters in the presence of ligase and digested over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for CDNAs greater than 400bp and 1000 bp, respectively. The CDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with ECOR I and XND or The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF. cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual CDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTS from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CMCGMAAGCTMAGCTMAGCT) and 25% strandth Pichna PDNA clones were generated with the universal M13 reverse primer (CMCGMAGCTMAGCTMAGCT) and 25% strandth Pichna PDNA clones were generated with the concert96 miles and contained with the contained with the concert96 miles were generated with the contained with the contained with the contained with the concert96 miles and contained with the contained with the contained with the contained with the contained with 
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Length:
Matches:
Conservative:
Mismatches:
Indels: 602.00 93.75% 86.72% 89.05% 4.96-70 Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: ORIGIN

155

SASE COUNT

534 111 9 8 0 Gaps: Query Match: DB:

US-10-019-455A-6 (1-128) x BQ564134 (1-534)

STATTATGGATAAACTTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTGTCTTTATCT 122 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100 9 1 MetAlaArglleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 63 123 81 a g ò à g à g ઠે

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/Gav_stage="Post natal day 5 to 13"
/Glowe lib="Mouse Organ of Corti; Vector: pBluescript"
/Glome lib="Mouse Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6: 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
cappule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
cappule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
cappule of the cochlea was cartiad out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
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to manufacturer's instructions. Reverse transcription and
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Gigapack III Gold Cloning kit (catalog # 237612), both
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manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker- primer and transcribed using
Molloney murine leukemia virus reverse transcriptes (MMLV-RT) and S-methyl GTP. The second strand synthesis was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
ECOR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Clontech, Paplo Alto, CA)
and Clontech Chroma Spin-1000 (Clontech, Paplo Alto, Contended of Clontech, Paplo Alto, Clontech, Paplo Alto, Clontech
                                                                                                                                                                                                                                                                                                                    560 bp mRNA linear EST 19-JUN-2002 gil35f01.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gil35f01.5', mRNA sequence.
BQ569741
BQ569741.1 GI:21473058
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 560)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 135 row: f column: 01
Seg primer: M13RP1 reverse primer (ABI).
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/clone="gil35f01"
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1. .560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
Mus musculus
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/strain="BALB/c"
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Unpublished
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
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BQ569741
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FEATURES

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE JOURNAL

FEATURES

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columns to enrich for CDNAs greater than 400bp and 1000 bp, respectively. The CDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with Gigapak ECOR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance halper phage (catalogue # 21203) was adopted to resistance halper phage (catalogue # 21203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, and growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concerts6(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTS from the 5' end of the CDNA clones were generated with the universal MI3 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Poster City, CA). Sequencing reactions were performed on MY Terrad thermal cyclers (MN Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Poster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 43% of genes are present in GenBank and have know function; 13% are uncharacterized BSTS and 1 others
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Alignment Scores: 5.25e-70 Length: 560 Score 602.00 Matches: 111 Scorett Similarity: 93.75% Mismatches: 8 Est Local Similarity: 86.72% Mismatches: 8 Query Match: 13 Gaps: 0

BASE COUNT

US-10-019-455A-6 (1-128) x BQ569741 (1-560)

PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluWetGlyValValGlyTyrPhe 100 126 ATTICICIOGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 185 186 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAACGGAGCTGGAGA 245 9 80 65 21 IlePheMetAspArgLeuAlaSerLysLysLysLeuCysAlaAspAspGluCysValTyrThr 40 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 6 Areschassararrearreirrecritesessecritereserarerarersecesseares 61 81 ò a à 엄 δ ద ò S S ò d

8 8 8

RESULT 6 BQ564944 LOCUS BC

BQ564944 608 bp mRNA linear EST 19-JUN-2002 ION g127g09.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone g127g09 5', mRNA sequence.

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BDS66494 GI:21468261
BDS66494 GI:21468261
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Miss musculus (house mouse)
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us-10-019-455a-6.rst

FEATURES Source

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Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MT Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
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gil08g04.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
Elone gil08g04 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Contact: Kachar,B.

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National Institute of Deafness and other Communication Disorders 50/4445 South Drive, NIH, Bethesda, MD 20892-8027, USA National Institute of Deafness and other Communication Disorders 50/4445 South Drive, NIH, Bethesda, MD 20892-8027, USA Tal: 301-402-1559
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 696)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H., Kouda, D., Shibata, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Sano, H., Sasaki, D., Shibata, K., Sano, H., Sasaki, T., Tagawa, A., Takabani, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN, Mouse, ESTS (Arakawa, T., et al. 2001)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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ESTs and 20% are unidentified.
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URL:http://genome.gsc.riken.go.jp/
12% are uncharacterized
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 157-1711 (2000)

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Func. Genomics 2 pre, L72-L66 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
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Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new agai. K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Ratahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
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head"
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 bp mRNA linear BST 19-JUN-2002
gi42g03.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
Glone gi42g03 5', mRNA sequence.
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204 Angalanggecangangtrangtrangtrangkangkanangalangkangkang 263
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
                                                                                       LyslysglyglnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu
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Seg primer: M13RP1 reverse primer (ABI).
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Fax: 301-402-1765
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reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney wurine lettemta virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Ptu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The CDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for CDNAs greater than 400pp and 1000 bp. respectively. The cDNA was then directionally ligated to the UnizAP X vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the vectored library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlabad, CA) as instructed by the manufacturer. ESTB from the 5' end of the CDNA clones were generated with the universal MI3 reverse primer (CAGAAAACAGCTATGACC) and 25% strength BigDye terminator sequencing reactions were performed on MT Terrad thermal cyclers (MP Research, Walthem, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Poster City, CA). The frequency distribution of the library is as follows: 72% of genes have I copy, 14.3% 2, 12% 3.10; 1.4% 11-50 and o.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have high in GenBank by our open function; 23% have the sincharacterized ESTS and 20% are unidenti
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85.94%
88.31%
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Best Local Similarity:
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120

254 TITIGGGCTGGCAGTGTTATGGTGACCACCAGGATGAGAATGGGAATTGTAGGTTATTTC 313

101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr

194 AAGAAAGGGCAGGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG

LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu

61

81

80

134 ATTICICIGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 193

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EST 19-JUN-2002
                                                                                G84 bp mRNA linear EST 19-JUN-2002
g106c09.71 Mouse Organ of Corti cDNA pBluescript Mus musculus CDNA
EQ563768
314 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 373
                                                                                                                                                                                                                                                EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 684)
                                                                                                                                                                                                                                                                                                             National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA Tel: 301-402-1765
Fax: 301-402-1765
Email: kacharb@nidcd.nih.gov
Plate: 06 row: column: 09
Seq primer: MI3RPI reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                              1. .684
/organism="Mus musculus"
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                         121 ThraspileAspPhePheCysGlu 128
                                      374 ACGGATATTGACTTCTTCTGTGAA 397
                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
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EST.
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Structural Cell Biology
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the Uni-ZAP XR vector, which had been predigested with BCOR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XII Blue MRF. cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual CDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96 (TM) plasmid purification kit (Invitrogen, Carlabad, CA) as instructed by the manufacturer. ESTS from the 5' end of the CDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing reactions were performed on M7 Tetrad thermal cyclers (M1 Research, Waltham, M2), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72 of genes have I copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-16. As to gene function, 45% of genes are present in Genbank and have know function; 23% have whits in Genbank but do not have assigned function; 12% are uncharacterized ESTS and 20% are unidentified."
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gl73g09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gl73g09 5', mRNA sequence.
BQ566932.1 GI:21470249
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us-10-019-455a-6.rst

ORGANISM

KEYWORDS SOURCE

AUTHORS TITLE JOURNAL

FEATURES

REFERENCE

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                                                                                                                                                                        EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
Unpublished
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 409)
                                                                                                                                                                                                                                                                                                                                                            Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Fal: 301-402-1765
Email: kacharb@midcd.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 73 row: g column: 09
Seg primer: M13RP1 reverse primer (ABI).
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/clone="gi73g09"
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Mus musculus (house mouse)
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strength BigDye terminator sequencing chemistry (Applied Biosystems, Poster City, CA). Sequencing reactions were performed on MJ Terrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25
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Structural Cell Biology
National Institute of Deafness and other Communication Disorders
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                                                                                                        Maltham, Ma), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Blosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
   South Drive, NIH, Bethesda, MD 20892-8027, USA
50/4249 South L._
Tel: 301-402-1599
Fax: 301-402-1765
Email: kacharb@nidcd.nih.gov
Plate: 37 row: b column: 12
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
_ 490
                                                                                              db xref="taxon:10090"
                                                                             'mol_type="mRNA"
'strain="BALB/c"
                                                                                                      clone="gi37b12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191
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BASE COUNT

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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Bovinae, Bos.

1 (bases 1 to 52)

Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T., Casas, E., Wray, J. E., White, J., Cho, J., Pahrenkrug, S. C., Bennett, G. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-McKom, C. G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J. W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsnLeu 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VallysGluGlnArgValTyrGlnGluAlaThrLysGluValProThrThrAspIleAsp 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 IIGAITCTTITGTTITGGGGCCTICGGGGTICTAIGTGCGGGCAIGGGGTATTAIGGAT 158
                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                          GlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrpAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                    5 LeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGlyIlePheMetAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144645 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
BE236443
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                                            Conservative:
Mismatches:
Indels:
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              Length:
Matches:
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459 TTCTTCTGGGAA 470
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Fax: 402 762 4390
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                                                                       Best Local Similarity:
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                                                   Percent Similarity:
Alignment Scores:
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BY233622 RIKEN full-length enriched, adult inner ear Mus musculus
cDNA clone F930026J20 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 365)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 --------GTCTATGGCAATCAGTCTGAGGATGAAATGGGAACCGTGGGTTAT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 PheproArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValPro 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LyslysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 PheTrpalaGlySerValTyrGlyAsp---GlyGlnAspGluMetGlyValValGlyTyr 99
                                                                                             /organism="Bos taurus"
/mol type="mRNA"
/db_xref="taxna"
/db_xref="taxna"
/lab_host="pooled"
/lab_host="DH10B"
/clone lib="MARC 4BOV"
/note="vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue From day 20 and day 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetalaarglleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly
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102
6
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Matches:
Conservative:
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FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: S4 row. c column: 18
Seq primer: ATTTAGGTGACACTATAG
Location/Qualifiers
                                                                                                                                                                                                                                                         126 g
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Mus musculus
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83.72%
79.07%
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Deackerhush, J. Schriml, N.W. Kanasin, A. Wittada H., Baralov, S.

Deackerhush, J. Schriml, N.W. Kanasin, A. Wittada H., Baralov, S.

A. Frezer, K. S., Casterelland, T., Garibold, M., Gissi, C., Godzik, A.,

A. Gongh, J. Carimond, S. Casterelland, M. H., Gissi, C., Godzik, A.,

A. Gongh, J. Carimond, S. Casterelland, B. H. Gissi, C., Godzik, A.,

A. Gongh, J. Carimond, S. Casterelland, B. H. Kansawa, Y. Kedisterki, R. W.,

A. Ring, E.D. Kanala, A. Kawaji, H. Kansawa, Y. Kedisterki, R. W.,

A. Ring, E.D. Kanala, A. Kawaji, H. Kansawa, Y. Carimond, J. Randaland, B. B. Z. Miland, A. Kanala, M. Philats, P. Philas, P. Denins, J. C., Sengle, C. A. Seto,

Randandanden, S. Bavasi, T. Reed, J. C. Reed, D. J. Red, J. Red, J. Red, J. C. Red, D. J. Red, J. R. Randala, R. K. Barala, M. Westerston, R. Mangi, M. Mangawa, R. Schnider, C. Sengle, C. A. Seto,

R. D. Tonia, M. Wester, R. Wangari, T. Wall, K. Kanaji, J. Aisawa, R. M. Mangawa, M. Kanala, M. Westerston, R. Mangi, J. Mangawa, R. M. Mangawa, J. Wandish, R. Wangi, J. Mangawa, R. M. Mangawa, J. Wandish, R. Wall, K. Kanai, J. Mangawa, R. K. Shingawa, A. Wandish, R. Wandish, M. Wall, K. Sanai, D. Shibata

K. Shingawa, A. Wandish, M. Wandawa, M. Sanak, R. Sanai, D. Shibata

K. Shingawa, A. Wandish, M. Wandawa, M. Sanak, M. Sanak, M. Sanak, M. Sanak, M. Mangawa, M. Wandish, M. Wandawa, M. Wandish, M. Wandawa, M. Wandish, M. Wandish, M. Mangawa, M. Wandish, M. Wandawa, M. Wandish, M. Wandish, M. Wandish, M. Wandawa, M. Wa
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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ567343 604 bp mRNA linear BST 19-JUN-2002 gi88408.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi88408 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                    PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
                                                                                                                                                                                                                      204 AAGAAAGGGCAGCAGCATCTATGTTTACTCCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                        264 TTTGGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
                                                                                                                                                                                                                                                                                                                       203
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 604)
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                                                                                                                                                                                                                                                                                                                                                       LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kachar, B. Structural Cell Biology Structural Cell Biology National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
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/dev.stage="Post natal day 5 to 13"
/clone lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti, Vector: pBluescript; The
                                                                                                                                                                                                                                                                                        IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal
                                                                                                                                                                                                                                                                                                           24 ATGGCAAGGAIATTGATTCTTTTGCTTGGGGGCCTTGTGGTTCTATGTGCCGGCATGGT
                                                                                                                                                         MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCC 365
          365
97
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                         Matches:
Conservative:
Mismatches:
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Fax: 301-402-1765
Email: kacharb@nidcd.nih.gov
Plate: 88 row: d column: 08
Seg primer: MI3RPI reverse primer (ABI).
Location/Qualifiers
             Length:
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                                                                                           Gaps:
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/clone="gi88d08"
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/strain="BALB/c"
                                                                                                                           US-10-019-455A-6 (1-128) x BY232622
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92.11%
85.09%
75.74%
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                                              Percent Similarity:
Best Local Similarity:
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Alignment Scores:
Pred. No.:
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                                                                             Query Match:
DB:
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             No.:
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BQ567343
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TITLE
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COMMENT
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organ of Corti (OC) was fine dissected from a total of 386 CC as follows: 102 samples from post-natal (P) day 5: 72 from P6: 60 from P7: 46 from P6: 18 from P9: 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spital ligament wer removed and the sensory and spital ligament were removed and the sensory and spital ligament were removed and the sensory and spital ligament were removed and the sensory of catalog # K1539-02; Invitrogen, Carlado, CAI, according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Unit-Zap XR vector kit (catalog # 237211, Stateagen) and Unit-Zap XR vector kit (catalog # 237211, Stateagen) and Unit-Zap XR vector kit (catalog # 237211, Stateagen) and Unit-Zap XR vector kit (catalog # 237211, Stateagen) and Unit-Zap XR vector kit (catalog # 23721, Stateagen) and Unit-Zap XR vector kit (catalog # 23721, Stateagen) and Unit-Zap XR vector kit (catalog # 23721, Stateagen) and Unit-Zap XR vector kit (catalog # 237612), both from Stateagen (La Jolla, CA, USA), according to manufacturer's instructions. Britely: 1.5 ug mana was primed with the linker- primer and transcribed using a hybrid oligo-180 dusing a whyrid oligo-180 dusing a whyrid oligo-180 dusing with Xho. I The condensates and digested with Row I The Colle with Pfu DNA polymerase, ligated with Book I adapter of the DNA polymerase and digested over Pharmacia Size Sept00 (Pharmacia, Uppsaa, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNA sequentially size fractionally ligated to the Unit Animacia, Statesgened with Animacia, Suratagened search place of the phage library was estimated to be 11,100,000 recombinants. Stratagened search place of the phage library was estimated or bescue plasmid DNA from the Phages. Upon plating of the phage library and search pl strength BigDye tearninator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MT Terrad thermal cyclers (MM Research, Faltham, MA), and analyzed on 3700 automated capillary sequencers using Pob's polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 7% of genes have 1 copy, 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

0004400 004 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 1.37e-56 502.00 96.00% 92.00% Percent Similarity: Best Local Similarity: Query Match:

US-10-019-455A-6 (1-128) x BQ567343 (1-604)

49 AspTyrAsnAlaProAspCysArgPhelleAsnValLysLysGlyGlnGlnIleTyrVal 68

0.7	<b>~</b>	30	90	0 #	88	00
 FATGTT 1	Tyrgly 8	rarddr 1	Slugln 1	SAGCAG 2	CysGlu	rergaa
	69 TyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrpAlaGlySerValTyrGly 88	121 TACTCCCAAGCTGGTAACAGAAAACGGAGCTGGAGAGTTTTGGGCTGGCAGTTTTAGGCTTATATGGT 180	89 AspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsnLeuValLysGluGln 108	181 GACCACCAGGATGAGGAAATTGTAGGTTATTTCCCCAGCAACTTGGTGAAGGAGCAG 240	109 ArgValTyrGlnGluAlaThrLysGluValProThrThrAspIleAspPhePheCysGlu 128	241 CGTGTATACCAGGAGGCCACCAAGGAGATCCCAACCACGGATATTGACTTCTTCTTGTGAA 300
  aagggca	rpalagi	GGGCTGG	rgAsnLe	GCAACT	Aspileas	SATATTG
GICAAG	GluPhe1	GAGTTT	PhePro	TTCCCC	ThrThr	Accacc
CATCGAT	yAlaGly	SAGCTGG	1GlyTy	raggita	luValPro	AGATCCC
 rGTAGGTT	31uAsnG	SAAAACG	31yvalva	GAATTG	ThrLysG	ACCAAGG
CCCAGAC	uValLys(	GGTAACA	pg]uMet	TGAGATG	nGluAla	GGAGGCC
	erLysLe	CCAAGCT	lyGlnAs	ACCAGGA	alTyrGl	TATACCA
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Search completed: December 29, 2003, 22:00:44 Job time : 1330.28 secs

us-10-019-455a-6.rng

Run on:

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Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=CQGT2_1VGPTO_SPOOlUG1955/runat_29122003_160347_230/app_query.fasta_1.1770
-Q=CQGT2_1VGPTO_SPOOlUG1019455/runat_29122003_160347_230/app_query.fasta_1.1770
-LODEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODEL=LOCAL_OUTPRPT=pc -NOFM==ext - HRAPSIZ=500 -MINICENE0 - MAXLEN=200000000
-USRE=USR10019455_@CGN 1 1 0 @runat_29122003_160347_230 -NCPU=6 -ICPU=3
-NO MMAR -LARGEQÜERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LOMGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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(c) 1993 - 2003 Compugen Ltd.
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Ygapop 10.0 , Ygapext (
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution

SUMMARIES

Description	Human MLP nucleoti 5.17883 Human growth regul 1.25741 Human growth regul 1.25741 Human growth regul 1.25741 CDNA encoding huma 1.25741 Human growth regul 1.259068 Human growth regul 1.259068 Human growth regul 1.259068 Human growth regul 1.259079 Human growth regul 1.259079 Mouse MLP nucleoti 1.259079 Mouse MLP nucleoti 1.259079 Mouse MLP nucleoti 1.259079 Mouse MLP nucleoti 1.259079 Mouse MLP nucleoti 1.259079 Mouse MLP nucleoti 1.259079 Mouse MLP nucleoti 1.259079 Mouse MLP nucleoti 1.259079 Mouse MLP nucleoti 1.259079 Mouse MLP nucleoti 1.259079 Mouse MLP nucleoti 1.259079 Mouse MLP nucleoti 1.259079 Mouse MLP nucleoti 1.259079 Mouse MLP nucleoti 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Meanoma inhibitor 1.259079 Me	ID NO:
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standard; cDNA; 387

(first entry)

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26-FEB-2002
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                                                                                                                                                                                                                                                                    The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis.

AAF59063 to AF59099 and AB69122 to AAB69132 represent sequences used
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                                                                                                                                                                                   Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                                                                                 Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetAlaArgileLeuLeuLeuDheLeuDroGlyLeuValAlaValCysAlaValHisGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleSerLeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPheIleAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTICICIGGCIAGIGCICAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe
                                                                                                                 Noguchi Y,
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Matches:
Conservative:
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                                           29-JUN-2000; 2000WO-JP04278.
                                                                    99JP-0186718
                                                                                            (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                   Ogi K,
                                                                                                                                                    WPI; 2001-159271/16.
P-PSDB; AAB69123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity:
                                                                                                                   Nishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
WO200102564-A1
                                                                    30-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                     11-JAN-2001
                                                                                                                               Tanaka H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated novel secreted polypeptide (I) and polynucleotide (II). (I) and (II) are useful for treating cancer, discases, wound healing disorder, infections, haematopoietic disorders, inflammatory disorders, infertility, neurological and psychiatric diseases, cardiovascular diseases, respiratory diseases, renal diseases, or gastrointestinal diseases. These may also be used to expression, production, function and/or metabolism of the genes, as vaccines for inducing immunological response in a mammal, and in screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. The polypeptides can be used as immunogens to produce antibodies immunospecific for the polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New secreted proteins or polypeptides, useful for treating e.g. cancer, autoimmune diseases, wound healing disorder, infections, haematopoietic disorders, inflammatory disorders, infertility, cancer
                                                                       antiinflammatory; neuroprotective; nephrotropic; cardiovascular; human; cancer; autoimmune disease; wound healing disorder; infection; haematory-order; infammatory disorder; infertility; neurological disease; psychiatric disease; cardiovascular disease; respiratory disease; cardiovascular disease;
                                                     protein; cytostatic; immunosuppressive; vulnerary; vaccine;
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/*tag= a
/product= "Human secreted protein"
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DNA encoding novel secreted protein #12.
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 44; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-APR-2000; 2000US-196603P. 24-APR-2000; 2000US-199417P.
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signature analysis, and Sanger sequencing techniques. This expressed sequence tag was used in the assembly of a full-length converse sequence (see AAH26343) encoding a novel human growth regulatory-like polypeptide (GRLP, see AAB2671). The GRLP belongs to the same protein family as growth regulatory proteins, compand melanoma derived growth regulatory proteins precursor (64% similarity and 45% identity over 111 amino acids) or melanoma inhibitory activity, cattle cartilage-derived retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid-sensitive protein in the prophylaxis, treatment (including gene therapy) and diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma cell
                                                                                                                                                                                                                                                                                                                                                                  growth and tumours, including neuroectodermal tumours such as gliomas. The polynucleotides can also be used to design probes and primers, for chromosome and gene mapping, in the recombinant production of protein, in the generation of antisense, ribozyme and peptide-nucleic acid molecules, and to produce transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 426 BP; 119 A; 73 C; 113 G; 120 T; 1 other;
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                                                      METALAARGILELEULEULEUPHELEUPROGIYLEUVALALAVALCYSALAVALHISGIY
                                                                                                                                                             121 ATTICICIGECTAGIECTCAAGAATTATAATGCCCCGGACTGTAGATTCATTAACGTT
                                                                                                                                                                                                                                                                                                                                                                        LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                         181 AAAAAAGGCCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe
                                                                                                                                                                                                                                                                    41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Growth regulatory-like polypeptide; human; cartilage; melanoma; neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ပ်
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT,
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          US-10-019-455A-6 (1-128) x AAS17583 (1-387)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH26341 standard; cDNA; 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-2001; 2001WO-US02455.
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ID AAH1

ID AAH1

ID AAH1

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120
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                                                                                                                                                                                                                                               79 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGGTGTCTATACT 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, angiogenesis, PRO protein, cardiovascularisation, wound; cancer, atherosclerosis, cardiac hypertrophy, gene therapy, endothelial disorder, cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                       259 TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGAGAGGGGTTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC
                                                                                                                                                                                                                           21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr
                                                                                                                                                                                                                                                                                               41 IleSerLeuAlaSerAlaGluAspTyrAsnAlaProAspCysArgPheIleAsnVal
                                                                                                                                                                                                                                                                                                                                139 ATTICICIGGCIAGIGCICAAGAAGATIATAATGCCCCGGACTGIAGATICATTAACGIT
                                                                                                                                                                                                                                                                                                                                                                    61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.
   Conservative:
Mismatches:
Indels:
   Length:
Matches:
                                                                                                                      US-10-019-455A-6 (1-128) x AAH26341 (1-426)
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9.05e-87
676.00
100.00%
100.00%
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us-10-019-455a-6.rng

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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atheroselarosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; angiogenesis, cardiant, cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerctic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertropiy, atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; theumatoid arthritis; myocardial infarction; thromophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 ATTCTCTGGCTAGTGCTCAAGAATTATAAATGCCCCGGACTGTAGATTCATTAACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGlyMetGlyValValGlyTyrPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA
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useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                     521
0 0 0
0 0
                                                                                                                                                                                                                                                  Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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676.00
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                                                          Claim 1; Fig 359; 567pp;
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Best Local Similarity:
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J, Hillan KJ, Marsters SA, Pan J,
CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2001; 2001WO-US06520.
01-MAR-2001; 2001WO-US06666.
09-MAR-2001; 2001US-080206.
14-MAR-2001; 2001US-0808689.
22-MAR-2001; 2001US-0816744.
05-APR-2001; 2001US-0828366.
10-MAY-2001; 2001US-0854280.
                                                                                                                                                                              20-JUL-2000; 2000US-219556P.
25-JUL-2000; 2000US-220624P.
28-JUL-2000; 2000US-220664P.
28-JUL-2000; 2000US-220664P.
17-AUG-2000; 2000US-222695P.
17-AUG-2000; 2000US-0643657.
23-AUG-2000; 2000WG-US23528.
24-AUG-2000; 2000WG-US23328.
15-SEP-2000; 2000US-230978P.
15-SEP-2000; 2000US-000000P.
                                                                                                                                                                                                                                                                                                                                                                          18-SEP-2000; 2000US-0665350.
24-OCT-2000; 2000US-242922P.
08-NOV-2000; 2000WO-US30952.
10-NOV-2000; 2000WO-US30953.
01-DEC-2000; 2000WO-US30973.
20-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.
22-JAN-2001; 2000US-07676609.
                                                                                                                                                                                                                                                                                                      2000WG-US23328.
2000US-233978P.
2000US-0664610.
2000US-0665350.
2000US-0665350.
2000US-0709238.
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25-WAY-2001; 2001US-0866034.
25-WAY-2001; 2001WG-US17092.
30-WAY-2001; 2001US-0870574.
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20-JUN-2001; 2001WO-US19692.
28-JUN-2001; 2001WO-US00000.
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                                                                                                                                                     09-JUL-2001; 2001WO-US21735
              antiarteriosclerotic; gene;
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
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GERRITSEN M E.
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STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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FERRARA N.
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                                                                                 WO200208284-A2
                                                 Homo sapiens
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                                                                                                                    31-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH) (BAKE/) (FERK/) (GERR/) (GERR/) (GODD/) (GODD/) (GURN/) (GURN/) (GURN/) (HILL/) (HILL/) (MARS/) (PAON/)
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337

277

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23-JUN-2000; 2000US-213637P.
26-JUL-2000; 2000US-219556P.
25-JUL-2000; 2000US-220664P.
28-JUL-2000; 2000US-220664P.
28-JUL-2000; 2000US-220664P.
29-JUL-2000; 2000US-US-22669P.
17-AUG-2000; 2000US-US-22669P.
17-AUG-2000; 2000US-US-2369P.
18-SEP-2000; 2000US-0664610.
18-SEP-2000; 2000US-0664610.
18-SEP-2000; 2000US-0669SP.
18-SEP-2000; 2000US-0669SP.
18-SEP-2000; 2000US-069SP.
18-SEP-2000; 2000US-069SP.
18-SEP-2000; 2000US-069SP.
19-SEP-2000; 2000US-0709238.
01-DEC-2000; 2000WO-US-308F.
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2001US-0802706.
2001US-0808689.
2001US-0816744.
2001US-0828366.
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10-MAY-2001; 2001US-0854280.
25-MAY-2001; 2001US-0866028.
25-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001WS-0866034.
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22-UAN-2001; 2001US-0767609.
28-FEB-2001; 2001US-0796498.
28-FEB-2001; 2001WO-US06520.
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2001WO-US17443.
                                                    20-JUN-2001; 2001WO-US19692
                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001; 2001WO-US17800
                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                  WO200200690-A2.
                                                                                                                                                                                                                                                                                       14-MAR-2001; 2
22-MAR-2001; 2
05-APR-2001; 2
 Homo sapiens.
                                                                                                                                                                                                                                                                     01-MAR-2001;
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                                  03-JAN-2002
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Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF; Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-090516/12. P-PSDB; ABB84996.

One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal

Claim 2; Fig 359; 565pp; English.

ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
antianglogenic, hypotensive, vulnerary and antiarteriosclerotic
activities, and can be used in gene therapy. The PRO polynucleotides,
cactivities, agonists and antagonists are useful for treating or diagnosing
a cardiovascular, endothelial or angiogenic disorder in a mammal,
c g. cardiac hypertrophy, trauma, cancer, age-related macular
degeneration, atherosclerosis, hypertension, arterial restenosis,
theumatoid arthritis, angina, mycoardial infarctions, thrombophlebitis,
lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
carcinoma) and wound healing. The PRO polynucleotides have applications
in molecular biology, including use as hybridisation probes, and in
chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
probes used in the exemplification of the present invention.

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98 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGGTGTGTCTATACT 157
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                                                                                                                                              278 TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGGAGTCGTGGGTTATTTC
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                                                                                                                                                                                             21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr
                                                                                                                                                                                                                                                                     158 ATTICTCTGGCTAGTGCTCAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT
                                                                                                                                                                                                                                                                                            61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu
                                                                                                                                                                                                                                                                                                                                            81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe
                                                                                                                                                                                                                                               41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha; gene; ss.
                                   521
128
0
0
0
Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding human PRO protein, Seq ID No 71.
                                                                                                  Gaps:
                                                                                                                       US-10-019-455A-6 (1-128) x ABL88251 (1-521)
                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ThraspileAspPhePheCysGlu 128
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2000US-220638P.
2000US-220664P.
2000US-220666P.
2000US-220893P.
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2000US-220605P.
2000US-220607P.
                                  1.21e-86
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                                                                      Best Local Similarity:
Query Match:
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                                                             Percent Similarity:
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25-JUL-2000; 2
25-JUL-2000; 2
25-JUL-2000; 2
26-JUL-2000; 2
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25-JUL-2000;
25-JUL-2000;
                        Alignment Scores:
Pred. No.:
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(first entry)
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P-PSDB; AAM23569.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                      WO200154477-A2.
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                                                                                                                                               12-OCT-2001
                                                                                                                                                                                                                       Homo sapiens
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Pred. No.:
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                                                                                                 RESULT
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                                                                                                                                                                                                                          One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAAAAGGCCACCAGATCTATGTGTACTCAAAGCTGGTAAAAAGAAAATGGAGCTGGAGAA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr 40
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                                                                                                                         A, Godowski PJ;
Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal
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                                                                                                                         Goddard A,
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                         Gerritsen ME, Goddard
Smith V, Stephan JF,
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                                                                                                                                                                                                               Claim 2; Figure 71; 359pp; English
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 28-JUL-2000, 2000MO-US20710.
23-AUG-2000, 2000MO-US23522.
24-AUG-2000, 2000WO-US23328.
15-SEP-2000, 2000US-0000000.
10-NOV-2000, 2000US-255646P.
01-DEC-2000, 2000US-255646P.
20-DEC-2000, 2000WO-US35678.
20-DEC-2000, 2000WO-US3650.
20-DEC-2000, 2000WO-US3650.
20-DEC-2000, 2000WO-US3650.
20-DEC-2000, 2000WO-US3650.
25-MAY-2001, 2001WO-US17092.
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676.00
100.00%
100.00%
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                                                                                                                         Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,
                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                 WPI; 2002-172001/22.
P-PSDB; AAU83627.
                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA
120
                                                 397
     ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr
                            diseases, diagnostics, raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                           cow; fruit fly; yeast; hamster; macaque; horse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; not tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
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128
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Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                            Human EST-derived coding sequence SEQ ID NO:
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Matches:
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Zhang J, Werhman T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polypeptide for treatment of antibodies and research use -
                                                                                                          ThraspileAspPhePheCysGlu 128
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                                                                                                                               ACGGATATTGACTTCTTCTGCGAG
                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                          AAH98228 standard; cDNA; 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
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AAH26343) encoding novel human growth regulatory-like polypeptide (GRLP, see AAB82671) was subsequently obtained. Human GRLP belongs to the same protein lamily as growth regulatory proteins, growth factors, human melanoma derived growth regulatory proteins precursor (64% similarity and 45% identity over 111 amino acids) or melanoma inhibitory activity, cartilage-derived retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid-sensitive proteins. GRLP polypeptides and polymucleotides of the invention can be used in the prophylaxity irreatment (including gene therapy) and disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma cell
                                                                                                                                                                         growth and tumours, including neuroectodermal tumours such as glomas. The polynucleotides can also be used to design probes and primers, for chromosome and gene mapping, in the recombinant production of protein, in the generation of antisense, ribozyme and peptide-nucleic acid molecules, and to produce transgenic animals.
                                                                                                                                                                                                                                                             Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                              Query Match:
DB:
                                                                                                                                                                                                                                                                                                        Pred. No.:
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                                                                                                                                                                                                                                                                                                                       CCCAGGAACTTGGTCAAGGAACAGGGGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 378
                                                                                                                                                             ATTTCTCTGGCTAGTGCTCAAGAATTATAATGCCCCGGACTGTAGATTCATTAACGTT 198
                                                                         40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system disorders.
                                                                                                                                                                                                                                              | IlePheMetAspArgLeuAlaSerLySLySLeuCysAlaAspAspGluCysValTyrThr
                                                                                                                                IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal
                                                                                                                                                                                     LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu
                    MetalaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly
                                                                                                  ATATITATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of a novel nucleic acid that was assembled from human thymus cDNA library-derived Hyseq clone identification number 16372272 (see AAH26341). A recursive algorithm was used too extend the clone by pulling additional sequences from different databases. A full-length sequence (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Growth regulatory-like polypeptide; human; cartilage; melanoma; neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
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Length:
Matches:
Conservative:
Mismatches:
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RESULT 10
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                                                                                                                                                                                                                                     Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
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                                                                                                                                                                                                                                                                                                                                      present invention describes novel MLP proteins and their encoding
                                                                                                                                                                    Yoshimura
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The present sequence is that of a novel nucleic acid encoding human growth regulatory-like polypeptide (GRLP, see AAB82671).

The sequence was assembled using human thymus CDNA library-derived Hyseq clone identification number 1637272 (see AAB26341) as seed, using software programs to pull additional sequences from Hyseq's proprietary database containing expressed sequences from Hyseq's proprietary database containing expressed sequences from Hyseq's proprietary database containing expressed sequences?

The predicted protein has a mol wt. of 14 kDa unglycosylated. GRLP belongs to the same protein family as growth regulatory proteins, belongs to the same protein family as growth regulatory protein precursor (64% similarity and 45% identity over 111 amino acids) or melanoma inhibitory activity, cattle cartilage-derived retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid-sensitive proteins. GRLP polypeptides and polynucleotides of the invention can diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma celling growth and tumours, including neuroectodermal tumours such as and and an also be used to design probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system disorders.
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                                                                                                                                      Growth regulatory-like polypeptide; human; cartilage; melanoma;
neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
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                                                                                                    Human growth regulatory-like polypeptide cDNA.
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AAH26343 standard; cDNA; 1201 BP.
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haematopoiesis regulating activity, tissue growth activity, immunosouppressive or immunostimulant activity, activin/inhibin activity, chemotactic/chemoKinetic activity, haemostatic and thrombolytic activity, use in cancer diagnosis and therapy, drug screening, receptor/ligand activity, antiinflammatory activity, and treatment of leukaemia, nervous system disorders, arthritis and inflammation.
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Mismatches:
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                                                                                                    Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint diseases
     Yoshimura K;
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     Noguchi Y,
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     Mogi S,
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 Ohkubo s,
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                                                                                                                                                                                             Claim 11; Page 93; 111pp; Japanese.
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P-PSDB; AAB69125.
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ID AAF5
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MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter; inhibitor; ds.
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                                                                                                                                                                                 Ogi K,
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                                                                             WO200102564-A1
                                                                                                                                          30-JUN-1999;
                                                         Mus musculus.
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joint

The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant extivities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and johrt diseases as well as pathologic angiogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention. Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other; 947 1111 9 0 Conservative: Mismatches: Indels: Length: Matches: Alignment Scores:

US-10-019-455A-6 (1-128) x AAF59084 (1-947) 1.03e-75 602.00 93.75% 86.72% 89.05% Percent Similarity: Best Local Similarity: Query Match: DB:

AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAACGGAGCTGGAGGG 250 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluWetGlyValValGlyTyrPhe 100 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80 TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr 131 191 81 251 61 101 엄 ò g ઠે a à g ò 원 à

20 9 40

384 111 9 0 0

5.37e-76 600.00 93.75% 86.72% 88.76%

Best Local Similarity: Query Match: DB:

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Alignment Scores:

70 40

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No.:

Length: Matches: Conservative: Mismatches: Indels:

Sequence 384 BP; 98 A; 72 C; 109 G; 105 T; 0 other;

US-10-019-455A-6 (1-128) x AAF59098 (1-384)

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311 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 370 The present invention describes novel MLP proteins and their encoding MNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing to treating bone and joint diseases as well as pathologic angiogenesis.

AAF55063 to AAF56099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention. ¥ joint S, Noguchi Y, Yoshimura MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter; inhibitor; ds. Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and Mogi SEQ ID NO:46. Claim 13; Page 105-106; 111pp; Japanese. s, 394 Nishi K, Ogi K, Ohkubo ThraspileAspPhePheCysGlu 371 ACGGATATTGACTTCTTCTGTGAA ВР 29-JUN-2000; 2000WO-JP04278. 99JP-0186718. AAF59098 standard; DNA; 384 Rat MLP nucleotide sequence (TAKE ) TAKEDA CHEM IND LTD (first entry) 2001-159271/16. P-PSDB; AAB69130. WO200102564-A1. 30-JUN-1999; 23-APR-2001 11-JAN-2001. Rattus sp. Tanaka H; AAF59098; diseases 121 Itoh Y, AAF59098 

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US-10-019-455A-6 (1-128) x AAF59079 (1-330)
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Best Local Similarity:
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ATGTTTATGGATAAACTTTCTTATAGAAGTTGTGTGCAGATGAGGAGTGTGTCTATACC
                    IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal
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P-PSDB; AAB69126.
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Tanaka H;
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HisGly1lePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal

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Length:
Matches:
Conservative:
Mismatches:
Indels:

1.15e-74 590.00 100.00% 100.00% 87.28%

Gaps:

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                                                59 ASDVAILYSLYSGIYGINGINIIETYYVAITYYSEKLYSLEUVAILYSGIUASNGIYALA
121 AACGTTAAAAAAGGCAGCAGCAGCAGTATGTGTGTACTACAAAGCTGGTAAAAAAAGAAAATGGAGCT
                                                                                                                                                                 TATTTCCCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTT
                                                                                                TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal
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                                                                                                                                                                                                                 CCCACCACGGATATTGACTTCTTCTGCGAG 330
                                                                                                                                                                                                                                                                                                                                                      nucleotide sequence SEQ ID NO:25
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Sequence 330 BP; 91 A; 60 C; 91 G; 88 T; 0 other; exemplification of the present invention.

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The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis.

AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
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Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;

	38	09	28	120	78	180	86	240	
330 99 4 0	19 HisGlyllePheMetAspArgleuAlaSerLysLeuCysAlaAspAspGluCysVal	:::          :::	TyrThrileSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle		59 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla	GATGTCAAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCT	79 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly	GGAGAGTTTTGGGCTGGCAGTGTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGT	
Length: Matches: Conservative: Mismatches: Indels: Gaps:	grenAlaSerLysLysLe		rAlaGlnGluAspTyrAs:	AGCACAGGAAGATTACAA	nileTyrValTyrSerLy	GATCTATGTTTACTCCAA	rValTyrGlyAspGlyGl	TGTTTATGGTGACCACCA	
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-LOOPCL=0 - LOOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62
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-THR_MIN=0 - ALIGN=15 - MODE=LOCAL - OUTFMT=pco - NORM=ext - HEAFSIZE=500 - MINLEN=0
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APPLICANT: Mize, Nancy K
APPLICANT: Boyle, Bryan J
APPLICANT: Boyle, Bryan J
APPLICANT: Ford, John E
APPLICANT: Arterburn, Matthew C
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Song, Yong
APPLICANT: Song, Yong
APPLICANT: Sjaastad, Michael
ITTLE OF INVENTION: Polypeptides and Polynucleotides
TITLE OF INVENTION: Polypeptides and Polynucleotides
CURRENT APPLICATION NUMBER: US/10/216,038
CURRENT APPLICATION NUMBER: US/10/216,038
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PRIOR FILING DATE: 2000-05-02
PRIOR PELICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 8
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Sequence 71, Application US/10218765; Publication No. US20030187201A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P.; APPLICANT: Desnoyers, Luc; APPLICANT: Gentriesn, Mary; APPLICANT: Goddard, Audrey; APPLICANT: Goddowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                        1.34e-93
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CRGANISM: Homo Sapien
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; Sequence 71, Application US/2030149239A1
; Publication No. US20030149239A1
; Publication No. US20030149239A1
; General Information:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Stephan, Jean-Philippe F.
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; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: ACIDE ENCODING THE SAME
; TITLE OF INVENTION: ACIDE ENCODING THE SAME
; FILE REFERENCE: P3530PLC3
; CURRENT APPLICATION NUMBER: 10/119,480
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR PILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
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PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
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R APPLICATION NUMBER: 60/100385
R FILING DATE: 1998-09-15
R FILING DATE: 1998-09-15
R RILING DATE: 1998-09-15
R APPLICATION NUMBER: 60/100390
R FILING DATE: 1998-09-16
R PILING DATE: 1998-09-18
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R FILING DATE: 1998-09-18
R FILING DATE: 1998-09-18
R FILING DATE: 1998-09-17
R APPLICATION NUMBER: 60/10147
R APPLICATION NUMBER: 60/101738
R FILING DATE: 1998-09-23
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RAPPLICATION NUMBER: 60/106905

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R FILING DATE: 1998-09-09
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FILING DATE: 1999-01-12
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APPLICATION NUMBER: 60/115565
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APPLICATION NUMBER: 60/119549
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APPLICATION NUMBER: 60/123618
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APPLICATION NUMBER: 60/125259
FILING DATE: 1999-03-19
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Saith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLCJ9
CURRENT PRILOR DATE: 2002-08-12
FRIOR APPLICATION NUMBER: US/10/19,480
FRIOR FILING DATE: 1997-09-17
FRIOR FILING DATE: 1997-09-17
FRIOR APPLICATION NUMBER: 60/06287
FRIOR FILING DATE: 1997-0-17
FRIOR APPLICATION NUMBER: 60/06287
FRIOR FILING DATE: 1997-10-17
FRIOR APPLICATION NUMBER: 60/063549
FRIOR FILING DATE: 1997-10-17
FRIOR APPLICATION NUMBER: 60/069873
FRIOR FILING DATE: 1997-12-17
FRIOR APPLICATION NUMBER: 60/078910
FRIOR FILING DATE: 1988-03-20
FRIOR FILING DATE: 1988-03-25
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/08441
PRIOR APPLICATION NUMBER: 60/08532
PRIOR PILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/08539
PRIOR FILING DATE: 1998-06-17
PRIOR PRIOR APPLICATION NUMBER: 60/089532
PRIOR PILING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08995
PRIOR APPLICATION NUMBER: 60/08905
PRIOR APPLICATION NUMBER: 60/0905
PRIOR APPLICATION NUMBER: 60/090691
PRIOR APPLICATION NUMBER: 60/090691
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PRIOR FILING DATE: 1998-06-27
PRIOR PRIOR APPLICATION NUMBER: 60/091692
PRIOR PILING DATE: 1998-06-27
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DR APPLICATION NUMBER: 60/078910

DR APPLICATION NUMBER: 60/078294

DR FILING DATE: 1998-03-26

DR PLING DATE: 1998-03-27

DR APPLICATION NUMBER: 60/079728

DR APPLICATION NUMBER: 60/081819

DR PILING DATE: 1998-04-15

DR APPLICATION NUMBER: 60/081819

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DR APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/095318
FILING DATE: 1998-04
FILING DATE: 1998-08-04
FILING DATE: 1998-08-10
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APPLICATION WINBER: 60/096146
FILING DATE: 1998-08-11
APPLICATION NUMBER: 60/096791
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APPLICATION NUMBER: 60/097986
FILING DATE: 1998-08-26
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APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Marcy
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paris
APPLICANT: Goddard, Paris
APPLICANT: Goddard, Paris
APPLICANT: Grinald, J. Christopher
APPLICANT: Grinald, J. Christopher
APPLICANT: Siephan, Jean-Philippe F.
APPLICANT: Siephan, Jean-Philippe F.
APPLICANT: Wood, Milliam I.
TITLE OF INVENTION: SECRETE AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC3+
CURRENT APPLICANTON NUMBER: 10/10/203
CURRENT APPLICANTON NUMBER: 60/062913
PRIOR PILING DATE: 1997-10-11
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-21
PRIOR PILING DATE: 1997-10-21
PRIOR PILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/06349
PRIOR APPLICATION NUMBER: 60/06349
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PRIOR APPLICATION NUMBER: 60/079294
PRIOR PILING DATE: 1998-03-26
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ProArgAsnLeuvallysGluGlnArgVallyrGlnGluAlaThrLysGluValProThr 120
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Matches:
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                                                                                                                                                                                                                                                           398 ACGGATATTGACTTCTTCTGCGAG
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Publication No. US20030187202A1
GENERAL INFORMATION:
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                                                PRIOR APPLICATION NUMBER: 60/126773
PRIOR PILING DATE: 1939-03-29
PRIOR PILING DATE: 1939-03-29
PRIOR PILING DATE: 1939-04-05
PRIOR FILING DATE: 1939-04-05
PRIOR FILING DATE: 1939-04-121
PRIOR PILING DATE: 1939-04-21
PRIOR PILING DATE: 1939-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR PILING DATE: 1939-04-27
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PRIOR PILING DATE: 1939-08-17
PRIOR APPLICATION NUMBER: 60/14030
PRIOR FILING DATE: 1939-08-17
PRIOR APPLICATION NUMBER: 60/160345
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APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Ratanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
ITILE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330PLG31
CURRENT APPLICATION NUMBER: 10/119, 480
RIOR PLING DATE: 2002-04-09
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-31
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PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-11
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Mismatches:
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Publication No. US20030187204A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerriteen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Baker, Kevin P.
APPLICANT: Benoyers, luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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  97
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  38 AIGGCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA
                                                           21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr
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NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
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ORGANISM: Homo Sapien
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; Sequence 71, Application US/10219068
; Publication No. US20030187205A1
; GENERAL INFORMATION:
; APPLICANT:
    APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Satch, Victorial
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Stephan, Jean-Philippe F.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; ILLE REFERENCE: P3530PIC31
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/07958
PRIOR PRIOR DATE: 1998-03-27
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NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
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ORGANISM: Homo Sapien
US-10-219-067-71
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CURRENT AFFILMS DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
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APPLICANT: Desnoyers, Luc.

APPLICANT: Gerritean, Mary
APPLICANT: Geodard, Mary
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APPLICANT: Goodard, Mary
APPLICANT: Goodard, Paul U.
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APPLICANTENT: Matanabe, Colin L.
APPLICANTENT: M
ProArgAsnLeuVallysCluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
                               338 CCCAGGAACTTGGTCAAGGAACAGCGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 397
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Sequence 71, Application US/10219073
Publication No US20030187207A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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CORGANISM: Homo Sapien
US-10-219-073-71
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                                                                      APPLICANT: Goddard, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J. Christopher
APPLICANT: Grimalil, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colos Band
FILMS DATE: 1997-10-13
PRIOR APPLICANTION NUMBER: 60/06247
PRIOR PILMS DATE: 1997-10-21
PRIOR PILMS DATE: 1997-10-21
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PRIOR APPLICANTON NUMBER: 60/06973
PRIOR PILMS DATE: 1998-03-26
PRIOR PILMS DATE: 1998-03-26
PRIOR APPLICANTON NUMBER: 60/079284
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ORGANISM: Homo Sapien
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Pred. No.:
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddowski, Paul J.
APPLICANT: Goddowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Surith, Victoria
APPLICANT: Surith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC49
CURRENT APPLICATION NUMBER: US/10/219,475
CURRENT FILING DATE: 2002-08-13
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                                                                                                                                           101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
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                                                                                                        41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
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PRIOR PLICATION NUMBER: 00/119, 480

PRIOR PELING DATE: 2002-04-09

PRIOR PLING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-10-13

PRIOR PELING DATE: 1997-10-28

PRIOR PILING DATE: 1997-10-28

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PRIOR PELING DATE: 1997-10-31

PRIOR PELING DATE: 1998-03-20

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ORGANISM: Homo Sapien
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Alignment Scores:

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APPLICANT: Baker, Kevin P.
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Paul J.
APPLICANT: Godweki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimey, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Sephan, Jean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, Milliam I.
APPLICANT: Wood, Milliam I.
APPLICANT: ACIDS ENCODING THE SAME
FILE REPERENCE: P3530PLC38
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Mismatches:
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PRIOR PELING DATE: 2002-04-09
PRIOR PELING DATE: 2002-04-09
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/063549
PRIOR PILING DATE: 1997-10-18
PRIOR PELING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR PILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
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CORGANISM: Homo Sapien
US-10-219-483-71
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Best Local Similarity:
Query Match:
DB:
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US-10-219-525-71
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Sequence 71, Application US/10219483

Publication No. US20030187210A1

Sequence 71, Application No. US20030187210A1

Sequence 71, Application No. US20030187210A1

APPLICANT: Beenoyers, Luc

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Ganney, Austin L.

APPLICANT: Gurney, Austin L.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE

FILE REFERENCE: P3530PLC43

CURRENT APPLICATION NUMBER: US/10/219,483

CURRENT PILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: 10/119,480
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PRIOR APPLICATION UNMBER: 60/079656
PRIOR PILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
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                                                                                                            TYPE: DNA
CORGANISM: Homo Sapien
US-10-219-480-71
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Pred. No.:
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21 llephemetaspargLeuAlaSerLysLeuCysAlaAspAspGluCysValTyrThr
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Gaps:
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PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/062287
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-18
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/06913
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR PILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
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97

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338 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 397
                                                 121 ThraspileAspPhePheCysGlu 128
                                                                                               398 ACGGATATTGACTTCTTCTGCGAG 421
                                                                                                                                                                                          Sequence 71, Application US/10219526; Publication No. US20030187212A1; GENERAL INFORMATION:
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ORGANISM: Homo Sapien
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Best Local Similarity:
Query Match:
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                                                                                                            APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: BEGETETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILER REFERENCE: P3530P1C29
CURRENT APPLICATION NUMBER: US/10/219,525
CURRENT FILING DATE: 2002-04-09
PRIOR PILING DATE: 2002-04-09
PRIOR PELICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/06287
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
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PRIOR FILING DATE: 1998-03-22
PRIOR FILING DATE: 1998-03-22
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PRIOR FILING DATE: 1998-03-22
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                                 Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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APPLICANT: Besnoyers, Luc
APPLICANT: Gerrifest, Mary
APPLICANT: Gerrifest, Mary
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Stephan, Jean-Philippe F
APPLICANT: Stephan, Jean-Philippe F
APPLICANT: Stephan, Jean-Philippe F
APPLICANT: Stephan, Jean-Philippe F
APPLICANT: Watanabe, Colin L
APPLICANT: Watanabe, Colin L
APPLICANT: Watanabe, Colin L
APPLICANT: Wood, William I
IIIIE OF INVENTION: SECRETED AND TRANSHEMBRANE POLYPEPTIDES AND NUCLEIC
ITLE OF INVENTION: SECRETED AND TRANSHEMBRANE POLYPEPTIDES
APPLICANT: Wood, William I
III SPERENCE: P3330PL41
FILE REFERENCE: P3330PL41
FILE REFERENCE: P3330PL41
FILE REPERENCE: P3330PL41
FRIOR APPLICATION NUMBER: U0/119, 480
FRIOR APPLICATION NUMBER: 00/062287
FRIOR APPLICATION NUMBER: 00/063849
FRIOR FILING DATE: 1997-10-17
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FRIOR FILING DATE: 1997-10-31
FRIOR APPLICATION NUMBER: 60/063849
FRIOR FILING DATE: 1997-10-31
FRIOR APPLICATION NUMBER: 60/063849
FRIOR FILING DATE: 1998-03-25
FRIOR RELIGING DATE: 1998-03-25
FRIOR RELIGING DATE: 1998-03-25
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FRIOR FILING DATE: 1999-03-27
FRIOR APPLICATION NUMBER: 60/079284
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FRIOR FILING DATE: 1999-03-27
FRIOR APPLICATION NUMBER: 60/079294
FRIOR FILING
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ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
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                                                                                                                                                1 MetalaargileLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly
                                                                                                                                                                                                                                                                                                    41 IleSerLeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPheIleAsnVal
Mismatches:
Indels:
Gaps:
                                                                                 US-10-019-455A-6 (1-128) x US-10-219-530-71 (1-521)
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  Local Similarity: 100.00% Match: 100.00%
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APPLICANT: Baker, Kevin P.
APPLICANT: Gedard, Audrey
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Judery
APPLICANT: Gerritsen, Jean J.
APPLICANT: Grimeldi, J. Christopher
APPLICANT: Grimeldi, J. Christopher
APPLICANT: Gerritsen, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION NUMBER: US/10/19, 480
RIOR APPLICATION NUMBER: 60/05287
RRIOR APPLICATION NUMBER: 60/05287
RRIOR APPLICATION NUMBER: 60/05349
RRIOR FILING DATE: 1997-10-13
RRIOR FILING DATE: 1999-10-21
RRIOR APPLICATION NUMBER: 60/06349
RRIOR FILING DATE: 1998-03-20
RRIOR APPLICATION NUMBER: 60/079294
RRIOR APPLICATION NUMBER: 60/079294
RRIOR APPLICATION NUMBER: 60/079284
RRIOR RILING DATE: 1998-03-20
RRIOR APPLICATION NUMBER: 60/079284
RRIOR APPLICATION NUMBER: 60/079284
RRIOR APPLICATION NUMBER: 60/079284
RRIOR APPLICATION NUMBER: 60/079284
RRIOR RILING DATE: 1998-03-20
RRIOR APPLICATION NUMBER: 60/079284
RRIOR APPLICATION NUMBER: 60/079284
RRIOR APPLICATION NUMBER: 60/079284
RRIOR APPLICATION NUMBER: 60/079284
RRIOR APPLICATION NUMBER: 60/079284
RRIOR APPLICATION NUMBER: 60/070894
RRIOR APPLICATION NUMBER: 60/07
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                                                                                            LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu
         41 IleSerLeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPheIleAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   521
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                             ThraspileAspPhePheCysGlu 128
                                                                                                                                                                                                                                                                                                                                                                                 398 ACGGATATTGACTTCTTCTGCGAG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 71, Application US/10219530; Publication No. US20030187213A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.34e-93
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100.00%
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; ORGANISM: Homo Sapien
US-10-219-530-71
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Pred. No.:
Score:
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US-10-219-530-71
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Appli Appl Appl Appli Appli

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Title: Perfect score: Sequence:

Run on:

Scoring table:

Searched:

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Sequence 193, Applemence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 13, Appli Sequence 181, Appli Sequence 181, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli
                                                                                                                                                                                         Sequence 83, P
Sequence 81, P
Sequence 1, P
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Sequence 11,
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APPLICANT: Ullich Bogdan
APPLICANT: Ullich Bogdan
APPLICANT: Ullich Bogdan
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe & Lynch
STREET: New York
COURTRY: New York
STATE: New York
COUNTRY: USA
CONFUTER: NEW YORK
COUNTRY: USA
TIPPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: USA
FILLING DATE: 29-UN1Y-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-UN1Y-1994
FILING DATE: 20-UN1Y-1994
FILING DATE: 20-UN1Y-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: DE P 43 24 247.2
RIGHER APPLICATION NUMBER: DE P ATORNEY/AGENT INFORMATION:
AMADE: ANALOW INFORMATION:
3 US-08-996-139-14
3 US-08-995-659-14
4 US-09-577-780-14
4 US-09-577-780-14
4 US-09-66-14
4 US-09-871-291-14
4 US-09-871-291-14
4 US-09-871-291-14
4 US-09-971-291-14
4 US-09-971-291-14
4 US-09-134-078-11
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4 US-08-916-4218-1
3 US-09-134-078-57
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US-08-459-967-7
US-08-459-967-7
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US-08-459-871-7
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US-09-019-632-1
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REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION: 17ELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-434-255-5
US-08-459-967-5
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US-08-578-649-1
'S Sequence 1, Application US/08578649
'Patent No. 5770366
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-MODEL=frame+ pan.model-DEV=xlh
-Q-Cgn2_1/USPGTC ppool/US10019455/runat_29122003_160348_277/app_query.fasta_1.1770
-Q-(cgn2_1/USPGTC) spool/US10019455/runat_29122003_160348_277/app_query.fasta_1.1770
-Q-(cgn2_1/USPGTC) spool/US10019455/runat_20UFFIX=rni-MINMATCH=0.1 -LGOPCL=0
-LOODEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCNE=ptc -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HBASIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10019455_@CGN 1 1 142 @runat_29122003 160348_277 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Sequence 4, Appl
Sequence 8, Appli
Sequence 24, Appli
Sequence 24, Appl
Sequence 48, Appl
Sequence 79, Appl
Sequence 79, Appl
Sequence 1, Appli
Sequence 28, Appl
Sequence 28, Appl
                                                                                                                                                                                                (without alignments)
1388.315 Million cell updates/sec
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                                                                                                                                                                        December 29, 2003, 16:24:24 ; Search time 40.6947 Seconds
                                                                                                                                                                                                                                                                                                              1 MARILLLFLPGLVAVCAVHG......RVYQEATKEVPTTDIDFFCE 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                                  GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                              - nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-578-649-1
US-08-578-649-4
US-08-578-649-4
US-08-578-649-8
US-08-578-649-24
US-08-578-649-3
US-08-578-649-3
US-08-578-649-3
US-08-578-649-3
US-09-300-958A-30
US-09-300-958A-28
US-09-300-958A-28
US-09-356-952-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     569978 seqs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext (
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext (
Delop 6.0 , Delext '
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Maximum DB seq length: 2000000000
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Match Length DB
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Database :

257.5 253.5 232.5 210.5 1190 164.5 86.5 86.5 86.5 86.5 86.5

Result

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Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 CTGGCTGCCTGGGCTATTTCCCCAGTAGCATTGTCCGAGAGGACCAGACCTGAAA 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 ------ValHisGlyIlePheMetAspArgLeuAlaSerLysLeuCysAlaAsp 34 GGACCTGGTGTCAGGGGTGTCCTATGCCCAAGCTGGCTGACGGAGGTGCGGAC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysArgPhelleAsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLys 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
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                                                                                                                                                                                                                                                                                                                                                                                                               40 ATGGCCCGGTCCTGGTGCCTT-----GGTGTCATCATCTTGCTGTCTCCCTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 AspGluCysValTyrThrIleSerLeuAlaSerAlaGluGluAspTyrAsnAlaProAsp
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APPLICANT: Wilch Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOWA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                    US-10-019-455A-6 (1-128) x US-08-578-649-1 (1-459)
                                                                                                                                                                                                                                                                     Length:
Matches:
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257.50
60.29%
41.18%
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 base pairs
TYPE: mucleic acid
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112..432
                                                                                                                                                         sig_peptide
40.111
                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity:
Query Match:
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FEATURE:
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LOCATION:
US-08-578-649-1
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US-08-578-649-18
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82 TrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyVal---ValGlyTyrPhe 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 ATGGCTGTGGCCCTTCAGGACTACATGGCCCCCGACTGCCGGTTCCTGACCGG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 ATGCCAAAATTAGCAGATCGTAAATTATGTGCAGAATCAGGAGTGCAGCCACCCTATCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 GlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu---Phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 MetAspArgleuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThrIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: 1BM PS/-
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 20-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 4..6
OTHER INFORMATION: /function= "Startcodon Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-019-455A-6 (1-128) x US-08-578-649-18 (1-330)
                                                                                                                                                                                                                                                     NAME: Andrew L. Tidjoloff
REGISTRATION NUMBER: 31.575
REFERENCE/DOCKET NUMBER: 30.575
REFERENCE/DOCKET NUMBER: 30.575
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INPORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [ndels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ThraspileasphePheCysGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 GACAAATGGGATTTCTACTGCCAG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08578649; Patent No. 5770366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.85e-28
253.50
64.81%
45.37%
37.50%
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide 7..327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_RNA
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Best Local Similarity:
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Pred. No.:
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US-08-578-649-4
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DB:
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183

81

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95 Glyval---valGlyTyrPheProArgAsnLeuvalLysGluGlnArgValTyrGlnGlu 113
                                                                                                                                                                                        395 GCAGCCCGCCTATTTCCCCAGTAGCATTGTCCGGGAGGACCTGAACTTGAAACTT 454
                                                                   76 AsnGlyAlaGlyGlu---PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMet 94
                                                                                                                 114 AlaThrLysGluValProThrThrAspIleAspPhePheCysGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305
17
17
33
3
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Sequence 8, Application US/08578649

Patent No. 5770366

GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Brightte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inch 1.44 Mb storage diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-019-455A-6 (1-128) x US-08-578-649-8 (1-305)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10022
COMPUTER READABLE FORM:
MUDIUM TYPE: 3.5 inch 1.44 Mb storage dis COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: DEM PS/2
COMPUTER: DEM PS/2
COMPUTER: DEM PS/2
COMPUTER: DEM PS/2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-Uuly-1994
CLASSIFICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-Uuly-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOBER 1035-PFF/.
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 base pairs
mwnb: mm.nleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: join[1..29, 277..305)
OTHER INFORMATION: /function= "Primer"
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210.50
61.62%
44.44%
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805 Third Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 805 Third
CITY: New York
STATE: New York
COUNTRY: USA
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 GluCysValTyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCyg 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------MetAspArgleuAlaSerLysLysLeuCysAlaAspAsp 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 ArgPhelleAsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGlu 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 LeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGlyIlePhe---
                                                                                                                                                                                                                                                                                                            CATPLE 10042

CAPPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: 1 mb F9/
COPERATION SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLEASSIFICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andew L. Tiajoloff
REGISTRATION NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
NAME: Andew L. Tiajoloff
REGISTRATION NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFRARE: (212) 688-9200
                                      APPLICANT: Ulrich Bogdan
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Relfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STRAT: New York
COUNTRY: USA
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Matches:
Conservative:
Mismatches:
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58.52%
37.78%
34.39%
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110..178
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179..499
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Best Local Similarity:
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY:
; LOCATION:
US-08-578-649-4
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LOCATION:
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LOCATION:
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Pred. No.:
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89 AspGlyGln---AspGluMetGlyValValGlyTyrPheProArgAsnLeuValLysGlu 107
                                                                                                                                                                                 127 roczákácra-----aagáscergásagererrichasagasásagererrengan 177
              50 TyrashalaProAspCysArgPheIleAsnValLysLysGlyGlnGlnIleTyrValTyr 69
30 LysLeuCysAlaAspAspGluCysValTyrThrIleSerLeuAlaSerAlaGluAsp 49
                                                                                                             70 SeriysLeuValLysGluAsnGlyAlaGlyGlu---PheTrpAlaGlySerValTyrGly 88
                                                                                                                                                                                                                                                   238 GACCAGACCCTGAAACCTGGCAAAGTCGATGTGAAGACAGATAAATGGGATTTCTAC 294
                                                                                                                                                                                                                          108 GlnargvalTyrGlnGluAlaThrLysGluValProThrThrAspIleAspPhePhe 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(40..111, 40..166, 214..347, 393..503, 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Neinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Falfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/08578649
Patent No. 5770366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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40..111
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LOCATION:
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LOCATION:
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94 GGACCTGGTGTCTGGGGGTGCTCTTGCCCAAGCTGGCTGACCGGAAGCTGTGCGGAC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 GACCCTATCTCCATGGCTGTGGCCCTTCAGGACTACATGGCCCCCGGACTGCCGATTCCTG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 -----ValTyrGlyAspGlyGlnAspGluMetGlyVal---ValGlyTyrPhePro 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 GACGTGGAGTGTCATGGGGGCTGCCANTTTCCCCTTTCTCTTTTTCAGAAATGGGATTTC 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 ACCATTCACCGGGGCCAAGTGTATGTCTTCTCCAAGCTG-----AAGGGCCGT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 CTTCCCCAGGTTCAGGGAGATTACTATGGAGATCTGGCTGCTCGCCTGGGCTATTTCCCC 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 ArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThrThr 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 Aspile-----Asphe 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 ------ValHisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAsp 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 AspGluCysValTyr---- 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 ---ThrileSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPhelle 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: one-of(194, 369, 527)
COTHER INFORMATION: /note= "N in positions 194, 369
COTHER INFORMATION: and 527 denotes an indefinite number and sequence US-08-578-649-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetalaargileLeuLeuLeuPheLeuProGlyLeuValalaValCysAla----
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26
39
62
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Indels:
                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 3, Application US/08578649
; Patent No. 5770366
                                                                                                                                                                                                                                                                                                                                 2.1e-18
190.00
45.36%
31.15%
28.11%
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                                                                                                    393..503
                                                                                                                                                         549..569
                                                   214..347
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                                                                                       exon
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                                                                                                                                                                                                                                                                                                                       Alignment Scores:
             FEATURE:
NAME/KEY:
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NAME/KEY:
LOCATION:
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NAME/KEY:
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US-08-578-649-3
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DB:
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1552 GATGIGCIGCATICCCTATICCTICCCTAGACCCTAICTCCAIGGCTGIGGCCCTT 1611
                                                                                                                                                                                                                                                                                                                    1492 CAGGÁGTGCAGCCGTAAGAATGGGGAAGGGGTAGAATTGGGCTTGGGTGTTAGCCTGTGTG 1551
1378 ATGGCCCGGTCCCTGGTGTCTT-----GGTGTCATCATCTTGCTGTCTGCCTTCTCC 1431
                                                                                                                                                                                                                                                                                                                                                                          68 ValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu---PheTrpAlaGlySerVal 86
                                                                                                                                                                                                            -------ValTyrThrIleSerLeuAlaSerAlaGln 47
                                                                                                                                                                                                                                                                                          48 GludspTyrdsnAlaProdspCysArgPhelleAsnValLysLysGlyGlnGlnIleTyr 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48, Application US/08306691B
; Sequence 48, Application US/08306691B
; Patent No. 573403
; Patent No. 573403
; Patent No. 573403
; Patent No. 573403
; Patent No. 573403
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
                                             18 ------ValHisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSES: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER ISM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
RICASSFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION NUMBER: 30,480
REFRENCE/DOCKET NUMBER: 8321
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5734039-
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
                                                                                                                                                                                                                  38 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2757 base pairs
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86.50
51.43$
32.86$
12.80$
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STRANDEDNESS: double
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Best Local Similarity:
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OTHER INFORMATION: /note= "N in position 2216
OTHER INFORMATION: denotes an indefinite number ans sequence of
OTHER INFORMATION: nucleotides"
                                APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Brightte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Relfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STRATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
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Matches:
Conservative:
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Indels:
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TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9300
TENGUENCE CHARACTERISTICS: (213) 688-9300
TENGUENCE CHARACTERISTICS: (213) 688-9300
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                                                                                                                                                                                                                                                                                                                    OPERATING STORM: PC-DOS
SOFTWARE: Mordperfect
CURRENT APPLICATION DATA:
PILING DATE: 29-UNIY-1994
CLASSIFICATION DATA:
RAPLICATION NUMBER: DE 943 24 247.2
FILING DATE: 20-UNIY-1993
ATTORNEY AGENT TOWNER: DE P43 24 247.2
FILING DATE: 20-UNIY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
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                 Ulrich Bogdan
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LOCATION: 1378..1449
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1586..1719
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1378..1504
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NAME/KEY:
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LOCATION:
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LOCATION:
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Query Match:

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1 MetAlaArglleLeuLeuPeuPheLeuProGlyLeuValAlaValCysAla----

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2325 GCCAAAGCCCGCTATGACTTCTGCGCCCGTGACCGTTCAGAGCTGTCGCTCAAGGAGGGT 2384
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52.24%
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                                                                                   2385 GACATCATC----
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Best Local Similarity:
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PCT-US93-06251-79
Sequence 79, Application PC/TUS9306251
Sequence 79, Application PC/TUS9306251
Sequence 79, Application PC/TUS9306251
Sequence 79, Application Fric and Rife, Jason P.
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INNENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INNENTION: Trivalent Synthesis of Oligonucleotides NUMBER OF INVENTION: Trivalent Synthesis of Oligonucleotides and Arylphosphonates
NUMBER OF ENUMBERS: 93
CORRESPONDENCE ADDRESS:
STREET: 400 Garden City Plaza
CITY: Garden City
CITY: CORRESPONDENCE ADDRESSER
CITY: CORRESPONDENCE ADDRESSER
CITY: CORRESPONDENCE ADDRESSER
                                                                                                                                                                                   ---GTTGGCTGGTTCCCTGCCAAC 2471
                                                                                                         84 GlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsn 103
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                                                                                                                                                           64 GlnGlnileTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrpAla 83
                                                                                        63
                                                                                     44 AlaSerAlaGluAspTyrAsnAlaProAspCysArgPheIleAsnValLysLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
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Matches:
Conservative:
Mismatches:
Indels:
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                                                    US-10-019-455A-6 (1-128) x US-08-306-691B-48 (1-2757)
                                                                                                                                                                                                                                                                                                                                              2472 TACGTGGAGGAGAT-----TATTCTGAA 2495
                                                                                                                                                                                                                                                             2433 GGGGAGATCTATGGCCGG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: DIGIGILO, FTANK S.
REGIESTRATION NUMBER: 31,346
REFRENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFX: 516-742-4366
TELEFX: 516-742-4366
TELEFX: 530 901 SANS UR
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2257 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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86.50
51.43%
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                                                                                                                                      2325
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Query Match:
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wcclelland, Michael

APPLICANT: Wcclelland, Michael

APPLICANT: Wcclelland, Michael

APPLICANT: Trenkle, Thomas

TITLE OF INVENTION: Using Same

FILE REPERENCE: P-PH 3457

CURRENT APPLICATION NUMBER: 60/083,331

PRIOR FILING DATE: 1999-04-27

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1998-04-7

PRIOR FILING DATE: 1999-0-04

NUMBER OF SEQ ID NOS: 85

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 30

LENGTH: 4762
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                                                  2432
                                                                                                                              81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
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                                                                                             84 GlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsn 103
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64 GlnGlnijeTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrpAla 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LyslysglyglnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu
                                           |||:::::::::|||
----AAGATCCTTAACAAGAAGGACAGCAAGGCTGGTGGCGA
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-019-455A-6 (1-128) x US-09-300-958A-30 (1-4762)
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Matches:
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; Patent No. 2548864
; GENERAL INFORMATION:
; APPLICANT: Barbacid, Mariano
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TYPE: DNA ORGANISM: Saccharomyces cerevisiae
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SEQ ID NO 11
LENGTH: 5398
                                                                                                                                                                                                                                                                                                                                                                                                                 0.0225
79.00
50.00%
29.49%
11.69%
                                                                                                                                                                                                                                  TYPE: DNA
CRGANISM: Homo sapiens
FRATURE:
NAME/KEY: unsure
LOCATION: (428)
LOCATION: (462)
LOCATION: (462)
US-09-300-958A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-300-958A-28

Sequence 28, Application US/09300958A

Patent No. 6495319

GENERAL INFORMATION:

APPLICANT: Welsh, John

APPLICANT: Trenkle, Thomas

TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 GlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsn 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 AlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLysLysGly 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 GlnGlnijeTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrpAla 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2793
22
14
21
13
                                                                                  CITY: Princeton
STATE: New Jersey
COUTRY: U.S.A.
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE PC compatible
COMPUTER: BE PC compatible
COMPUTER: BE PC compatible
COMPUTER: BE PC compatible
COMPUTER: BE PC compatible
COMPUTER: USPELICATION DATA:
APPLICATION NUMBER: US/07/646,537B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
TITLE OF INVENTION: Vav Proto-Oncogene Protein NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-019-455A-6 (1-128) x US-07-646-537B-1 (1-2793)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2516 TATGTGGAGGAAGAC-----TATTCCGAA 2539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 LeuValLysGluGlnArgValTyrGlnGlu 113
                  NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2477 ĠĠĠAGATCŤĀĊĠĊĊGG-------
                                                                                                                                                                                                                                                                 APPLICATION:
BILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Gaul, Timothy J.
REGISTRATION NUMBER: 33,111
REGISTRATION NUMBER: DC10
TELECOMMUNICATION:
TELEPHONE: (609) 921-4526;
TELEPHONE: (609) 921-4526;
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.50
51.43%
31.43%
12.65%
                                                                   P.O. Box 4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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LOCATION:
US-07-646-537B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 AlaGlnGluAspTyrAsnAlaProAspCysArgPhelleAsnValLysLysGlyGlnGln 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WESOLS 122
US-09-356-952-11
Sequence 11, Application US/09356952
Fatent No. 6117663
GENERAL INFORMATION:
APPLICANT: Borlack-Sjodin, Ann
APPLICANT: Borlack-Sjodin, Ann
APPLICANT: Borlack-Sjodin, Ann
APPLICANT: Borlack-Sjodin, Ann
APPLICANT: Borlack-Sjodin, Ann
APPLICANT: Borlack-Sjodin, Ann
APPLICANT: Borlack-Sjodin, Ann
APPLICANT: Cale, Philip
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION THEREOF
GURRENT APPLICANTON NUMBER: US/09/356,952
GURRENT APPLICANTON NUMBER: 60/19
EARLIER APPLICANTON NUMBER: 60/093,631
SEARLIER FILING DATE: 1998-07-21
MUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 ValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsnLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 ---GGAAGGAGGATGAATAAATTCAAATCCCGTGTTGCACCTGCACCACAAAATT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 LysGluGlnArgValTyrGlnGluAlaThriysGluValProThrThrAsplle 123
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23
16
12
12
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Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: Using Same
FILE REFERENCE: P-PH 3457
CURRENT APPLICATION NUMBER: US/09/300,958A
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/083,331
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-02-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PALENT UN VET: 2.0
SOFTWARE: PALENT UN VET: 2.0
SEQ ID NO 28
LENGTH: 467
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9
                                                                                                                                                                                                                         LysLysGlyGlnGlnileTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
                                                                                                                  26 LeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThrileSerLeuAlaSer 45
                                                                                                                                                                       -----AspCysArgPhelleAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILLING DATE: 22 DECEMBER 1997
CLASSIFICATION:
     5398
223
21
21
11
                               Conservative:
Mismatches:
Indels:
                                                                                            US-10-019-455A-6 (1-128) x US-09-356-952-11 (1-5398)
      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
FILING DATE: 14 OCTOBER 1997
APPLICATION DATA: 0.0 NARCH 1997
FILING DATE: 0.0 NARCH 1997
PRIOR APPLICATION DATA: 0.0 NARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY, AGENT INFORMATION:
NAME: PERKINS, PALTICIA ANNE
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)233-0644
                                                                                                                                                                                                                                                                                                                               101 ProArgAsnLeuValLysGluGlnArg 109
                                                                                                                                                                                                                                                                                                                                                  AlaGlnGluAspTyrAsnAlaPro-
                   78.50
49.44%
25.84%
11.61%
                                Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-996-139-14
Alignment Scores:
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970 -----ACACTGGTCAGCGAGGTTGAGACGCAAGGAGACCTCTCGAGGAGACTTCCCACA 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       922 TGTGCGGCAGGTGGGCCCTGGGCAAAGTCAAGAATTCTAAGACGTTC----- 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
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649 GTTCIGCICCICTICAICICIGIGGIAGIAGIGGCIGCCAICAICTICGGGGTTIACIAC 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           709 AGGAAGGGAAGGGAAAGCGCTGACAGCTAATTTGTGGAATTGGGTCAATGATGCTTGCAGT 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 ---LeualaSerLysiysLeuCysalaAspAspGluCysValTyrThrIleSerLeuAla 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 SeralaginGluAspTyrAsnAlaProAspCysArgPheileAsnValLysLysGlyGln 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 IleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGlyllePheMet 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 GlnileTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrp----
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Sequence 14, Application US/08995659

Sequence 14, Application US/08995659

Patent No. 6242213

Patent No. 6242213

APPLICANT: Anderson, Dirk M.

APPLICANT: Anderson, Dirk M.

APPLICANT: Maraskovsky, Eugene

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

MUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department
                                                                                                                                                                                                                                                                                                                                       1878
30
26
48
38
                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-019-455A-6 (1-128) x US-08-996-139-14 (1-1878)
                                                                                                                                                                        ORGANISM: Murine
IMMEDIATE SOURCE:
LIBRARY: Murine Fetal Liver Epithelium
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1878 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTT-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                           0.245
78.00
39.44%
21.13%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 AspArg-----
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                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                           CLONE: MURANK
                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                              US-08-996-139-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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970 -----ACACTGGGGGGGTTGAGACGCAAGAGACTCTCGAGGAAGATTCCCACA 1023
                                                                                                                                                                                                                                     101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
                                                                                                                                                           83 -----AlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
                                    45 SeralaginGluAspTyrAsnAlaProAspCysArgPheileAsnValLysLysGlyGln 64
                                                                                   65 GlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrp----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION NUMBER: US/09/6,139
FILING DATE: CINCHOWN:
APPLICATION NUMBER: US/N 08/813,509
FILING DATE: OT MARCH 1997
APPLICATION NUMBER: US/N 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/ABGNT INFORMATION:
REFERENCE/DOCKET NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELEPHONE: (206)587-0430
TELEPHONE: (206)587-0430
TELEPHONE: GOOD 14:
NUMBER: 1978 base pairs
                                                                                                                                                                                          Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09215649A Patent No. 6271349 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98101
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                  1024 GAGGAT 1029
                                                                                                                                                                                                                                                                                                                           121 ThrAsp 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---LeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThrIleSerLeuAla 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 IleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGlyIlePheMet 23
                                                                                            COMMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
CORRATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
FILING DATE: 22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-019-455A-6 (1-128) x US-08-995-659-14 (1-1878)
                                                                                                                                                                                                                                       FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)233-0644
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1878 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: Murine Fetal Liver Epithelium CLONE: muRANK
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.44%
21.13%
11.54%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Murine IMMEDIATE SOURCE:
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Best Local Similarity:
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                      Seattle
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US-08-995-659-14
                                        STATE: W1
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970 -----ACACTGGTCAGCGAGGTTGAGACGCAAGGAGACTCTCGAGGAAGATTCCCACA 1023
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                                                                                                                                                                                                                                                                                                                                                                                     26 ---LeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThrIleSerLeuAla 44
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30
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48
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Matches:
Conservative:
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LIBRARY: Murine Fetal Liver Epithelium CLONE: muRANK
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| NAME/KEY: CDS | LOCATION: 1..1875 | SEQUENCE DESCRIPTION: SEQ ID NO: 14: US-09-215-649A-14
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on: December 29, 2003, 22:08:26 ; Search time 1216 Seconds (without alignments) 12918.830 Million cell updates/sec	O.
Title: VS-10-019-455A-4 Perfect score: 384 Sequence: 1 atggcaagaatattgttactatattgacttcttctgcgag 384	
Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0	
Searched: 2888711 segs, 20454813386 residues	
Total number of hits satisfying chosen parameters: 5777422	
Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries	
Database : GenEmbl:*  1: 9b ba:* 2: 9b hq:* 4: 9b pl:* 5: 9b com:* 6: 9b pat:* 7: 9b pb.* 10: 9b pl:* 11: 9b pl:* 12: em fin:* 13: em fin:* 14: em fin:* 15: em fin:* 16: em pat:* 17: em pat:* 18: em pl:* 18: em pl:* 18: em pl:* 19: em pat:* 10: em pat	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.		Score	Query Match	Query Match Length	DB	ID	Description
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	н	384	100.0	384	9	BD010802	802
	7	384	00	384	9	BD093103	103 Novel
	м	384	00	521	9	AX358818	818
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	13	330	•	330	9	BD093117	Novel
	14	287	74.7	384	9	BD010805	5 Novel
	15	287	•	384	9	BD093106	6 Novel
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	25	249		330	9	BD010836	
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## ALIGNMENTS

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Yoshimura,K. and Tanaka,H.

Novel polypeptide and its DNA.

Patent: WO 0102564-A 3 11-JAN-2001;

TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
CGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
OS HOMO Sapiens (human)
PN WO 0102564-A/3
PD 11-JAN-2001
PF 29-UUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PR 30-JUN-1999 JP 99P 186718
PR 7ASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
                                                                                                                                                                                                                  YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
CIZNI5/12, CIZNS/10, CIZP21/02, CO7KL4/47, CO7KL6/18, AG1K45/00, PC
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02,C12R1:19)
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Homo sapiens
Eukarycia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches 0;
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Sequence 71 from Patent WO0193983.
AX358818
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
70 c 106 g 109
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Ver onoguchi, koji YoshiMuRa, HIDEYUKI TANAKA
CI2N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PC C12P21/08,C12N15/00,A61K37/02,C12N5/00
CC CC Location/Qualifiers
FH Key 1.384
FT source 1.384
FT /organism='Homo sapiens (human)'.
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/organism='Homo sapiens (human)'.
Location/Qualifiers
                  Patent: JP 2001069994-A 3 21-MAR-2001;
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/db_txef="taxon:9606"
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                                                   Homo sapiens (human)
JP 2001069994-A/3
21-MAR-2001
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Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.
Matches 384; Conservative
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PN JP 200106
PD 21-MAR-20
PR 29-JUN-20
PR YASUAKI I
PI YUKO NGGU,
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Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis
Patent: WO 0208284-A 359 31-GAN-2002;
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard, Audrey (US); Godowski, Paul J. (US); Gerritsen, Mary E. (US); Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US); Pani, James (US); Pani, Nicholas F. (US); Stephan, Jean-Philippe F. (US); Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
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100.0%; Pred. No. 3.4e-107;
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Sequence 359 from Patent W00208284.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                      Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I. Secreted and transmembrane polypeptides and nucleic acids encoding
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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rative 0; Mismatches 0; Indels
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                                                                                                                      Parent: WO 0193983-A 71 13-DEC-2001;
Genentech Inc. (US)
Location/Qualifiers
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Sequence 71 from Patent WO0208288.
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Matches 384; Conservative
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Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C. Dinis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C. Direct Submitssion
Submitted (109-FEB-2000) Pathology, Brigham and Women's Hospital, 75
Francis Street, Boston, MA 02115, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRI 06-JUL-2000
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1 (bases 1 to 846)
Robertson, N.G., Haller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Penis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C. A novel conserved cochlara gene, OTOR: identification, expression analysis, and chromosomal mapping Genomics 66 (3), 242-248 (2000)
                                                                            1 ATGGCAAGAATATTGTTACTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA
                                                                                                                         301 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC
                218 AAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAAGGAGCTGGAGAA
                                                            TTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC
AAAAAAGGGAGCAGATCTATGTGTACTCAAAGCTGGTAAAAAGAAAATGGAGCTGGAGAA
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Best Local Similarity 100.0%; Pred. No. 3.6e-107;
Matches 384; Conservative 0; Mismatches 0; Indels (
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Homo sapiens otoraplin (OTOR) mRNA, complete cds.
AF233261
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/note="similar to cdrap/mia"
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/product="otoraplin"
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/mol_type="mRNA"
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1. .846
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Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                       Compositions and methods for the diagnosis and treatment of disorders involving anglogenesis Patent: WO 0200690-A 359 03-JAN-2002; Genentech, Inc. (US)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDBYUKI TANAKA
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDBYUKI TANAKA
PC CIZANIS/09, A61K38/00, A61K45/00, A61K48/00, A61K48/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K45/00, A61K48/00, A61K
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    Length 865;
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Query Match 100.0%; Score 384; DB 9; I
Best Local Similarity 100.0%; Pred. No. 3.6e-107;
Matches 384; Conservative 0; Mismatches 0;
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/organism='Homo sapiens (human)'.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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368 ACGGATATTGACTTCTTCTGCGAG 391
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/codon_start=1
/poduct=fibrocyte-derived protein"
/protecin_id="AAA642356.1"
/db_xref="GI:11991844"
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Submitted (19-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue du Dr. Roux, Paris 75015, France
Location/Qualifiers
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1 (bases 1 to 865)
2 (bener-Salmon, M., Frenz, D., Liu, W., Verpy, E., Voegeling, S. and
                45 ATGGCAAGAATATTGTTACTTTTTCCTCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="20"
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AF243505
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Rendtorff, N.D., Frodin, M., Attie-Bitach, T., Vekemans, M. and
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                                                     Length 923;
                                                                               Indels
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AJ243552.1 GI:12619172
melanoma inhibitory activity like protein; Mial
Homo sapiens (human)
Homo sapiens
                                                     100.0%; Score 384; DB 6; L
100.0%; Pred. No. 3.7e-107;
.ive 0; Mismatches 0;
              u
              260
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/organism="Homo Bapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 ACGGATATTGACTTCTTCTGCGAG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 ACGGATATTGACTTCTGCGAG 384
/db_xref="taxon:9606"
_147 c 213 g
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Rendtorff, N.D.
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                                                        Query Match
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Matches 384; Conservative
                 303 a
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HSA242552
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1 (bases 1 to 923)

1 (bases 1 to 923)

1 (bases 1 to 924)

Yoshimura, K. and Tanaka, H.

Novel polypeptide and its DNA

Patent: WO 0102564-A 21 11-3AN-2001;

PAREDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
GGI, SHOIGHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
CIZNIS/12,C12NS/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC
A61K38/17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.JAN-2001
29-JUN-2000 WO 2000JP004278
30-JUN-1999 JP 99P 186718
YASUJAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n38/11/,
A61K39/395,A61K49/16,A61P19/02,A61P19/08,A61K31/7088//(C12P21/
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                                                                                       1 ATGGCAAGAATATTGTTACTTTTCCTCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA
                                                               Gaps
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                                   100.0%; Score 384; DB 6; Length 923; 100.0%; Pred. No. 3.7e-107; ive 0; Mismatches 0; Indels
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/organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BD093121 923 bp
Novel polypeptide and its DNA.
BD093121
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WO 0102564-A/21
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Homo sapiens (human)
Homo sapiens
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                                          Query Match
Best Local Similarity 100.
Matches 384; Conservative
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BD093121
LOCUS
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JOURNAL
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                ORIGIN
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Tommerup, N.
Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation (Genomics 71 (1), 40-52 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSA242552 1422 bp mRNA linear PRI 29-JAN-2001
Homo sapiens mRNA for melanoma inhibitory activity like protein
(MIAL gene).
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                                                                                                                                                                                                                                                                                                        AAAAAAGGCCAGCAGCATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240
                                                                                                                                                                                                                                                                                                                                                                                             TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 300
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                  93
                                                                                                                             61 ATALTIALGGACCGICTAGCTICCAAGAAGCICTGIGCAGATGAIGAGAGGIGTGIATACI
                                                                                                                                                                                                                    121 ATTICTCTGGCTAGGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT
                                                                                                                                                                                                                                           Submitted (21-MAY-1999) Rendtorff N.D., Department of Medical Genetics, Institute of Medical Biochemistry and Genetics, Blegdamsvej 3, 2200 Copenhagen N, DENWARK Revised by anthor 03-AUG-1999 Related sequence: AJ243939 (Mus musculus mRNA) Related sequences: AJ243939 (Mus musculus mRNA) Related sequences: AJ25324 to AJ252327 (genomic sequence).
                                                                    1 ATGGCAAGAATATTGTTACTTTTCCTCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA
Gaps
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SHINICHI MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
                                                                                                                                                                                                                             PAT 31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TATACTATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 TATTTCCCCAGGAACTTGGTCAAGGAACAGCGTGTACCAGGAAGCTACCAAGGAAGTT 354
241 TATTTCCCCAGGAACTTGGTCAAGGAACAGCGTGTAACCAGGAAGCTACCAAGGAAGTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATACTATTTCTCTGGCTAGTGCTCAAGAATATATAATGCCCCGGACTGTAGATTCATT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACGTTAAAAAAGGGCAGCAGCAGTTTATGTGTACTCAAAGCTGGTAAAAAGAAAATGGAGCT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAGAATTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGT 294
                                                                                                                                                                                                                                                                                                                                                                            Ducactoria September 1  

Busing September 2  

Busing September 3  

Busing September 3  

Busing September 4  

Busing September 5  

Busing September 6  

Busing September 6  

Busing September 7  

Busing September 7  

Busing September 7  

Busing September 8  

Busing September 9  

Busing September 9
CO7K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50,
133/53//
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GGAGAATTTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGTGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO,
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100.0%; Pred. No. 1.5e-90;
ive 0; Mismatches 0;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
a 60 c 91 g 88
                                                                                                                                                                                                                             330 bp Novel polypeptide and DNA thereof. BD010816
                                                                         361 ACGCATATTGACTTCTTCTGCGAG 384
                                                                                                                   384
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                                                                                              361 ACGGATATTGACTTCTTCTGCGAG
                                                                                                                                                                                                                                                                                                  BD010816.1 GI:18639189
                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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                                    301
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BD010816
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                                                                                                                                                                                                                                                                                                                  /translation="martillerpglyavcavhglpmprlaskklcaddbcvytisla
sagedynapocrpinvkkgoglyvysklvkengagefwagsvygdbgdbmgvvgyfpr
nlvkegrvygeatkevpttdldffce"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="WIAL"
/product="melanoma inhibitory activity like protein"
:1. .115
                                                                                                                                                                     product="melanoma inhibitory activity like protein"
                                                                                                                                                                                                                                             /codon_start=1
/codon_start=1
product="melanoma inhibitory activity like protein"
/protect="melanoma inhibitory"
/protect="q1:12619173"
/db_xref="G1:12619173"
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Pred. No. 3.9e-107;
; Mismatches 0;
         /map="20p11.22-12.2"
/tissue_type="brain and cochlea"
/dev_stage="fetal"
1. .1422
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/gene="MIAL"
/number=2
115^116
/gene="MIAL"
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257^258
/gene="MIAL"
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364. .387
/gene="MIAL"
/number=4
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/gene="MIAL"
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/gene="MIAL"
                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="MIAL"
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YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
CI2N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ATTTCTCTGGCTAGTGCTCAAGAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 TITIGGCTGGCAGTGTTATGGTGATGGCCAGGACGAGGATGGGAGTCGTGGGTTATTTC 300
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                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 toase; 1 to 38, 1 to 39, K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H.

Yoshimura,K. and Tanaka,H.

Parent: JP 2001069994-A 21-MaR-2001;

TAKEDA CHEMICAL INDUSTRIES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGCAAGAATATTGTTACTTTTCCTCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA
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                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.7%; Score 287; DB 6;
84.3%; Pred. No. 2.8e-77;
iive 0; Mismatches 60;
                                                                                           DNA
301 CCCACCACGGATATTGACTTCTTCTGCGAG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107
                                                                                     Novel polypeptide and DNA thereof.
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/organism='Mus sp. (mouse)'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus sp."
/mol type="genomic DNA"
/db_xref="taxon:10095"
                                                                                                                                                                                                                                                                                                                       Mus sp. (mouse)
JP 2001069994-A/6
21-MAR-2001
29-JUN-2000 JP 2000195911
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JP 2001069994-A/6.
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Best Local Similarity 84.3
Matches 323; Conservative
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                                                                                                           DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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JOURNAL
                                                                  RESULT 14
BD010805
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                                                                                                                                                                                                                                                                     Ito, X., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and its DNA
Patent: WO 0102564-A.17 11-2NA-2001,
TAKEDA CHEMICAL INDUSTRIES LTD, YASUKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDBYUKI TANAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
C CI2N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC
A61K38/17,
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02,C12R1:19)
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29-JUN-2200 WO 2000JP004278
30-JUN-1999 JP 99P 186718
YASUAKI 1TO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 CATGGAATATITATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGT 114
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                                                                                                                               PAT 27-AUG-2002
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                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 330)
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                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.9%; Score 330; DB 6; I
ilarity 100.0%; Pred. No. 1.5e-90;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers.
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                          355 CCCACCACGGATATTGACTTCTTCTGCGAG 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .330
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                     ф
                                                                                                                                 Novel polypeptide and its DNA.
BD093117
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
WO 0102564-A/17
                                                                                                                                                                                BD093117.1 GI:22638705
                                                                                                                                                                                              WO 0102564-A/17.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Sim
Matches 330;
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Yoshimura,K. and Tanaka,H.
Novel polypeptide and its DNA
AL Patent: WO 0102564-A [11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES ITD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,
HIDEYUKI TANAKA
OS Mus sp. (mouse)
PN WO 0102564-A/6
PD 11-JAN-2000
PP 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PR XASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI
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CIZNIS/12,CIZNS/10,CIZP21/02,CO7K14/47,CO7K16/18,A61K45/00, PC
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 384)
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84.3%; Pred. No. 2.8e-77;
iive 0; Mismatches 60;
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/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"
a 68 c 111 g 107
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Novel polypeptide and its DNA.
BD093106
                     361 ACGGATATTGACTTCTTCTGTGA 383
      ACGGATATTGACTTCTTCTGCGA 383
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WO 0102564-A/6.
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Best Local Similarity 84.3
Matches 323; Conservative
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PC A61K39/3
PC 02,C12R1
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Oy 361 ACGGATATTGACTTCTTCTGCGA 383

Db 361 ACGGATATTGACTTCTTCTGTGA 383

Search completed: December 30, 2003, 04:07:56

Job time : 1218 secs
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BQ564607 gil9h02.y
BQ568498 gil09c02.
BQ564134 gilld01.y
                                                                                   ; Search time 1278.03 Seconds (without alignments) 7302.593 Million cell updates/sec
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Query Match 74.7%; Score 287; DB 13; Length 398;
Best Local Similarity 84.3%; Pred. No. 1.6e-75;
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
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/dev_stage="Fost matal day 5 to 13"
/clone lib="Mouse Organ of Corti con Paluescript"
/clone lib="Mouse Organ of Corti; Vector: pBluescript; The
/note="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         488 bp mRNA linear EST 19-JUN-2002
glighO2.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gilghO2 5', mRNA sequence.
BQ564667
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                                                                                61 ATAITITATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT 120
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA Tel: 301-402-1599 Fax: 301-402-1765 Email: kacharb@nidcd.nih.gov
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Seg primer: M13RP1 reverse primer (ABI).
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/clone="gi19h02"
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/strain="BALB/c"
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epichellum was carefully disserved out of the microtary of the district of the microtary of the micro Pastitrack Kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 23761), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo (dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using moloney murine leukemia virus reverse transcribts was pointed with the linker-primer and transcribed using moloney murine leukemia virus reverse transcribts with Noney murine leukemia virus reverse transcribts with Synthesized with DAA polymerase and RNase H. Complementary bNA was blunt ended with Ffu DNA polymerase, ligated with Ato I. The cDNA was sequentially size fractionated virth Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 by respectively. The cDNA was then directionally ligated to the blage library was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF' cells, the Combinants. Stratagen's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescue library, individual cDNA was estimated to be 11,100,000 recombinants. Stratagen's ExAssist Interference plating from 200 ul of saturated culture with the Charler of the phage interference purified from 200 ul of saturation kit (TWN plasmid DNA from the place interestion of the phage interference plating of the fauturated culture with the Charler of the phage interestion kit (TWN plasmid DNA plasmid DNA place in the Charler plasmid strength BigDye terminator sequencing chemistry (Applied Blosystems, Poster City, CA). Sequencing chemistry (Applied Blosystems, Poster City, CA). Sequencing reactions were performed on MT Terrad thermal cyclers (MT Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Blosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have I copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have bits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified." Concert96(TM) plasmid purification kit (Invitrogen, Carlabad, CA) as instructed by the manufacturer. BSTs from the 8' end of the CDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25% 61 ATAITTAIGGACCGICTAGCITCCAAGAAGCICTGTGCAGAIGATGAGGTGTGTCTATACT 120 ATTICICIGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT 180 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240 1 AIGGCAAGAAIAITGITACTITICCTCCGGGTCTTGIGGCCTGTAIGTGCTGTGCAIGGA 60 7 ArescaAssararrearrerrrectresessectrerestrerraristiscessestaser 66 epithelium was carefully dissected out of the modiolus. Gaps °, Length 488; 60; Indels Query Match
74.7%; Score 287; DB 13;
Best Local Similarity 84.3%; Pred. No. 1.7e-75;
Matches 323; Conservative 0; Mismatches 60; 143 121 181 SASE COUNT

TITTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGGATGGGAGTCGTGGGTTATTTC 300 247 TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC 306

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/ Geav stage="Post natal day's to 13" / Glore lib="Wouse Organ of Corti CDNA pBluescript" / Glore lib="Wouse Organ of Corti; Vector: pBluescript: The note="Organ: Organ of Corti; Vector: pBluescript: The organ of Corti; Vector: pBluescript: The organ of Corti; Vector: pBluescript: The organ of Corti; Vector: pBluescript: The organ of Corti; Vector: pBluescript: The organ of Corti; Vector: pBluescript: The organ of Corti; Vector: pBluescript: The organ of Corti; Vector: pBluescript: The organ of Corti; Vector: pBluescript: The Dorgation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bonny capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fastrack kit (catalog # K1593-O2; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR digapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer severse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer severse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker primes and transcribed using synthesized with the linker primer severse transcribed using synthesized and digested with Rub Na polymerase and RNAsse H. Complementary DNA was blunt ended with the presence of ligase and digested with Na Lubra promerase and RNAsse H. Complementary DNA was blunt the presence of ligase and digested
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gil09c02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gil09c02 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 514)
CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360
                                           Contact: Kachar,B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
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Seg primer: M13RP1 reverse primer (ABI).
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Mus musculus
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/strain="BALB/c"
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Fax: 301-402-1765
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ORGANISM

AUTHORS TITLE JOURNAL

REFERENCE

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over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) and Cloumns to enrich for CDNAs greater than 4000p and 1000 bp the bull of the CDNA was then directionally ligated to the bull of the Uni-22p XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XII Blue MRF' cells, the yield of the phage library was estimated to be 11,00,000 recombinants. Stratagene's Exhasist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid MnA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTS from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry Applied Biosystems, Poster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (M1 Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; as follows: 72% of genes are present in GenBank, but do not have assigned function; 23% have hits in GenBank, but do not have assigned function; 23% have bits in GenBank, but do not have sesigned function; 23% have better and paracterized ESTS and 20% are unidentified.
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14.7%; Score 287; DB 13; Length 514;
Best Local Similarity 84.3%; Pred. No. 1.8e-75;
Matches 323; Conservative 0; Mismatches 60; Indels (
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BQ564134 534 bp mRNA linear EST 19-JUN-2002 gilld01.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gilld01 5', mRNA sequence.

DEFINITION

BQ564134

BQ564134.1 GI:21467451 EST.

ACCESSION VERSION KEYWORDS

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and spiral ligament were removed and the sensory
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//woulv-WI) and 5-methyl dCTP. The second strand was
//columns to enrich for conks greater than 400ps and 1000 by
//columns to enrich for conks greater than 400ps and 1000 by
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 534)
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Structural Cell Biology
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
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Plate: 11 row: d column: 01
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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musculus (house mouse)
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       Mus musculus
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Unpublished
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Query Match
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Matches 323; Conservative
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strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on My Terrad thermal cyclers (My Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72 of genes have 1 copy; 14.38 2; 128 3-10; 1.48 11-50 and 0.18 51-150. As to gene function, 45% of genes are present in GenBank and have know function, 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 TTTTGGGCTGCCAGTGTTAATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360
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National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: kacharb@midcd.nih.gov
Plate: 135 row: f column: 01
Seg primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 ACGGATATTGACTTCTTCTGCGA 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
1 (bases 1 to 560)
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Matches 323; Conservative
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Best Local &
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KEYWORDS
SOURCE
ORGANISM
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TITLE
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ORIGIN
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BQ569741
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/dev stagge=Posts natal day 5 to 13"
/dev stagge=Posts natal day 5 to 13"
/clone 11b="Wouse Organ of Corti; Vector: ppluescript"
/clone 11b="Wouse Organ of Corti; Vector: ppluescript; The
organ: Organ of Corti; Vector: ppluescript; The
organ of Corti; (10C) was fine dissected from a total of 386
OC as follows: 10C samples from post-natal (10) day 5; 72
from pto 2 and 24 from pto 18 from pto 20 from pto;
from pto 2 and 24 from pto 18 from pto 20 from pto;
from pto 2 and 24 from pto 3; 18 from pto 20 from pto;
from pto 2 and 24 from pto 3; 18 from pto 20 from pto;
from pto 2 and 24 from pto 3; 18 from pto 20 from pto;
from pto 2 and opened in Leibowitz medium. The bony
capsule of the cochiea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
pital ligament were removed and the sensory
for all RNA was extracted using the micro Fasttrack kit
(catalog # K1593-02; Invitrogen; Carlebad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 23721), Stratagene) and Uni-Zap XR
dispace from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 15; up mRNA was
interpreted a sinstructions. Briefly: 15; up mRNA was
primed with the linker- primer and transcribed using
primed with the linker- primer and transcribed using
primed with the linker- primer and transcribed using
monory murine leukemia virus reverse transcribed using
primed with Mol. I The CDNA was sequentially size fractionated
voer pharmacia Size Sep400 (Pharmacia, Ungapeta)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
and Clontech Alto, which had been predigested with
Ecok I and Xho I. The phage inharavy was estimated to be 11,100,000
recombinants: Stratagene's Exassist Interference
resistance helper phage (catalogue # 211203) was adopted
resistance helper phage (catalogue # 21203)
car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on Mu Tetrad thermal cyclers (Mu Research, Maltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have I copy; 14.3% 2; 12% 3-10; 1.4% 11.50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank and not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 560;
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Pred. No. 1.8e-75;
0; Mismatches 60;
                                    .. .560
'organism="Mus musculus"
                                                                                                    /mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="gil35f01"
                                                                                                                                                                                                                                                                         'sex="male and female"
ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.7%;
84.3%;
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/Gev stage="Post natal day 5 to 13"
/clone_lbb="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti, Vector: pBluescript; The
organ of Corti (DC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
et from P12 and 24 from P13. After xilling animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
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g127g09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone g127g09 5', mRNA sequence.
                                                                                                                                                                                                                                                                121 ATTICTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT 180
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Mammalia, Eutheria, Rodentia, Sciurognathi, Gridae, Murinae, Mus.
1. (bases 1 to 608)
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                              6 ATGCCAAGGATATTGATTCTTTTGCTTGGGGCCTTGTGGGTTCTATGTGCCGGGCATGGT 65
1 ATGGCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA 60
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Seq primer: M13RP1 reverse primer (ABI).
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sex="male and female"
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Plate: 27 row: g column: 09
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'strain="BALB/c"
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Structural Cell Biology
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and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack Kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR digapack III Gold Cloning kit (catalog # 237612), both from Stratagene [La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using boloney murine leukemia vitus reverse transcribed using boloney murine leukemia vitus reverse transcribed using synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with PG DNA polymerase, ligated with BCOR I adapters in the presence of ligase and digested with RNO I. The CDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Dpsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with ECOR I and Xho I. The phagemid was packaged with Green Planta Columns to enrich for cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with ECOR I and Xho I. The phagemid was packaged with Green Planta Columns to enrich for cDNA was then directionally ligated to resouch library was estimated to be 11,100,000 recombinants: Stratagene's EARsist Interference resistance helper phage (catalogue # 21203) was adopted to rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate; Plasmid DNA from the phages. Upon plating of the phage instructed by the manufacturer. ESTE the careful paramid purification of the CDNA valuniants of the S' end of the CDNA clones were generated with the bull was a instructed by the manufacturer. STF from the S' end of strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on My Tetrad thermal cycless (Wy Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have bits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

0; Gaps 74.7%; Score 287; DB 13; Length 608; 84.3%; Pred. No. 1.9e-75; 60; Indels 0; Mismatches Matches 323; Conservative Best Local Similarity Query Match BASE COUNT ORIGIN

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61 ATAITTAIGGACCGICTAGCITCCAAGAAGCICTGTGCAGAIGAGTGTGTGTGTATACT 120 193 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG 252 73 GTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGCGGATGAGGAGTGTGTCTATACT 132 121 ATTICTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT 180 133 ATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 192 181 AAAAAAGGCAGCAGCAGTTTTGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240 1 ATGGCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCCTGTATGTGCTGTGTGCATGGA 60 13 Arggcaaggararrgarrctrrrrgcrrggggccrrgrggrgrrargrgcggggarggr 72 à 8 ద ð ద ਨੇ 셤

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/clone="gilobgod"
/clone="gilobgod"
/dev-gaselge="post natal day 5 to 13"
/dev-gasege="post natal day 5 to 13"
/devestage="post natal day 5 to 13"
/devestage="post natal day 5 to 13"
/clone lib="Mouse Organ of Corti; Vector: pBluescript" The
/clone lib="Mouse Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bull
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total NAW was extracted using the micro Fasttrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
digapeck III Gold Cloning kit (catalog # 237212), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(df) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker- primer and transcribed using
Moloney mutine leukemia wirus reverse transcribed using
month and particulations. Briefly the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the server of the serv
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253 TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC 312
                                                                 301 CCCAGGAACTTGGTCAAGGAACAGCGTGTACCAGGAAGCTACCAAGGAAGTTCCCAGC 360
                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 630)
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Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
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Plate: 108 row: g column: 04
Seg primer: M13RP1 reverse primer (ABI).
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/mol_type="mRNA"
/strain="BALB/c"
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Mus musculus
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SOURCE

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with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo, Alto, Ab) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The CDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Giapak III Gold and, upon tiration on XL1 Blue MRF cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference dresistance helper phage (stanlogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescue plasmid DNA from the phages. Upon plating of the crescue plasmid DNA from the phages. Upon plating of the concerts(TM) plasmid purification kit (Invitrogen, Concerts(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTS from the 5' end of the CDNA clones were generated with the universal M13 reverse primer (AccGAAACAGCTATGAC) and 25% strength BigDye terminator sequencing reactions were performed on M1 Terrad thermal cyclers (M1 Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPF polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have I copy: 14.3% 2; 12% of genes are present in GenBank and have know function, 45% of genes are present in GenBank and have sasigned function; 12% are uncharacterized ESTS and 20% are unidentified."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 GTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGCGGATGAGGAGTGTGTCTATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 287; DB 13;
Pred. No. 1.9e-75;
0; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ACGGATATTGACTTCTTCTGCGA 383
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larity 84.3%;
Conservative (
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Matches 323;
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ORIGIN
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GI:15393547

BB611549 BB611549.1

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SOURCE

COMMENT

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EST 19-JUN-2002
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474 bp mRNA linear EST 19-JUN-2002
clone g142g03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                             61 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT 120
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Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 474)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ATTICTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT 180
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1 ATGGCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTTGTGCATGTA 60
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Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGCTTATTTC
                                                                                                                                                                                                                0; Gaps
                                                                                                                                                      74.7%; Score 287; DB 10; Length 696; 84.3%; Pred. No. 2e-75;
                                                                                                                                                                                Pred. No. 2e-75;
0; Mismatches 60; Indels
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/dev_stage="Post natal day 5 to 13"
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Plate: 42 row: g column: 03
Seg primer: M13RP1 reverse primer (ABI).
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/mol_type="mRNA"
/strain="BALB/c"
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                                                                                                                                                                                                                      Matches 323; Conservative
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                                                                                                                                                                Query Match
Best Local Similarity
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                                                                      204 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                      BASE COUNT
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KEYWORDS
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BQ565637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.
                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 696)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Mateauyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagama, M., Tagawa, A., Takakashi, F., Takeda, Y., Tanaka, T., Toya, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to Rot = 10.0 and subtraction to Rot = 50.0. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inote="Site_1: XhoI, Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. ist strand cDNA was primed with a primer [5" of Strand CONA WAS GAGAGGARGCARGAGGATCTTTTTTTTTTTVN 3"], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-reseges riken.go.jp,
URL:http://genome.ges.riken.go.jp,
URL:http://genome.ges.riken.go.jp,
Caninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
C.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapped discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B.,
wagi,K., Pujiwake,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-22 Suebhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="RIKEN full-length enriched, 13 days embryo
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                    Tagani,M., Tagawa,A., Takahashi,F., Takeda,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
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/dev_stage="13 days embryo"
/lab_host="SOLR"
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/db_xref="taxon:10090"
/clone="3110083012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .696
                                            Mus musculus (house mouse)
Mus musculus
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                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                      AUTHORS
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                      KEYWORDS
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/clone lib="Mouse Organ of Corti cDNA pBluescript" The cross of Corti (OCC) was fine dissected from a total of 386 organ of Corti (OCC) was fine dissected from a total of 386 organ of Corti (OCC) was fine dissected from a total of 386 organ of Corti (OCC) was fine dissected from a total of 572 from PD1 if the DD1 if it is the DD1 if it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA).

In frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1-4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

ö 1 ATGCCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA 60 14 Argecaacgararrearreirrecrrecececerrererrerarerecececearder 73 0; Gaps DB 13; Length 474; 61; Indels Query Match 74.3%; Score 285.4; DB 1. Best Local Similarity 84.1%; Pred. No. 5.1e-75; Matches 322; Conservative 0; Mismatches 61 120 t 78 C BASE COUNT ORIGIN

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/dev stage="Post natal day 5 to 13"
/dev stage="Post natal day 5 to 13"
/clone lib="Mouse Organ of Corti cDNA pBluescript"
/clone lib="Mouse Organ of Corti; Vector: pBluescript; The
/note="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (CD) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P5; 60 from P7; 46 from P8; 18 from P3; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bulla
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiclus. 684 bp mRNA linear EST 19-JUN-2002 3106:09:y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi06:09 5', mRNA sequence. EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing Unpublished Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and 181 AAAAAAGGGCAGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240 301 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 684) library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to 194 AAGAAAGGGCAGCAGCTCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 300 254 ritirócácticácaciciritaricatcaccaccacacacacacatacaarticaagatatatitc 313 National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA Email: kacharb@nidcd.nih.gov Plate: 06 row: c column: 09 Seq primer: MI3RP1 reverse primer (ABI). Location/Qualifiers organism="Mus musculus" /db_xref="taxon:10090" /clone="gi06c09" /sex="male and female" 374 ACGGATATTGACTTCTTCTGTGA 396 361 ACGGATATTGACTTCTTCTGCGA 383 Mus musculus (house mouse) /mol_type="mRNA" /strain="BALB/c" Structural Cell Biology National Institute of De BQ563768.1 GI:21466749 Contact: Kachar, B. Tel: 301-402-1599 Fax: 301-402-1765 1. .684 Mus musculus Kachar, B. 241 source DEFINITION ORGANISM AUTHORS TITLE ACCESSION JOURNAL RESULT 10 REFERENCE BQ563768 KEYWORDS FEATURES COMMENT

LOCUS

30566932

ACCESSION

SOURCE

KEYWORDS

REFERENCE

TITLE

JOURNAL

FEATURES

with Xno 1. The CUMA was Sequencially bize liarlindacture over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for CDNAs greater than 400bp and 1000 bp columns to enrich for CDNAs was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR i and Xho I. The phagemid was packaged with Gigapak II Gold and, upon titration on XLI Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference resistance helper phage (catalogue # 21223) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual colns were selected and grown in 36-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concertsoffy) plasmid purification kit (Intirogen, Carlebad, CA) as instructed by the manufacturer. ESTS from the 5' end of the CDNA clones were generated with the universal M13 reverse primer (CAGGAAAGGTTAGAC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified." manufacturer's instructions. Briefly: 1.5 ug mRNA was treverse transcribed using a hybrid oligo(df) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker primer and transcribed using Moloney murine leukemia vitus reverse transcribes (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was bluth ended with PFU DNA polymerase, ligated with BCR I adapters in the presence of ligase and digested with Xho I. The CDNA was sequentially size fractionated with Xho I. The CDNA was sequentially size fractionated

0; Gaps 74.3%; Score 285.4; DB 13; Length 684; 84.1%; Pred. No. 6.1e-75; ive 0; Mismatches 61; indels 0; ilarity 84.1%; Conservative ORIGIN

BASE COUNT

73 GTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGCGGATGAGGAGTGTGTCTATACT 132 121 ATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT 180 ATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 192 193 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGG 252 TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGGATGGGAGTCGTGGGTTATTTC 300 253 TITITGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC 312 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 372 1 ATGGCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGCGCTGTATGTGCTGTGCATGGA 60 13 Arescheseararitearrentineerreseseseerrerestrerarereseseseseerres 61 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT 373 ACGGATATTGACTTCTTCTGTGA 395 361 ACGGATATTGACTTCTTCTGCGA 383 Query Match Best Local Similarity Matches 322; Conserva' 301 133 241 313 g à Dp. à 엄 à 셤 Š g à g à

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/dev stage="Post mala!"
/dev stage="Post mala! day 5 to 13"
/clone lib="Mouse Organ of Corti cDNA pBluescript"
/clone lib="Mouse Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from Pol 6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibbwitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fastrack kit
(catalog # K1533-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
digapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker- primer and transcribed using
Moloney murine leukemia virus reverse transcriptase
(MMLY-RT) and S-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
columns to enrich for CDNAs greater than 400bp and 1000 by
respectively. The cDNA was sequencially size fractionated
with Who I. The pDNA was sequencially asserted with Grone Chrome Applance of Liagase and digested
with Moloney murine leukemia was sequencially asserted with BCOR I and Xho I. The phagemid was packaged with diggapak
III Gold of the phage library was estimated t
                     EST 19-JUN-2002
PQ566932 400se Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi73909 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Rodentia; Sciurognathi, Muridae; Murinae; Mus.
1 (bases 1 to 409)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST analysis of gene expression in the mouse Organ of Corti at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1765
Fax: 301-402-1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bmail: kacharb@midcd.nih.gov
plate: 73 row: g column: 09
Seq primer: M13RP1 reverse primer (ABI).
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                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                  BQ566932.1 GI:21470249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   onset of hearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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source FEATURES

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recombinants. Stratagene's Exassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the concerts of TWN plasmid purification kit (Invitrogen, Carlabad, CA) as instructed by the manufacturer. ESTS from the 5' end of the CDNA clones were generated with the universal M13 reverse primer (CAGGAAACGTATGAC) and 25% strength BigDyb terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Terrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of 1.4% 11-50 and in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCAC 359
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Pred. No. 6.1e-71;
0; Mismatches 62; Indels
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Best Local
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490 bp mRNA linear EST 19-JUN-2002 gi37bi2.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi37bi2 5', mRNA sequence.

DEFINITION RESULT 12 BQ565411 LOCUS

ACCESSION VERSION

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

Kachar, B.

AUTHORS TITLE

REFERENCE

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 490)

musculus (house mouse) BQ565411.1 GI:21468728

Mus

ORGANISM

KEYWORDS SOURCE

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/dex='malle and remale"
/dex='malle and remale"
/dex='malle and remale"
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/rore=Torgan: Organ of Corti: Vector: paluescript; The
/rore=Torgan: Organ of Corti: Vector: paluescript; The
/rore=Torgan: Organ of Corti: Vector: paluescript; The
/rore follows: 102 samples from post-natal (P) day 5, 72
from PD: 66 from PD; 46 from PB; 18 from PB; 20 from PD;
/rore pl: 2 and 24 from PB; 18 from PB; 20 from PD;
/rore pl: 2 and 24 from PB; 18 from PB; 20 from PD;
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/rore pl: 2 and 24 from PB; 30 from PB;
/rore pl: 2 and 24 from PB; 30 from PB;
/rore pl: 2 and 24 from PB; 30 from PB;
/rore pl: 3 and opened in Leibowitz medium. The bony
capsule of the cochiea was chipped away, stria vascularis
and spiral ilgament were removed and the sensory
/rore pl: 3 instructions Reverse transcription and
library construction were carried out with the Uni Zap XR
/rore pl: 3 instructions Riefly; 15 up mRNA was
/rore pl: 3 instructions Riefly; 15 up mRNA was
/rore pl: 4 and XP or instructions Reverse transcription
/rore pl: 4 and XP or instructions Proper and thicker-primer
/rore pl: 4 and XP or instructions Applaness and dispersed
/rore pl: 4 adapters in the presence of ligase and dispersed
/rore planned chrome Spin-1000 (Clontech, Palo Alco, CA)
/rospectively The CDNA was sequentially size fractionally ligated
/rore norich for cDNA was packages. Upon plating
/rore and library, individual cDNA dones were selected and
/rore planned DNA from the plages. Day and and and
/rore planned DNA was the directionally ligated to
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Contact: Kachar, B.
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
S0/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Fig. 301-402-1369
Fax: 301-402-1765
Email: kacharb@nidcd.nih.gov
                                                                                                                                                                                                                                                                   Plate: 37 row: b column: 12
Seq primer: M13RP1 reverse primer (ABI)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                            122 ITTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTTA 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACCA 361
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                                                                                                                                                                                                                                           BY232622
BY232622 RIKEN full-length enriched, adult inner ear Mus musculus
cDNA clone F930026J20 5', mRNA sequence.
genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
                                                                                                                                                                         2 IGGCAAGAATAITGTTACTITICCICCGGGTCTTGTGGCTGTAIGTGCTGTGCAIGGAA 61
                                                                                                                                                                                                                                                                                                                                                                              FGGAGAAT
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                                                                                                        67.8%; Score 260.4; DB 13; Length 490; 80.1%; Pred. No. 1.8e-67;
                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.8e-67;
0; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 CGGATATTGACTTCTTGCGA 383
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Mus musculus
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                                                                                                                                              306; Conservative
                                                                                                                             Similarity
                                                                                                                                                                                                                                               62
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                                                                                                             Query Match
                                                                                                                             Best Local
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GGC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
URL: Hutbp://Genome.goc.riken.go.jp,
URL: http://genome.goc.riken.go.jp,
Anizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Mumazaki, R., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct
,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,M., Imotani,K., Ishii, Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yaoshino,M., Waterston,R., Lander,E.,R., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Bncyclopedia Project of Genome Res. 11 (2), 281-289 (2001) cDNA library was defended and sequenced in Mouse Genome Bncyclopedia Project of Genome Solence Center and Genome Science Laboratory in Riken Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissues were provided by Kirk W. Beisel (Boys Town National Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NE 69131 USA ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ATAITTAIGGACCGICTAGCIITCCAAGAAGCICIGIGCAGAIGAIGAGIGIGICIAIACI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ATTICTCTGGCTAGTGCTCAAGAATATAATGCCCCGGACTGTAGATTCATTAACGTT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'clone_lib="RIKEN full-length enriched, adult inner ear"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGCAAGAATATTGTTACTTTTTCCTCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 ATGCCAAGGATATTGATTCTTTTGCTTGGGGGCCTTGTGGTTCTATGTGCCGGGCATGCT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.9%; Score 253; DB 13; Length 365; 83.9%; Pred. No. 2.7e-65; ive 0; Mismatches 55; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 t
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/clone="F930026J20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 g
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                                                                                                                                                                                                                                                                                                                  Nature 420, 563-573 (2002)
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Matches 286; Conservative
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EST 19-JUN-2002
                                                                                                                                                                                                                                BQ567343 604 bp mRNA linear EST 19-JUN-200; gi88408.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi88408 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                          EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing Unpublished
181 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240
                                                              TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 300
                                                                             264 TTTGGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGGAATTGTAGGTTATTTC 323
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 604)
                  204 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Kachar,B.
Structural Cell Biology
Mational Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
                                                                                                                         301 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGC 341
                                                                                                                                            Email: kacharb@nidcd.nih.gov
Plate: 88 row: d column: 08
Seg primer: MI3RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
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1. .604
                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="gi88d08"
                                                                                                                                                                                                                                                                                                    BQ567343.1 GI:21470660
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                                                                                                                                                                                                                                                                                                                                                     musculus
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                                                                                                                                                                                                                                                                                                                                                     Mus
                                                                 241
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                                                                                                                                                                                                                                                      DEFINITION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                          BQ567343
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synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligate and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The CDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue NRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistence helper phage (catalogue # 211203) was adopted to rescued library individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concerto (TM) plasmid purification kit (Invitrogen, Canterset) end of the cDNA clones were generated with the universal Ml3 reverse primer (CAGGARAACCTRAGACC) and 25% strength Richber 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            universal mis reverse primer. Curocontrol of Applied Blosystems, Foster City, CA). Sequencing chemistry (Applied Blosystems, Foster City, CA). Sequencing reactions were performed on MT Terrad thermal cyclers (MT Sesearch, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POS5 polymer (Applied Blosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have I copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GATTACAATGCCCCAGACTGTAGGTTCATCGATGTCAAGAAGGGCAGCAGATCTATGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 TACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAATTTTTGGGCTGGCAGTGTTATGGT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 GATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTCCCCAGGAACTTGGTCAAGGAACAG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GACCACCAGGATGAGATGGGGAATTGTAGGTTATTTCCCCAGCAACTTGGTGAAGGAGCAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAGAAGTIGIGIGGGAIGAGGAGIGIGIGITTIATACTATITCICTGGCAAGAAGCACAGGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 CGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACCACGGATATTGACTTCTTCTGCGA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 CGTGTATACCAGGAGGCCACCAAGGAGATCCCAACCACGGATATTGACTTCTTCTGTGA 299
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Bovidae; Bovinae; Bos.

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Contact: Smith TPL
Contact: Smith TPL
Contact: USDA, Ass, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Fax: 402 762 4350
Email: smithDemail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904-e. Vector identified by cross_match with the -minscore 18
por PRIMERS.
1 (bases 1 to 527)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGATGAGTGTCTATACT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 CCCAGGAACTIGGICAAGGAACAGCGIGIGIGIACCAAGGAAGTICCCACC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 ATATTTATGGACAGACTTGGTTCCAAGAAGCTGTGTGCAGATGATGAATGTGTCTATACT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 AAAAAAGACAGTGGATCTATGTTTACTCAAAGCTGGTCTATGGCAATCAGTCTG---- 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 TTTTGGGCTGGCAGTGTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGGCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA 60
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                                                                                                                             Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.1%; Score 234.8; DB 10; Length 527; 79.7%; Pred. No. 1e-59; Indels 36; Gaps iive 0; Mismatches 42; Indels 36; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: GTTTTCCCAGTCACGACG
Plate: 54 row: C column: 18
Seg primer: ATTTAGGTGACACTATAG.
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/db_xref="taxon:9913"
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Search completed: December 30, 2003, 06:07:13

Job time : 1283.36 secs

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December 29, 2003, 22:01:01; Search time 127.462 Seconds (without alignments) 8132.484 Million cell updates/sec
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                                                                                                                                                                                                                                                                                5105512
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                  2552756 segs, 1349719017 residues
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Maximum Match 100%
Listing first 45 summaries
                                                           OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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SUMMARIES

Description	Human MLP nucleoti	DNA encoding novel	Human growth regul	Human angiogenesis	Human PRO9873 cDNA	cDNA encoding huma	Human EST-derived	Human growth regul
ΩI	AAF59065	AAS17583	AAH26341	ABL95740	ABL88251	ABK33571	AAH98228	AAH26342
	22	24	22	24	24	24	22	22
% Query Match Length DB	384	387	426	521	521	521	891	891
* Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	384	384	384	384	384	384	384	384
Result No.		7	ო	4	Ŋ	9	7	00

Human MLP nucleoti	grow		Mouse MLP nucleoti	Mouse MLP nucleotí	Rat MLP nucleotide			Rat MLP nucleotide	Rat MLP nucleotide	Recombinant human	Sequence encoding	Melanoma inhibitor	Human antisense ol	Human prostate exp	Sequence encoding	Breast cancer rela	Breast cancer rela	Sequence encoding	fied f	Human gene express		ñ	130	Human TANGO 130 CD	Human TANGO 130 po	Human prostate exp		Human prostate exp	Human prostate exp	H	Human TANGO 130 po	Human protein enco	Human PRO19670 cDN	Human cDNA encodin	a)	Human PRO19670 cDN
383	343	179	990	384	860	080	660	093	192	783	050	083	732	229	052	502	012	061	055	828	695	459	850	245	849	035	751	878	625	852	851	775	140	460	738	249
AAF5908	AAH2634	AAF5907	<b>AAF5906</b>	AAF5908	AAF5909	AAF59080	<b>AAF</b> 5909	<b>AAF5909</b>	AAF5909	AAH4778	AAQ84050	AA17008	AAD1873	ABV59229	AAQ8405	ABL63602	<b>ABL6401</b>	AAQ84061	AAQ84055	AAZ14828	AAS22695	AAS22459	ABQ79850	AAZ51245	ABQ79849	ABV21035	ABV23751	ABV26878	ABV29625	ABQ7985	ABQ7985	AAH99775	AAF9214	ABS7446	ABL9573	ABL8824
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923	1201	330	384	947	384	330	330	307	261	433	459	459	459	555	581	442	442	330	305	300	429	884	1230	1263	1263	4409	4409	4409	4409	5724	8121	417	1060	1060	1060	1060
100.0	100.0	85.9	74.7	74.7	74.3	65.7	64.8	56.6	50.5	16.9	16.9	16.9	16.9	16.6	16.5	16.4	16.4	14.9	14.1	14.0	14.0	14.0	14.0	14.0	14.0			14.0	14.0	14.0		13.5		12.0	12.0	12.0
384	384	330	287	287	85	٠.	~**	217.4	193.8	64.8	64.8		64.8	63.8	63.2	62.8	62.8								53.6							52	46	46	46	46
Q	10	11	12	13	14	15	16	11	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

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Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
                                                                                                        MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter; inhibitor; ds.
                                                                                      Human MLP nucleotide sequence SEQ ID NO:4.
                     AAF59065 standard; DNA; 384 BP.
                                                                                                                                                                                                                                                            30-JUN-1999; 99JP-0186718.
                                                                                                                                                                                                                                                                                  (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                       29-JUN-2000; 2000WO-JP04278.
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                           WPI; 2001-159271/16.
                                                                                                                                                                                          WO200102564-A1.
                                                                                                                                                                    Homo sapiens.
                                                                 23-APR-2001
                                                                                                                                                                                                                11-JAN-2001.
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Tanaka H;
                                           AAF59065;
RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTGGGCTGGCAGTGTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGGACTGTAGATTCATTAACGTT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360
                                                                                                                     The present invention describes novel MLP proteins and their encoding DDAs. The MLP proteins and DNAs have antinifialmentery and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis.

AMFS9063 to AMFS9099 and AAE69122 to AAE69132 represent sequences used
                                                                                                                                                                                                                                                                                                                                  1 AIGGCAAGAATATIGTTACTTTTCCTCCCGGGTCTTGIGGCTGTAIGTGCTGTGTGCAAGAA 60
                                                                                                                                                                                                                                                                                                                                                  1 ATGGCAAGAATATTGTTTTTCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA 60
                          Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secreted protein, cytostatic, immunosuppressive, vulnerary; vaccine; antiinflammatory; neuroprotective, nephrotropic, cardiovascular; human, cancer, autoimmune disease; wound healing disorder; infection, haematopoietic disorder, inflammatory disorder; infertility; neurological disease; psychiatric disease; cardiovascular disease; respiratory disease; renal; gastrointestinal; ss.
                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                         ; Score 384; DB 22; Length 384; ; Pred. No. 9.7e-114; 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;
                                                                                                                                                                                                                      in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding novel secreted protein #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 ACGGATATTGACTTCTTCTGCGAG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 ACGGATATTGACTTCTTCTGCGAG 384
                                                                                             Example 1; Page 91; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS17583 standard; cDNA; 387 BP
                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                        Matches 384; Conservative
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
 P-PSDB; AAB69123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                      diseases
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The invention relates to an isolated novel secreted polypeptide (I) and purelectide (II). (I) and (II) are useful for treating cancer, autoimmune diseases, wound healing disorder, infections, haematopoietic disorders, inflammatory disorders, infertility, neurological and isorders, inflammatory disorders, infertility, neurological and specification of seases, respiratory diseases, repiratory diseases, renal diseases, abnormalities and disorders caused by abnormal expression, production, function and/or metabolism of the genes, as vaccines for inducing immunological response in a mammal, and in screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. The polypeptides can be used as immunogens to produce antibodies immunospecific for the polypeptides, and to identify membrane-bound or soluble receptors. The polymelostides, and to identify membrane-bound or soluble receptors. The polymocleotides may be used as diagnostic reagents, in chromosome localisation studies, and in tissue expression studies. The present sequence represents the coding sequence of novel human secreted protein #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ATATITATGGACCGICTAGCTICCAAGAAGCICTGIGCAGATGAIGAGGGTGTGTCTATACT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 Triridederreschererrargerearescheschenegagareschererescharrire 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Arescandaniarierracirritecrecesererreresecrerarerecreserandes 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New secreted proteins or polypeptides, useful for treating e.g. cancer, autoimmune diseases, wound healing disorder, infections, haematopoietic disorders, inflammatory disorders, infertility, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 384; DB 24; Length 387; 100.0%; Pred. No. 9.7e-114; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith RF, Xiang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other;
                                  /product= "Human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agarwal P, Murdoch PR, Rizvi SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 44; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMIK ) SMITHKLINE BEECHAM PLC.
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                                                                                                                                                                                                                                                                                                                       11-APR-2001; 2001WO-US11797.
                                                                                                                                                                                                                                                                                                                                                                                                           13-APR-2000; 2000US-196603P.
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Matches 384; Conservative
/*tag=
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                                                                                                                                     WO200179454-A1.
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0; Gaps

0; Indels

9 78 180

258

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The present sequence is that of Hyseq clone identification number 1637272, which was obtained from a human thymus CDMA library using standard PCR with primers specific for vector sequences flanking the inserts, sequencing by hybridisation sequence signature analysis, and Sanger sequencing techniques. This expressed sequence tag was used in the assembly of a full-length CDMA sequence (see AARESA3) encoding a novel human growth CDMA sequence (see AARESA3) encoding a novel human growth could tory-like polypeptide (GRLP, see AABESA7). The GRLP belongs to the same protein family as growth regulatory proteins growth factors, human melanoma derived growth regulatory proteins or melanoma inhibitory activity, catlle cartilage-derived cretinoic acid sensitive protein (CD-RAP, 44% identity and 64% retinoic acid sensitive protein (CD-RAP, 44% identity and 64% retinoic acid sensitive protein (CD-RAP, 44% identity and 64% retinoic acid sensitive protein (CD-RAP, 44% identity and 64% retinoic acid sensitive protein (CD-RAP, 44% identity and 64% retinoic acid sensitive proteins. GRLP polypeptides and polynucleotides of the invention can be used in the prophylaxis, treatment (including gene therapy) can diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma cell growth and tumours, including neuroectodermal tumours such as and primers, for chromosome and gene mapping, in the recombinant production of protein, in the generation of antisense, ribozyme and peptide-nucleic acid molecules, and to produce transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system disorders.
                                                                                                                                                                                                                                                                                                                Growth regulatory-like polypeptide; human; cartilage; melanoma; neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
                                                                                                                                                                                                                                                                    Human growth regulatory-like polypeptide clone 16372272.
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Example 1; Page 114; 119pp; English.
                                                                                                                                                  AAH26341 standard; cDNA; 426 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-2001; 2001WO-US02455.
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02-MAY-2000; 2000US-0563786.
                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                   02-OCT-2001
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                                                                                                          RESULT 3
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100.0%; Score 384; DB 22; Length 426; 100.0%; Pred. No. 1e-113;

Best Local Similarity

Query Match

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259 TTTTGGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGTTTTTC 318
                                                                                                                                                                                                                                                                                                                       319 CCCAGGAACTTGGTCAAGGAACAGCGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosciderosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; gene; ss.
                                                                                                         79 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT 138
                                                                                                                                                                                          181 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240
                                                                                                                                                                                                                                               241 ITTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 300
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                                                                                                                                                   1 ATGCCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA
                                                    19 ATGGCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA
                                                                                                                                    ATTICICIGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT
                                                                              61 ATATITATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           379 ACGGATATTGACTTCTTCTGCGAG 402
                                                                                                                                                                                                                                                                                                                                                            361 ACGGATATTGACTTCTTCTGCGAG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL95740 standard; cDNA; 521 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUL-2001; 2001WO-US21735.
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Matches 384; Conservative
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23-AUG-2000;
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07-SEP-2000;
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoardial infarctions, thrombophiebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.
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Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
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                 28-FEB-2001; 2001US-0796498.
28-FEB-2001; 2001US-0796498.
28-FEB-2001; 2001WO-US06666.
09-MAR-2001; 2001US-0802706.
14-MAR-2001; 2001US-080889.
22-MAR-2001; 2001US-08386.
10-MAY-2001; 2001US-083486.
10-MAY-2001; 2001US-0834280.
25-MAY-2001; 2001US-0854280.
                                                                                                                                                                                                                                                                                           25-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001WO-US17092.
30-MAY-2001; 2001US-0870574.
                                                                                                                                                                                                                                                                                                                                                                      2001WO-US17443.
2001WO-US17800.
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28-JUN-2001; 2001WO-US00000.
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GODDARD A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GODOWSKI P J.
GURNEY A L.
HILLAN K J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENENTECH INC.
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WATANABE C K.
WILLIAMS P M.
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FERRARA N.
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01-JUN-2001;
22-JAN-2001;
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                                                                                                                               CCCAGGAACTIGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360
                                                                                                                                          TITIGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 300
                                                                                                                                                                                                                                                                                                                                                     Human; anglogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agnosis; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restences; angina; thematoid arthritis; mycardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
                                                                                              Human PRO9873 cDNA sequence SEQ ID NO:359.
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22-MAR-2001; 2001US-0816744.
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17-AUG-2000;
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ABK33571;
                       RESULT 6
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                                                                         ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
ABB85003. The PRO proteins and polymucleotides have cardiant, cytostatic,
antiangiogenic, hypotensive, vulnerary and antiatteriosclerotic
activities, and can be used in gene therapy. The PRO polymucleotides,
activities, and can be used in gene therapy. The PRO polymucleotides,
cardiachyscular, endothelial or angiogenic disorder in a mammal,
c a cardiach hypotrophy, trauma, cancer, age-related macular
c e.g. cardiach hypotrophy, trauma, cancer, age-related macular
c degeneration, atherosclerosis, hypertension, arterial restenosis,
c rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
c rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
c cardinoma) and wound healing The PRO polymucleotides have applications
c in molecular biology, including use as hybridisation probes, and in
chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
c probes used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                  One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
                                                                                                                                                                                                                   Paoni NF;
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                                                                                                                                                                                                               Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JP, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                    Goddard A;
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05-APR-2001; 2001US-0858366.

10-MRY-2001; 2001US-0858208.

10-MRY-2001; 2001US-0856228.

25-MRY-2001; 2001US-0866028.

25-MRY-2001; 2001US-0866034.

25-MRY-2001; 2001US-087092.

30-MRY-2001; 2001US-0870574.

30-MRY-2001; 2001WO-US17443.
                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                        Ferrara N,
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P-PSDB; ABB84996.
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One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antegonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human dermal
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                                                                                                                                                                                                     Human, secreted protein, PRO; tumour, lung cancer; colon cancer, breast cancer; prostate tumour, rectal tumour, liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha; gene; ss.
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Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                      cDNA encoding human PRO protein, Seq ID No 71.
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2000WO-US23522.
2000WO-US23328.
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2000US-220664P.
2000US-220666P.
2000US-220893P.
ABK33571 standard; cDNA; 521
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                                                                                                            (first entry)
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                                                                                                            08-MAY-2002
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fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. BRR3356-ABR33657 represent human PRO protein coding sequences of the invention.
                                                                                                                                                                                                   61 ATAITIAIGGACCGICIAGCIICCAAGAAGCICIGIGCAGAIGAIGAGGGGIGIGICIATACI 120
                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                             158 ATTICTICTIGGCIAGTGCTCAAGAATATTATAATGCCCCGGACTGTAGATTCATTAACGTT 217
                                                                                                                                                                                                                                                                                                       181 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240
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                                                                                                                                                                                                                                                                                                                                                       TTTTGGGCTGGCCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 300
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                                                                                                                                                                                                                                                                                                                                                                                                         CCCAGGAACTIGGICAAGGAACAGCGIGTGTACCAGGAAGCTACCAAGGAAGTICCCAACC 360
                                                                                                                                                                                                                                                                                                                                                                                                                     338 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 397
                                                                                                                                                                                                                           ATAITITAIGGACCGICTAGCIICCAAGAAGCICTGIGCAGAIGAIGAIGAGAGIGICIATACI 157
                                                                                                                                                   38 ATGGCAAGAATATTGTTTTTTCTCCCCGGGTCTTTGTGGCTGTATGTGCTGTGCATGGA 97
                                                                                                                                                                                                                                                                                                                       121 ATTICTCTGGCTAGTGCTCAAGAATTATAATGCCCCGGACTGTAGATTCATTAACGTT
                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; blodyversity; gene therapy; nutrition; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
                                                                                                 Query Match
100.0%; Score 384; DB 24; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.1e-113;
Matches 384; Conservative 0; Mismatches 0; Indels 0;
                                                                          Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human EST-derived coding sequence SEQ ID NO: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RA, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 ACGGATATTGACTTCTTGCGAG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGGATATTGACTTCTTCTGCGAG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH98228 standard; cDNA; 891 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (BSTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ATTTCTCTGGCTAGTGCTCAAGAATTATAATGCCCCGGACTGTAGATTCATTAACGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AAAAAAGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TITTGGGCTGGCAGTGTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 ATÁTTTATGGÁCCGTCTAGCTTCCAÁGAAGCTCTGTGCAGATGATGAGAGTGTGTCTATACT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 ATTICTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 ATGGCAAGAATATTGTTACTTTCCTCCCCGGGTCTTGTGGGCTGTATGTGCTGTGCATGGA 78
                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGGCAAGAATAITGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                    Isolated polypeptide for treatment of diseases, diagnostics, raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth regulatory-like polypeptide; human; cartilage; melanoma; neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 384; DB 22; Length 891; 100.0%; Pred. No. 1.4e-113; tive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human growth regulatory-like polypeptide partial cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 ACGGATATTGACTTCTTCTGCGAG 384
                                                                                                                                                                                           Claim 1; Page 236; 1275pp; English.
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                                                                                                                           antibodies and research use
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Matches 384; Conservative
WPI; 2001-476164/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the invention.
                            P-PSDB; AAM23569
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25-JAN-2001; 2001WO-US02455.

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cccadgaactrogreaagaacagcorororacaggaagcraccaaggaagrrcccacc 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAITTAIGGACCGICIAGCTICCAAGAAGCICIGIGCAGAIGAIGAGGGGGGTGICIATACT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTICICIGGCIAGIGCICAAGAAGAITAIAAIGCCCCGGACIGIAGAIICAIIAACGII 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triridescriescaererrianesrearesceaesaceaeareseaereseaeresearric 318
                                                                                                                                                                                                                         Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system
                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of a novel nucleic acid that was assembled from human thymus cDNA library-derived Hyseq clone identification number 16372272 (see AAH26341). A recursive identification number 16372272 (see AAH26341). A recursive sequences from different databases. A full-length sequence (see AAH26343) encoding novel human growth requlatory-like polypeptide (RRLP, see AABB2671) was subsequently obtained. Human GRLP belongs to the same protein family as growth regulatory proteins, belongs to the same protein family as growth regulatory proteins, carometric, human melanoma derived growth regulatory protein or melanoma inhibitory activity, cattle cartilage-derived retinoic acid sensitive protein (CD-RAP, 44% identity and 64% retinoic acid sensitive protein (CD-RAP, 44% identity and 64% retinoic acid sensitive protein (CD-RAP, 44% identity and 64% retinoic acid sensitive protein (cD-RAP, 64% identity and 64% retinoic acid sensitive growth and polynucleotides of the invention can diagnosis of disorders and diseases caused by, or involving, and diagnosis of disorders and maintenance, inhibition of melanoma cell content and maintenance, inhibition of melanoma cell content and maintenance, inhibition of melanoma cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antisense, ribozyme and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      production of protein, in the generation of antisense, ribozyme an peptide-nucleic acid molecules, and to produce transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for chromosome and gene mapping, in the recombinant f protein, in the generation of antisense, ribozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The polynucleotides can also be used to design probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth and tumours, including neuroectodermal tumours such as
                                                                                                                                Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 384; DB 22; 100.0%; Pred. No. 1.4e-113;
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                                                                                                                                Arterburn MC,
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                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 115; 119pp; English
                                                                                                                                    Ford JE,
                                  25-JAN-2000; 2000US-0491404.02-MAY-2000; 2000US-0563786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 384; Conservative
                                                                                                                                      Boyle BJ,
                                                                                                                                                                                                WPI; 2001-483233/52
                                                                                                (HYSE-) HYSEQ INC
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                                                                                                                                                         Drmanac RT;
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Gaps

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Indels

Length 891;

138

78

198 240

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DNAS. The MLP proteins and DNAS have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAS can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ATTICTCTGGCTAGTGCTCAAGAATTATAATGCCCCGGACTGTAGATTCATTAACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AAAAAAGGGCAGCAGCAGTTCTATGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 ATTICICTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention describes novel MLP proteins and their encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGGCAAGAATATTGCTTCTTCCTCCGGGTCTTGTGGCTGTATGTGCTGTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                           MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Noguchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 384; DB 22;
100.0%; Pred. No. 1.5e-113;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohkubo S, Mogi S,
                                                                                                                                                                                     Human MLP nucleotide sequence SEQ ID NO:29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 99-100; 111pp; Japanese.
379 ACGGATATTGACTTCTTCTGCGAG 402
                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0186718.
                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-2000; 2000WO-JP04278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TAKE ) TAKEDA CHEM IND LTD
                                                                                             AAF59083 standard; DNA; 923
                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishi K,
                                                                                                                                                                                                                                                                                                                               WO200102564-A1
                                                                                                                                                                                                                                                                   inhibitor; ds
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                                                                                                                                                           23-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanaka H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases
                                                                                                                           AAF59083;
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                                                                                 AAF59083
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274 TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGGAGTCGTGGGTATTTC 333
                                                                          TITIGGGCTGGCAGTGTTATGGTGATGGCCAGGACGAGGAGGGGGAGTCGTGGGTTATTTC 300
                                                          CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of a novel nucleic acid encoding human growth regulatory-like polypeptide (GRLP, see AAAB2671).
The sequence was assembled using human thymus cDNA library-derived Hyseq clone identification number 16372272 (see AAB26341) as seed, using software programs to pull additional sequences from Hyseq's proprietary database containing expressed sequence arg sequences, and by gel sequencing using primers to extend both 5' and 3' ends. The predicted protein has a mol.wt. of 14 kba unglycosylated. GRLP belongs to the same protein family as growth regulatory protein, growth factors, human melanoma derived growth regulatory protein precursor (64% similarity and 45% identity over 111 amino acids)
                                                                                                                                                                                                                                                                                                                                                    Growth regulatory-like polypeptide; human; cartilage; melanoma; neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ford JE, Arterburn MC, Tang YT, Liu C;
                                                                                                                                                                                                                                                                                                                     Human growth regulatory-like polypeptide cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 115-116; 119pp; English.
                                                                                                                                       394 ACGGATATTGACTTCTTCTGCGAG 417
                                                                                                                       361 ACGGATATTGACTTCTGCGAG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                AAH26343 standard; cDNA; 1201 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-2001; 2001WO-US02455
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02-MAY-2000; 2000US-0563786
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33..101
/*tag= b
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/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483233/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
or melanoma inhibitory activity, cattle cartilage-derived
retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
similarity over 126 annino acids) and other retinoic acid-sensitive
proteins.
GRLP polypeptides and polymucleotides of the invention
can be used in the prophylaxis, treatment (including gene therapy)
and diagnosis of disorders and diseases caused by, or involving,
cartilage development and maintenance, inhibition of melanoma cell
growth and tumours, including neuroectodermal tumours such as
gliomas The polymucleotides can also be used to design probes
and primers, for chromosome and gene mapping, in the recombinant
production of protein, in the generation of antisense, ribozyme and
production of protein, in the generation of antisense, ribozyme and
production of protein, in the generation of antisense, ribozyme and
production of protein, and cell proliferation octivity,
into any also have cytokine and cell proliferation octivity,
immunosupressive or immunostimulant activity, activity,
immunosupressive or immunostimulant activity, activity, inhibin
activity, chemotactic/chemoKinetic activity, haemostatic and
thrombolytic activity, use in cancer diagnosis and therapy,
drug screening, receptor/ligand activity, antinflammatory
arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 AAAAAAGGGCAGCAGGTCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 AAAAAAGGCCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGGTGTGTCTATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ATTICICICIGGCIAGIGCICAAGAAGATTATAAIGCCCCGGACTGTAGATTCATTAACGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 384; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1201 BP; 357 A; 188 C; 275 G; 381 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human MLP nucleotide sequence SEQ ID NO:23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 ACGGATATTGACTTCTTCTGCGAG 416
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The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis.

AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
                                                                                                                                                                                                  sare, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAGAATTTTGGCCTGGCAGTGTTTATGGTGATGCCAGGACGAGATGGGAGATGGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 CATGGAATATTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGATGAGTGTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 330; DB 22; Length 3; Pred. No. 2.5e-96; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 330 BP; 91 A; 60 C; 91 G; 88 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                              the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCACCACGGATATTGACTTCTTCTGCGAG 384
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                                                                                                                                    s,
                                                                                                                                                                                                                                                                               Claim 8; Page 97; 111pp; Japanese.
                                                                                                                                    Ohkubo
                                                                                                                                                                                                                                                                                                                                                                                                                                                85.9%; Sccilarity 100.0%; Pr
Conservative 0;
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                                                        29-JUN-2000; 2000WO-JP04278
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                                                                                                                                                                                           P-PSDB; AAB69126
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                                    11-JAN-2001
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                                                                                                                                                     Tanaka H;
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Score 287; DB 22; Pred. No. 2.1e-82; 0; Mismatches 60;

Query Match 74.7%; Best Local Similarity 84.3%; Matches 323; Conservative C

Length 384;

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1 ATGCCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA

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ATTICTCTGGGCTAGTGCTCAAGAAGATTATAATGCCCCGGGACTGTAGATTCATTAACGTT

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AAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA

181

181 241 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360 

ACGGATATTGACTTCTTCTGTGA 383 ACGGATATTGACTTCTCTGCGA 383

TITIGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGATTGGAATTGTAGGTTATTTC

241

301 301 361 361

TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC

120

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The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                     joint
                                                                                                                                                                                                                                                               Yoshimura
 MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
                                                                                                                                                                                                                                                                                                                                                                      opment of
bone and
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                                                                                                                                                                                                                                                               Noguchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;
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                                                                                                                                                                                                                                                                   Mogi
                                                                                                                                                                                                                                                                   Ohkubo S,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 93; 111pp; Japanese
                                                                                                                                                                                                          99JP-0186718.
                                                                                                                                                                                                                                      CHEM IND LID
                                                                                                                                                                                                                                                                    Ogi K,
                                                                                                                                                                                                                                                                                                                WPI; 2001-159271/16.
                                                                                                                                                                                                                                                                    Nishi K,
                                                                                                                                                                                                                                                                                                                              P-PSDB; AAB69125
                                                                                                                                                                                                                                         (TAKE ) TAKEDA
                                                                                                                    WO200102564-A1
                                                          inhibitor; ds
                                                                                                                                                                              29-JUN-2000;
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Tanaka H;
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Yoshimura

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ATATTTATGGACCGTCTAGCTTCCAAGAGGTCTGTGCAGATGATGAGTGTGTATAGT 120
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AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CCCAGGAACTIGGICAAGGAACAGCGIGIGIGIACCAGGAAGCIACCAAGGAAGTICCCACC 360
                                                                              Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGTGCATGGA
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                                                                                                                                                                                                                                                                                                                                                                                                        MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter; inhibitor; ds.
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Pred. No. 6.9e-82;
Trimitches 61; Indels
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 105-106; 111pp; Japanese.
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                                                                                                                                                          371 ACGGATATTGACTTCTTCTGTGA 393
                                                                                                                                       361 ACCGATATTGACTTCTGCGA 383
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                                                                                                                                                                                                                                                                     BP
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                                                                                                                                                                                                                                                                     AAF59098 standard; DNA; 384
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                                                                                                                                                                                                                                                                                                                                             entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAAAGGGCAGCAGTATGTATGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TITTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATAITTAIGGACCGICTAGCTICCAAGAAGCICTGIGCAGAIGAIGAGIGIGICTAIACI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in Arugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF5909 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGCCAAGAATATTGCTTACTTTTCCTCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;
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                                                                                                                                                                                                      Mouse MLP nucleotide sequence SEQ ID NO:30.
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                                                                                                 BP
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al Similarity 84.3%;
323; Conservative (
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                                                                                                 AAF59084 standard;
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48; Indels 22;

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Query Match 65.7%; Best Local Similarity 85.4%; Matches 281; Conservative

Length 330;

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234 180 294 240

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AAGAAAGGCCAGCAGATCTATGTTTTCCAAGCTGGTAACAGAAAATGGAGCTGGGCA 240
                                                                                                 TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 300
                                                                                                             CCCAGGAACTIGGICAAGGAACAGCGIGIGIACCAGGAAGCIACCAAGGAAGTICCCACC 360
                                                                                                                                                          cccascaacrigerragadascaacgasteraccascaccaccaacgastrocaacc 360
ATGITTATGGATAAACTTTCTTAAGAAGTTGTGTGCAGATGAGGAGTGTGTCTATACC 120
                   121 ATTICTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT 180
                                     AAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAAGAAAATGGAGCTGGAGAA
                                                                                                                                                                                                                                                                                                                        MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter; inhibitor; ds.
                                                                                                                                                                                                                                                                                                          Mouse MLP nucleotide sequence SEQ ID NO:25
                                                                                                                                                                                      361 ACGGATATTGACTTCTTCTGTGA 383
                                                                                                                                                                             ACGGATATTGACTTCTGCGA 383
                                                                                                                                                                                                                                                 AAF59080 standard; DNA; 330
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241 TATTTCCCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGTT 300
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                                                                                                                             61 TATACTATTTCTCTGGCAAGAGACACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATC 120
                                                                                                                                                                                                                                                                                                                                                                                                   295 TATTTCCCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTT 354
                                                                                                                                                                                                                            121 GATGTCAAGAAAGGGCAGCAGAATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCT
55 CATGGAATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTC
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                                                 235 GGAGAATTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGG
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The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of pronoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used

Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other; in the exemplification of the present invention.

Safe low-toxicity secretory cell function-regulatory protein and encoced DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint

Claim 10; Page 98; 111pp; Japanese.

Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

29-JUN-2000; 2000WO-JP04278.

11-JAN-2001.

99JP-0186718

30-JUN-1999;

(TAKE ) TAKEDA CHEM IND LTD

WPI; 2001-159271/16. P-PSDB; AAB69127.

Tanaka H;

Itoh Y,

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December 30, 2003, 04:08:13; Search time 315.339 Seconds (without alignments) 4172.254 Million cell updates/sec
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12: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
15: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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IES		6-0	6-16	8-7	9-0	9-0	9-0	9-0	9-0	.0-6	9-4	9-4	9-4	9-5	9-5	9-5
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115-10-219-531-71	US-10-219-	US-10	US-10-223	US-10-230	US-10-232-228	US-1	US-10-227-	US-10-230-	5 US-10-230-338-71	US-10-218-	US-10-230-414-	US-10	US-10	US-10	US-10-227	US-10-219	US-10-230	US-1	US-10-219	US-10-219	US-10-219	US-10-219-479	US-10-21	US-10-230-	US-10-232-	US-10-23	US-10-216-		US-10-219	
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## ALIGNMENTS

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RESULT 1

1 Sequence 1, Application US/10216038

1 Publication No. US200124573A1

1 Sequence 1, Application US/10216038

2 Sequence 1, Application Wo. US200124573A1

2 SEQUENCE No. US200124573A1

3 APPLICANT: Pord, John E

APPLICANT: Ford, John E

APPLICANT: Pord, John E

APPLICANT: Pord, Vong

APPLICANT: Pord, Vong

APPLICANT: Wise, Methods and Materials Relating to No. US20030124573A1e1 Growth F

TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1e1 Growth F

TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1e1 Growth F

TITLE OF INVENTION: Methods and Polymptides and Polympticotides

TITLE OF INVENTION: WORDER: US/10/216,038

CURRENT PLIANG DATE: 2000-06-02

PRIOR FILING DATE: 2000-06-02

PRIOR FILING DATE: 2000-01-25

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 1

LENGTH: 426

TYPE: DAA

COSTUMARE: PATERIT OF SEQ ID NOS: 8

SEQ UD NO 1

SEQ UD NO 1

SEQ UD NO 1

SEQ UD NO 1

SEQ UD NO 1

SEQ UD NOS: 8

CONTRARE PATERIES: MATERIA (426)

TYPE: DAA

CONTRARE INFORMATION: n = A, T, G, Or C

US-10-216-038-1

Best Local Similarity 100.0%; Score 384; DB 15; Length 426;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Descroyers, Luc
APPLICANT: Descroyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Mood, Milliam I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDE ENCODING THE SAME
TITLE OF INVENTION: ACIDE ENCODING THE SAME
FILE REFERENCE: P3530PLC19
CURRENT APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065287
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-12-17
PRIOR PLING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/069873
PRIOR PLING DATE: 1997-12-17
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                                                                                                                                                         Score 384; DB 13;
Pred. No. 7.1e-118;
Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 7.1
Matches 384; Conservative 0; Mismatches
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; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANIEM: Homo Sapien
US-10-216-163-71
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APPLICANT: Geddard, Audrey
APPLICANT: Gedwski, Paul J.
APPLICANT: Gramaldi, J. Christopher
APPLICANT: Gramaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Scephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: WATANAMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPRENCE: 19330PIC3
CURRENT APPLICATION NUMBER: 60/05213
PRIOR APPLICATION NUMBER: 60/05287
PRIOR APPLICATION NUMBER: 60/06349
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PRIOR APPLICATION NUMBER: 60/06349
PRIOR APPLICATION NUMBER: 60/06349
PRIOR APPLICATION NUMBER: 60/06393
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-26
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PRIOR FILING DATE: 1998-03-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319
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R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/079294
R FILING DATE: 1998-03-25
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R APPLICATION NUMBER: 60/079728
R APPLICATION NUMBER: 60/081819
R FILING DATE: 1998-04-15
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A FILING DATE: 1998-08-11
A APPLICATION NUMBER: 60/096791
A APPLICATION NUMBER: 60/097986
A FILING DATE: 1998-08-26
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APPLICATION NUMBER: 60/100627
FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100848
FILING DATE: 1998-09-18
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APPLICATION NUMBER: 60/095318
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APPLICATION NUMBER: 60/09596
FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/09598
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FILING DATE: 1998-09-10
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APPLICATION NUMBER: 60/099812
FILING DATE: 1998-09-10
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APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/090691
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
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FILING DATE: 1998-08-10
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FILING DATE: 1998-09-10
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FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/085323
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FILING DATE: 1998-05-15
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FILING DATE: 1998-05-22
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/091982
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PRIOR FILING DATE: 1938-09-17

PRIOR FILING DATE: 1938-09-24

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PRIOR PILING DATE: 1938-09-10-8

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PRIOR PILING DATE: 1939-0-12-3

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PRIOR PILING DATE: 1939-0-12-3

PRIOR PILING DATE: 1939-0-12-1

PRIOR PILING DATE: 1939-0-12-1

PRIOR PILING DATE: 1939-0-12-1

PRIOR PILING DATE: 1939-0-12-1

PRIOR PILING DATE: 1939-0-12-1

PRIOR PILING DATE: 1939-0-12-1

PRIOR PILING DATE: 1939-0-12-1

PRIOR PILING DATE: 1939-0-12-
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61 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT 120
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                 FILE REFERENCE: P3530PLC24
CURRENT APPLICATION: ALIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC24
CURRENT APPLICATION NUMBER: US/10/219,063
CURRENT FILING DATE: 2002-08-13
PRIOR PLING DATE: 1997-09-17
PRIOR PELICATION NUMBER: 66/06287
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-38
PRIOR FILING DATE: 1997-10-31
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           ENCODING THE SAME
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US-10-219-066-71
Sequence 71, Application US/10219066
Publication No. US20030187203A1
GENERAL INFORMATION:
APPLICANT: BAREr, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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Matches 384; Conservative
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ORGANISM: Homo Sapien
US-10-219-063-71
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Fublication No. US20030187202A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Geritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Stephan Ginaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan Jean-Philippe F.
APPLICANT: Stephan Jean-Philippe F.
APPLICANT: Stephan Jean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
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PRIOR FILING DATE: 1999-07-20
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/145227
PRIOR APPLICATION NUMBER: 60/145227
PRIOR PLING DATE: 1999-07-86
PRIOR FILING DATE: 1999-08-03
PRIOR FILING DATE: 1999-08-17
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PRIOR PLING DATE: 1999-11-09
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US-10-219-063-71
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Sequence 71, Application US/10219067 Publication No. US20030187204A1 GENERAL INFORMATION:
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; ORGANISM: Homo Sapien
US-10-219-067-71
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APPLICANT: Godowski, Autrey
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APPLICANT: Godowski, Autrey
APPLICANT: Godowski, Autrey
APPLICANT: Godowski, Autrein
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
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APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIOS ENFORMED THE SAME
TITLE OF INVENTION: ACIOS ENFORMED THE SAME
TITLE OF INVENTION: ACIOS ENFORMED THE SAME
TITLE OF INVENTION: ACIOS ENFORMED THE SAME
TITLE OF INVENTION: ACIOS ENFORMED THE SAME
TITLE OF INVENTION WINDER: US/10/219,066
CURRENT FILING DATE: 1097-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR PELLOR ON WHERE: 60/06349
PRIOR FILING DATE: 1997-10-17
PRIOR PELLOR ON WHERE: 60/064103
PRIOR FILING DATE: 1997-10-17
PRIOR PELLOR ON WHERE: 60/06973
PRIOR FILING DATE: 1998-03-20
PRIOR PELLOR ON WHERE: 60/079294
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PRIOR PELLOR ON WHERE: 60/079294
PRIOR PELLOR DATE: 1998-03-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 384; Conservative
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-219-066-71
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APPLICANT Desnoyers, Luc.
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APPLICANT Gerriteen, Mary
APPLICANT Godowski, Paul J.
APPLICANT Godowski, Paul J.
APPLICANT Godowski, Paul J.
APPLICANT Godowski, Paul J.
APPLICANT Grimaldal, J. Christopher
APPLICANT Grimaldal, J. Christopher
APPLICANT Smith, Victoria
APPLICANT Watanabe, Colin L.
APPLICANT Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPRENCE: P3530PLC31
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPRENCE: P3530PLC31
TOTHER OF APPLICATION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 60/063913
PRIOR APPLICATION NUMBER: 60/063913
PRIOR PLING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/06393
PRIOR APPLICATION NUMBER: 60/06393
PRIOR APPLICATION NUMBER: 60/079394
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PRIOR APPLICATION NUMBER: 60/079394
PRIOR PLING DATE: 1998-03-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ATTICTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 AAAAAAGGCCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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100.0%; Score 384; DB 13;
Best Local Similarity 100.0%; Pred. No. 7.1e-118;
Matches 384; Conservative 0; Mismatches 0;
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1 ATGGCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGGCTGTATGTGCTGTGCATGGA 60
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ORGANISM: Homo Sapien
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APPLICANT: Goddard, Addrey
APPLICANT: Goddard, Addrey
APPLICANT: Gordard, Austin L.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Matenabe, Colin L.
APPLICANT: Necod, William I.
APPLICANT: Necod, William I.
APPLICANT: Matenabe, Colin L.
APPLICANT: Necod, William I.
APPLICANT: NOWER: US/10/219,068
CURRENT APPLICATION NUMBER: US/10/219,068
CURRENT FILING DATE: 1090-20-0-17
FRIOR APPLICATION NUMBER: 60/06213
FRIOR APPLICATION NUMBER: 60/06213
FRIOR APPLICATION NUMBER: 60/06213
FRIOR APPLICATION NUMBER: 60/06313
FRIOR PELING DATE: 1997-10-13
FRIOR FILING DATE: 1997-10-11
FRIOR PELING DATE: 1997-10-11
FRIOR APPLICATION NUMBER: 60/06913
FRIOR APPLICATION NUMBER: 60/06913
FRIOR APPLICATION NUMBER: 60/079294
FRIOR RILING DATE: 1998-03-25
FRIOR APPLICATION NUMBER: 60/079294
FRIOR RILING DATE: 1998-03-25
FRIOR RILING DATE: 1998-03-27
FRIOR FILING DATE: 1998-03-27
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                              98 ATATITATIGGACCGICIAGCITCCAAGAAGCICTGIGCAGAIGAIGAGTGTGTGTTATACT 157
301 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGCAAGAATAITGTTACTTTTTCCTCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 ArgecaAgaArarretracrrrrccrcccccccrcrrcrcrcrargracrercreraccarcca 97
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                                                                                                                                                              398 ACGGATATTGACTTCTTCTGCGAG 421
                                                                                                                         361 ACGGATATTGACTTCTTCTGCGAG 384
                                                                                                                                                                                                                                                                                                                                        Sequence 71, Application US/10219068 Publication No. US20030187205A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                       US-10-219-068-71
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US-10-219-068-71
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LENGTH: 521
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GENERAL INCORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Benoyers, Luc
APPLICANT: Geraiteen, Mary
APPLICANT: Gedowski, Mary
APPLICANT: Gerialdi, J. Christopher
APPLICANT: Gerimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
CURRENT FILING DATE: 2002-09-13
PRIOR PLING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/05287
PRIOR APPLICATION NUMBER: 60/05287
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1998-10-32
PRIOR APPLICATION NUMBER: 60/06993
PRIOR APPLICATION NUMBER: 60/06993
PRIOR APPLICATION NUMBER: 60/06993
PRIOR APPLICATION NUMBER: 60/06993
PRIOR APPLICATION NUMBER: 60/079204
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                                                                      181 AAAAAAGGCCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240
                                                                                                                118 AAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAATGGAGCTGGAGAA 277
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NUMBER OF SEQ ID NOS: 246
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Best Local Similarity 100.0
Matches 384; Conservative
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; TYPE: DNA; CORGANISM: Homo Sapien US-10-219-073-71
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APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Gurney, Austin L.

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

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APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

PRIOR PAPLICATION NUMBER: 10/19,480

PRIOR FILING DATE: 1997-10-17

PRIOR PELING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/06329

PRIOR PELING DATE: 1997-10-26

PRIOR PELING DATE: 1997-10-26

PRIOR PELING DATE: 1997-10-26

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PRIOR PELING DATE: 1997-10-26

PRIOR PELING DATE: 1998-03-26

PRIOR PEL
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                                                                                                                                 98 ATATTTARGGACCGICTAGCTTCCAAGAAGCTCTGTGCAGATGAGTGAGTGTGTCTATACT 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
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Sequence 71, Application US/10219475

Sequence 71, Application US/10219475

Publication No. US2003018720841

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Austin L.

APPLICANT: Ginaldi, J. Christopher

APPLICANT: Ginaldi, J. Christopher

APPLICANT: Ginaldi, J. Christopher

APPLICANT: Ginaldi, J. Christopher

APPLICANT: Ginaldi, J. Christopher

APPLICANT: Ginaldi, J. Christopher

APPLICANT: Ginaldi, J. Christopher

APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

APPLICANT: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE

FILE REPERENCE: PSSO101C49

CURRENT APPLICATION NUMBER: US/10/219,475
                                                                                                                                                                                                                                                                                           61 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT 120
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                                                                                Gaps
                                                                            0;
Query Match 100.0%; Score 384; DB 13; Length 521; Best Local Similarity 100.0%; Pred. No. 7.1e-118; Matches 384; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2002-04-15
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1007-09-17
PRIOR PRILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06349
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/069913
PRIOR FILING DATE: 1997-12-17
PRIOR PLING DATE: 1997-12-17
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
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TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-480-71
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US-10-219-483-71
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APPLICANT: Desnoyers, Luc
APPLICANT: Geddard, Audres,
APPLICANT: Goddard, Audres,
APPLICANT: Goddard, Audres,
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Ausrin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Schan-Philippe F.
APPLICANT: Schan-Philippe F.
APPLICANT: ARTHADE, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: MACHADE, COLIN L.
APPLICANT: MACHADE, COLIN L.
APPLICANT: MACHADE, COLIN B.
APPLICANT: MACHADE, COLIN B.
APPLICANTON NUMBER: US/10/219,480
FRIOR APPLICATION NUMBER: 60/06213
FRIOR APPLICATION NUMBER: 60/06213
FRIOR APPLICATION NUMBER: 60/062287
FRIOR FILING DATE: 1997-017
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PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or FALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
                                                                                                                                                                                                                                                             Length 521;
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Publication No. US20030187209A1
GRNERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Deenoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                          US-10-219-475-71
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181 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 ATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT 217
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PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/064103

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-12-3

PRIOR FILING DATE: 1997-12-3

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-25

PRIOR PILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-03-27

PRIOR PRIOR APPLICATION NUMBER: 60/079728

PRIOR PILING DATE: 1998-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 246

LENGTH: 521

TYPE: NUMBER: NUMBER: 521
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APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Mary
APPLICANT: Goddard, Andrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, COLIN L.
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APPLICANT: Watanabe, COLIN L.
APPLICANT: Watanabe, COLIN L.
APPLICANT: Watanabe, COLIN L.
APPLICANT: Watanabe, COLIN L.
APPLICANT: WATANAWEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 ATGGCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGGCTGTATGTGCTGTGCATGGA
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Pred. No. 7.1e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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; Publication No. US20030187210A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 384; Conservative
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; ORGANISM: Homo Sapien
US-10-219-525-71
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LENGTH: 521
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100.0%; Score 384; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.1e-118;
Matches 384; Conservative 0; Mismatches 0; Indels 0
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          TILD KEEREMALE: F30207143,
CURRENT PELLING DATE: 2002-08-13
PRIOR FILING DATE: 2002-08-13
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/05213
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/06287
PRIOR PELLING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/06973
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
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Publication No. US20030187211A1
GENERAL INFORMATION:
APPLICANT: Bester, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
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FILE REFERENCE: P3530P1C43
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Viccoria
APPLICANT: Smith, Viccoria
APPLICANT: Smith, Viccoria
APPLICANT: Smath, Viccoria
APPLICANT: Matanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANTON: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
CURRENT FILING DATE: 2002-08-13
FRIOR FILING DATE: 2002-04-09
FRIOR PELING DATE: 1997-09-17
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100.0%; Score 384; DB 13;
Best Local Similarity 100.0%; Pred. No. 7.1e-118;
Matches 384; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGGATATTGACTTCTTCTGCGAG 384
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361 ACGGATATTGACTTCTTCTGCGAG 384
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Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Jean-Philippe F.
Watanabe, Colin L.
Wood, William I.
                                                                                                                                                                                                                                                                                                       ; Sequence 71, Application US/10219530; Publication No. US20030187213A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo Sapien
US-10-219-530-71
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TYPE: DNA
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## APPLICANT: Goddard, Audrey
## APPLICANT: Goddard, Audrey
## APPLICANT: Gramey, Austin U.
## APPLICANT: Smith, Victoria
## APPLICANT: Smith, Victoria
## APPLICANT: Smith, Victoria
## APPLICANT: Smith, Victoria
## APPLICANT: Smith, Victoria
## APPLICANT: Watanabe, Colin L.
## APPLICANT: Watanabe, Colin L.
## APPLICANT: Watanabe, Millippe F.
## APPLICANT: Watanabe, Millippe F.
## APPLICANT: WOOD, ## ALDS ENCODING THE SAME
## TILLE OF INVENTION: ACIDS ENCODING THE SAME
## TILLE OF INVENTION NUMBER: 60/05213
## PRIOR PILLING DATE: 1997-10-17
## PRIOR PILLING DATE: 1997-10-28
## PRIOR PILLING DATE: 1997-10-28
## PRIOR PILLING DATE: 1997-10-31
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US-10-219-526-71; Sequence 71, Application US/10219526; Publication No. US20030187212A1; GENERAL INFORMATION:
                                                                                                                      APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo Sapien
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APPLICANT:

TITLE OF INVENTION: SECRETED JAN TRANSMEMBRANB POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3530P1C54

CURRENT APPLICATION NUMBER: US/10/219,530

CURRENT APPLICATION NUMBER: US/10/19,480

PRIOR APPLICATION NUMBER: 60/059113

PRIOR PILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-10-17

PRIOR PLING DATE: 1997-10-17

PRIOR PLING DATE: 1997-10-17

PRIOR PLING DATE: 1997-10-17

PRIOR PLING DATE: 1997-11-17

PRIOR PLING DATE: 1997-11-17

PRIOR PLING DATE: 1997-11-17

PRIOR PLING DATE: 1997-11-17

PRIOR APPLICATION NUMBER: 60/069873

PRIOR APPLICATION NUMBER: 60/078910

PRIOR PLING DATE: 1998-03-20

PRIOR PLING DATE: 1998-03-20

PRIOR PLING DATE: 1998-03-20

PRIOR PLING DATE: 1998-03-20

PRIOR PLING DATE: 1998-03-26

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301 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360
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                                                   338 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 397
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        QY
        181 AAAAAAGGGCAGCAGCTATCTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA
        240

        Db
        218 AAAAAAGGCAGCAGTTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGTGGAGAA
        277

        QY
        241 TTTTGGGCTGGTGTTTATGGTGATGGCCAGGACGAGTGGTGGTTATTTC
        300

        Db
        278 TTTTGGGCTGGTGTTTATGGTGATGGCCAGGACGAGTCGTGGGTTATTTC
        330

        CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAGTCGTGGGTTATTTC
        337

        QY
        301 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAATTCCCACC
        360

        Db
        338 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC
        397

        QY
        361 ACGGATATTGACTTCTTGCGAG
        384

        Db
        398 ACGGATATTGACTTCTTTCTGCGAG
        421
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Search completed: December 30, 2003, 10:03:00 Job time : 318.339 secs

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December 30, 2003, 02:01:19; Search time 1831.44 Seconds (without alignments) 6953.486 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
                                  OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
                                                                                   US-10-019-455A-4
384
                                                                                               Perfect score:
                                                                                                                       Scoring table:
                                                                                                        Sequence:
                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                Database
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence 4, Appli	Sequence 12, Appl	Sequence 12, Appl	Segmence 12 Appl
ID	1 384 100.0 384 44 US-10-019-455A-4	PCT-US01-11797-12	2 PCT-US01-11797-12	174-10-257-174-12
DB	44	٦	7	4
Query Match Length DB ID	384	387	387	787
Query Match	100.0	100.0	100.0	100
Score	384	384	384	384
Result No.	н	7	ĸ	4

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Sequence 107188,
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Sequence 107188,
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US-09-528-409-107188

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US-09-933-524A-107188

US-10-216-038-1

US-10-218-038-1

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Sequence 4, Application US/10019455A

GENERAL INFORMATION:
APPLICANT: ITCH, YASUGARI
APPLICANT: OGG, KAZUNORI
APPLICANT: OGG, KAZUNORI
APPLICANT: OHCUBO, SHOICHI
APPLICANT: OHCUBO, SHOICHI
APPLICANT: OHCUBO, SHOICHI
APPLICANT: NOGUCHI, VUKO
ITILE OF INVENTION: NOUGH, PEPTIDE AND DNA THEREOF
FILE REFERENCE: 56804-46342
CURRENT APPLICATION UNDERF: US/10/019,455A
CURRENT APPLICATION UNDERF: 2002-04-22

NUMBER OF SEQUENCE: 2002-04-22
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US-10-219-071-71
US-10-219-072-71
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Score 384; DB 44; Length 384; Pred. No. 1.1e-107;

100.0%;

Query Match Best Local Similarity

SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 4 LENGTH: 384

TYPE: DNA ORGANISM: Homo sapiens

; NAME/KEY: CDS ; LOCATION: (1)..(384) US-10-019-455A-4

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Best Local Similarity 100.0%; Pred. No. 1.1e-107;
Matches 384; Conservative 0; Mismatches 0; Indels
    0; Indels
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PCT-US01-11797-12

PCT-US01-11797-12

Sequence 12, Application PC/TUS0111797

GENERAL INFORMATION:

APPLICANT: SMITHKLINE BEECHAM CORPORATION

APPLICANT: SMITHKLINE BEECHAM D.1.c.

TTTLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GPS0022

CURRENT APPLICATION NUMBER: PCT/US01/11797

CURRENT FILING DATE: 2000-04-13

PRIOR APPLICATION NUMBER: 60/199,417

PRIOR FILING DATE: 2000-04-24

NUMBER: OF SEQ ID NOS: 48

SOUTHARE: FREESEQ for Windows Version 3.0

SEQ ID NO 12

LENGTH: 387
    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REPERENCE: GP50022
CURRENT APPLICATION NUMBER: PCT/USO1/11797
CURRENT FILING DATE: 2001-04-11
PRIOR PEDIGATION NUMBER: 60/196,603
PRIOR PILING DATE: 2000-04-13
PRIOR PILING DATE: 2000-04-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FRASESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                            Sequence 12, Application PC/TUS0111797
SENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM P.1.c.
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Best Local Similarity
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LENGTH: 387
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APPLICANT: Tang, Y Tom
APPLICANT: Int, Chenghua
APPLICANT: Int, Chenghua
APPLICANT: Int, Chenghua
APPLICANT: Int, Chenghua
APPLICANT: Int, Chenghua
TITLE OF INVENTION: Methods and Materials Relating to Novel Growth Regulatory-like
TITLE OF INVENTION: Methods and Polynucleotides
TITLE OF INVENTION: Polypeptides and Polynucleotides
CURRENT APPLICATION NUMBER: PCT/US01/02455
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/563,786
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Best Local Similarity 100.0%; Pred. No. 1.1e-107;
Matches 384; Conservative 0; Mismatches 0;
            APPLICANT: RIZAL, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Smith, Randall F.
APPLICANT: Smith, Randall F.
APPLICANT: Stang, Zhaoying
FILE REFERENCE: GP50022
CURRENT APPLICATION NUMBER: US/10/257,174
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: ECT/US01/11797
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
SOFTWARE: PRESEQ for Windows Version 3.0
SECTION 0.12
LENGTH: 387
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Ford, John E
Arterburn, Matthew C
Murdoch, Paul R.
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APPLICANT: Mize, Nancy K
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US-10-257-174-12
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PCT-US01-02455-1
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                                                                                                                                                                                                Length 426;
                                                                                                                                                                                          100.0%; Score 384; DB 2; Length 4:
100.0%; Pred. No. 1.2e-107;
tive 0; Mismatches 0; Indels
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark
APPLICANT: Dickson, Mark
APPLICANT: Jones, Lee W.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 774
CURRENT APPLICATION NUMBER: US/09/528,409
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                                                                   NAME/KEY: misc_feature
i_LOCATION: (1)..(426)
control information: n = A, T, G, or C
PCT-US01-02455-1
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BER: 60/125,453
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PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 107188
LENGTH: 426
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; OTHER INFORMATION: n = A,T,C or G
US-09-528-409-107188
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Best Local Similarity 100.0
Matches 384; Conservative
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ORGANISM: Homo sapiens
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TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Mize, Nancy K
APPLICANT: Boyle, Bryan J
APPLICANT: Boyle, Bryan J
APPLICANT: Ford, John E
APPLICANT: Ford, John E
APPLICANT: Arterburn, Matthew C
APPLICANT: Tang, Y Tom
APPLICANT: Tang, Y Tom
APPLICANT: Tang, Y Tom
APPLICANT: Tang, Y Tom
APPLICANT: Div. Chenghua
APPLICANT: Div. Chenghua
APPLICANT: Div. Chenghua
APPLICANT: Div. Chenghua
APPLICANT: Div. Chenghua
APPLICANT: Div. Chenghua
APPLICANT: Div. Chenghua
APPLICANT: Div. Chenghua
APPLICANT: Div. Chenghua
FILE OF INVENTION: Polypeptides and Polynucleotides
TITLE OF INVENTION: Polypeptides and Polynucleotides
CURRENT APPLICATION NUMBER: 12001-01-25
PRIOR APPLICATION NUMBER: US 09/563,786
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR APPLICANT: DIV. CONC. 7
SOFTWARE: PatentIn version 3.0
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100.0%; Pred. No. 1.2e-107;
tive 0; Mismatches 0; Indels 0; Gaps
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                             09/491,404
                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)._(426)
OTHER INFORMATION: n = A, T, G, or C
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PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: US 09/4;
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 7
SCOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 426
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Matches 384; Conservative
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PCT-US01-02455-1
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LENGTH: 426
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                                                                        199 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 258
                                                                                                                                        241 TITIGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 300
                                                                                                                                                                      199 AAAAAGGGCAGCAGATCTAIGTGTACTCAAAGCTGGTAAAAGAAAAIGGAGCTGGAGAA 258
139 ATTICICIGGCTAGIGCICAAGAAGATTATAATGCCCCGGACIGTAGATTCATTAACGIT 198
                                                                                                                                                                                                                                  301 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 107188. Application US/09933524
GENERAL INFORMATION:
APPLICANT: Dranac. Ivan
APPLICANT: stache-Crain, Birgit
APPLICANT: Dickson, Mark
APPLICANT: Jones, Lee W.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 1.26
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CURRENT APPLICATION NUMBER: US/09/933,524

CURRENT FILING DATE: 2001-08-20

FRIOR PEPLICATION NUMBER: 09/528,409

FRIOR FILING DATE: 2000-03-17

NUMBER OF SEQ ID NOS: 116231

SOFTWARE: Hy-patent.pl Version 3.1

SEQ ID NO 107188

LENGTH: 426
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| LOCATION: (1)...(426)
| OTHER INFORMATION: n = A,T,C or G
US-09-933-524-107188
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US-09-933-524-107188
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APPLICANT: Mize, Nancy K
APPLICANT: Boyle, Bryan J
APPLICANT: Ford, John E
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Methods and Materials Relating to Novel Growth Regulatory-like
TITLE OF INVENTION: Polypeptides and Polynucleotides
                                                                                                                                                                                                                                                                                                                                                                        319 CCCAGGAACTTGGTCAAGGAACAGGGTGTGCCAGGAAGCTACCAAGGAAGTTCCCACC 378
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                                                                                              61 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT 120
                                                                                                                                                                                                              181 AAAAAAGGGCAGCAGCAGTTTTGTGTTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240
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                           19 ATGGCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA 78
       1 AIGGCAAGAAIAIIGIIACIIIIICCICCCGGGICIIGIGGCIGIAIGIGCIGIGCAIGGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/563,786A CURRENT FILING DATE: 2000-05-02 PRICR APPLICATION NUMBER: US/9/491,404 PRIOR FILING DATE: 2000-01-25
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LOCATION: (1). (426)
OTHER INFORMATION: n = A, T, G, or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/09563786A; GENERAL INFORMATION:
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Best Local Similarity 100.09
Matches 384; Conservative
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SOFTWARE: Patentin ve
SEQ ID NO 1
LENGTH: 426
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US-09-563-786A-1
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APPLICANT: TALELLY, MACLIEW APPLICANT: TALELY, Y TON
APPLICANT: Tang, Y TON
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Drwanac, Radoje T
APPLICANT: Song, Yong Michael
TITLE OF INVENTION: Methods and Materials Relating to Novel Growth Regulatory-like
TITLE OF INVENTION: Polypeptides and Polymucleotides
TITLE OF INVENTION: Polypeptides and Polymucleotides
TITLE OF INVENTION: POLYPEDTICAL NOVEL SONG-08-08
GURRENT APPLICATION NUMBER: US/10/216,038
CURRENT APPLICATION NUMBER: US 09/563,786
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 8
SOTTWARE: PATENTIN PATENTION 3.1
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LOCATION: (426)...(426)

POTHER INFORMATION: n = A, T, G, or C

US-10-216-038-1
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APPLICANT: Mize, Nancy K
APPLICANT: Boyle, Bryan J
APPLICANT: Ford, John E
APPLICANT: Arterburn, Matthew C
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
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Boyle, Bryan J
Ford, John E
Arterburn, Matthew C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
LENGTH: 426
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US-10-311-830-1
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     319 CCCAGGAACTIGGICAAGGAACAGCGIGIGIACCAGGAAGCIACCAAGGAAGIICCCACC 378
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                                                                                                                                                                                                                                                                 APPLICANT: Drmanac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark
APPLICANT: Jones, Lee W
APPLICANT: Ones, Lee W
APPLICANTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                CURENT APPLICATION NUMBER: US/09/933,524A;
CURRENT APPLICATION NUMBER: US/09/933,524A;
CURRENT FILING DATE: 2001-08-20;
PRIOR APPLICATION NUMBER: 09/528,409;
PRIOR FILING DATE: 2000-05-17;
NUMBER OF SEQ ID NOS: 116231;
SOFTWARE: HY-PARENT.pl Version 3.1;
SOFTWARE: Hy-Patent.pl Version 3.1;
SOFTWARE: 426
                                                                                                                                                                                                                        Sequence 107188, Application US/09933524A GENERAL INFORMATION:
                                                   361 ACGGATATTGACTTCTGCGAG 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LOCATION: (1)...(426)
; OTHER INFORMATION: n = A,T,C or G
US-09-933-524A-107188
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Best Local Similarity 100.0
Matches 384; Conservative
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US-09-933-524A-107188
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APPLICANT: Ye, Weilan IIILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND IIILE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
                                                                                                                           FILE REFERENCE: P325-P1C1
CURRENT APPLICATION NUMBER: US/10/081,056
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US CT/US01/21735
PRIOR FILING DATE: 2000-07-20
PRIOR PLILNG DATE: 2000-07-20
PRIOR PLILNG DATE: 2000-07-20
PRIOR PELING DATE: 2000-07-20
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR PLILNG DATE: 2000-07-26
PRIOR PLILNG DATE: 2000-07-27
PRIOR PLILNG DATE: 2000-08-07
PRIOR PLILNG DATE: 2000-08-07
PRIOR PLILNG DATE: 2000-08-17
PRIOR PLILNG DATE: 2000-08-17
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PRIOR PLILNG DATE: 2000-08-17
PRIOR PLILNG DATE: 2000-08-17
PRIOR PLILNG DATE: 2000-08-17
PRIOR PLILNG DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/230, 978
PRIOR PLILNG DATE: 2000-09-07
PRIOR PLILNG DATE: 2000-09-07
PRIOR PLILNG DATE: 2000-09-07
PRIOR PLILNG DATE: 2000-09-07
PRIOR PLILNG DATE: 2000-09-18
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PRIOR PLILNG DATE: 2000-09-18
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PRIOR APPLICATION NUMBER: US 09/709,238
PRIOR APPLICATION NUMBER: US 09/709,238
PRIOR APPLICATION NUMBER: PCT/US00/30952
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-10
PRIOR FILING DATE: 2000-11-10
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/747,259
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PLILING DATE: 2001-02-28
FILING DATE: 2001-02-28
APPLICATION NUMBER: PCT/US01/06666
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FILING DATE: 2001-05-25
APPLICATION NUMBER: PCT/US01/17092
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APPLICATION NUMBER: PCT/US00/34956
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APPLICATION NUMBER: US 09/802,706
FILING DATE: 2001-03-09
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APPLICATION NUMBER: US 09/816,744
FILING DATE: 2001-03-22
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APPLICATION NUMBER: US 09/796,498
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APPLICATION NUMBER: US 09/866,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 09/767,609
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              APPLICANT: Williams, P.Mickey
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                                                                                                                FILE REFERENCE: P3235P1C1
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APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Methods and Materials Relating to Novel Growth Regulatory-like
TITLE OF INVENTION: Polypeptides and Polynucleotides
FILE REFRESHOE: 21272-021 [HYS-7]
CURRENT APPLICATION NUMBER: US/10/311,830
CURRENT PILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 09/563,786
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR PILING DATE: 2000-05-02
PRIOR FILING PAIE: 2000-01-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VETSION 3.0
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LOCATION: (1)...(426)
OTHER INFORMATION: n = A, T, G, or C
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APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
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Paoni, Nicholas F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0
Matches 384; Conservative
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                                                                                                                                                                                                                                                                                                                SOFTWARE.
SEQ ID NO 1
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APPLICANT:
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APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Beenoyers, Luc Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, P. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC
CURRENT APPLICATION NUMBER: US/10/119,480
CURRENT FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 246
Prior Application removed - See File Wrapper or Palm
Prior Application removed - See File Wrapper or Palm
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 521;
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PRIOR APPLICATION NUMBER: US 09/870,574
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17443
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR PILING DATE: 2001-06-20
PRIOR PILING DATE: 2001-06-20
PRIOR PILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 383
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                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homosapiens
US-10-081-056-359
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APPLICANT: Stephan, Jeacoria
APPLICANT: Stephan, Jeacoria
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPREENCE: PASSAPPICA
CURRENT APPLICATION NUMBER: US/10/216,159A
CURRENT PILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: (0/059113
PRIOR APPLICATION NUMBER: 60/06387
PRIOR APPLICATION NUMBER: 60/06387
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/063973
PRIOR FILING DATE: 1998-01-20-7
PRIOR FILING DATE: 1998-01-20-7
PRIOR FILING DATE: 1998-01-20-7
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PRIOR APPLICATION NUMBER: 60/05994
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                                                                                                                                                                        Gaps
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                                                                                                              Length 521;
                                                                                                        Ouery Match 100.0%; Score 384; DB 46; Length 9 Best Local Similarity 100.0%; Pred. No. 1.3e-107; Matches 384; Conservative 0; Mismatches 0; Indels
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimey, Austin L.
APPLICANT: Surney, Austin L.
APPLICANT: Shinh, Victoria
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-119-480-71
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US-10-216-159A-71
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                                                                                                                                                                                                                                                                                                                        121 ATTICICIGGCIAGIGCICAAGAAGAITATAAIGCCCCGGACIGIAGAITCATIAACGIT 180
                                                                                                                                                                                                                                                                                                                                                                              181 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 240
                                                                                                                                                                                                                 0; Gaps
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
                                                                                                                                                            Query Match
100.0%; Score 384; DB 48; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.3e-107;
Matches 384; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapien
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Search completed: December 30, 2003, 09:01:32 Job time : 1836.61 secs

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RESULT 1
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Sequence 1, Appli
Sequence 1, Appli
Sequence 38, Appl
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Sequence 18, Appli
Sequence 8, Appli
Sequence 3, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 899 App
                                                                                                                                                          December 30, 2003, 01:34:27; Search time 31.014 Seconds (without alignments) 5464.987 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                 1 atggcaagaatattgttact.....atattgacttcttctgcgag 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-578-649-18
US-08-578-649-24
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US-08-28-24-463-14
US-08-28-161-4
US-09-359-161-4
US-09-767-515-2
US-09-767-515-2
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US-09-767-515-2
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US-09-671-949-1

US-09-270-139-94

US-09-270-139-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-578-649-1
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                                                                                                               OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                          Run on:
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Sequence 1, Appli Sequence 1, Appli Sequence 94, Appl Sequence 14, Appl

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                                                                                                               10933, A
55, Appl
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Sequence 9
Sequence 2
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Sequence 1
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Sequence
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MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: 1BM PS2.
ODERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION: UMBER: DE 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoloff
                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza
TITLE OF INFORTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES. 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
US-09-650-855-14
US-09-477-071-1
US-09-477-071-1
US-09-107-532A-3486
US-08-620-312D-161
US-08-868-786-1
US-09-134-001C-1171
US-09-741-150-3
US-09-741-150-3
US-08-252-991A-10933
US-08-285-190-1
US-08-785-190-1
US-08-785-190-1
US-08-785-190-1
US-09-453-702B-116
US-09-220-132-94
US-09-220-132-94
US-09-220-132-94
US-09-220-132-94
US-09-220-132-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Andrew L. Tiajoloff

REGISTRATION NUMBER: 31,575

REFERENCE/DOCKET NUMBER: 305-PFF/ALT
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-984
INPORMATION POR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 459 base pairs
TENGTHEN 459 base pairs
TENGTHEN 505 SEG ID NO: 1: SEQUENCE CHARACTERISTICS:
TENGTH: 459 base pairs
TENGTHEN 1001eic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADRESS:
AUDRESS:
Felfe & Lynch
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
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LOCATION: 40..
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 CCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACTATTCTCTGGCTAGTGCTCAAG 142
                                                                                                                                                                                                                                                   143 AAGATTATAATGCCCCGGACTGTAGATTCATTAACGTTAAAAAAGGGCAGCAGATCTATG 202
                                                                                                                                                                                                                                                                                                                                             194 Aggactacanggeeeeeeachgeegatreergaeearreegaggeeaaggeargarahig 253
                                                                                                                                                                                                                                                                                                                                                                                       203 TGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAATTTTGGGGCTGGCAGTGTTTATG 262
                                                                                                                                                                                                                                                                                                                                                                                                                           254 rerrerecaagere----aaggecerergegecererrergggaggeaggearerreagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 GTGATGGCCAGGACGAGATGGGAG---TCGTGGGTTATTTCCCCAGGAACTTGGTCAAGG 319
                                                                                                                                                  23 TCCTCCCGGGTCTTGTGGCTGTATGTGCATGGAATATTTATGGACCGTCTAGCTT 82
                                                                                                               9; Gaps
                                                                     16.9%; Score 64.8; DB 1; Length 459; 55.6%; Pred. No. 2.3e-11; tive 0; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08578649

Patent No. 5770366

GENERAL INFORMATION:
APPLICAWT: Ulrich Bogdan
APPLICAWT: Reinhard Buttner
APPLICAWT: Reinhard Buttner
APPLICAWT: Brigitte Kaluza
1TITE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NOMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette COMPUTER: IBM PS/2 OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOER 1035-PFF/ALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-2019-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-Uuly-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE; (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31,57
REFERENCE/DOCKET NUMBER: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                               Conservative
mat_peptide
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                                                                           Query Match
Best Local Similarity
Matches 170; Conserv
; NAME/KEY:
; LOCATION:
US-08-578-649-1
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303 CAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACCAC 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%; Score 63.2; DB 1; Length 581; 54.3%; Pred. No. 8.3e-11; tive 0; Mismatches 138; Indels
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ODERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Reinjatte Kaluza
ITITE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-U1Y-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
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805 Third Avenue
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APPLICATION NUMBER: US,
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179..499
STRANDEDNESS: single
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                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
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Best Local Similarity
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LOCATION:
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                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                             LOCATION:
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US-08-578-649-4
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268 GGCCAGGACGAGATGGGAG---TCGTGGGTTATTTCCCCAGGAACTTGGTCAAGGAACAG 324
208 TACTATGGAGATCTGGCTGCTCGCCTGGGCTATTTCCCCAGTAGCATTGTCCGAGAGGAC 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 TATAATGCCCCGGACTGTAGATTCATTAACGTTAAAAAAGGGCAGCAGATCTATGTGTAC 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.5%; Pred. No. 4.7e-09;
Matches 141; Conservative 0; Mismatches 91; Indels
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                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_RNA; LOCATION: 4..6; OTHER INFORMATION: /function= "Startcodon Met" US-08-578-649-18
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Patent No. 5770366
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Raluza
TILLE OF INVENTION: MELANOWA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 base pairs
TYPE: nucleic acid
STAMDENRES: single
TOPOLOGY: linear
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STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                     NAME/KEY: mat_peptide LOCATION: 7..327
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88 AAGCTCTGTGCAGATGATGAGTGTGTCTATACTATTTCTCTGGCTAGTGCTCAAGAAGAT 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uery Match
14.1%; Score 54.2; DB 1; Length 305;
Sest Local Similarity 57.7%; Pred. No. 4.9e-08;
fatches 139; Conservative 0; Mismatches 93; Indels 5
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MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
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APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kalusa
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                      NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET UNBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 883-384
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc RNA
LOCATION: join(1..29, 277..305)
STHER INFORMATION: /function= "Primer"
US-08-578-649-8
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-U1ly-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/08578649
Patent No. 5770366
                                                                                                                                                                                                                                                                                                      LENGTH: 305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: New York
COUNTRY: USA
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119 CTATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: one-of (194, 369, 527)
OTHER INFORMATION: /note= "N in positions 194, 369
OTHER INFORMATION: and 527 denotes an indefinite number and sequence OTHER INFORMATION: of nucleotides "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(40..111, 40..166, 214..347, 393..503, 549
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Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Brighte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reife & Lynch
PRIOR APPLICATION. 435

PRIOR APPLICATION DAYA:
APPLICATION DAYA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: AAACHEW L. Tiajoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: 31,575
REFERENCE/COCKET NUMBER: 31,575
REFERENCE/COCKET NUMBER: BOER 1035-PFF/ALT
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
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TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (312) 688-9200
SEQUENCE CHARACTERISTICS:
LENGTH: 596 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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ST: 805 Third Avenue
New York
New York
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Matches 62; Conserv
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LOCATION:
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NAME/KEY:
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denotes an indefinite number ans sequence of
nucleotides"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1649 Trcacccccccaagregiciaricrcriccaagcre 1686
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                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 MD storage diskette
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                          NAME: Andrew L. Titjoloff
REGISTRATION NUMBER: 31,575
REBERENCE DOCKET NUMBER: 31,575
REBERENCE DOCKET NUMBER: 31,575
RELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INPORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 3565 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
                                                                                                                         SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08232463; Patent No. 5670367; GENERAL INFORMATION; APPLICANT: DORNER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                         PC-DOS
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1378..1449
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                                                                                                       OPERATING SYSTEM:
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US-08-232-463-14/c
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LOCATION:
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COUNTRY:
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us-10-019-455a-4.rni

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LENGTH: 1929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 AATTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGAGTGGGAGTCGTGGGTTATT 298
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APPLICANT: Kossmann, Jens
APPLICANT: Rossmann, Jens
APPLICANT: Boxion, Botho
TITLE OF INVENTION: PROCESS AND DNA MOLECULES FOR INCREASING
TITLE OF INVENTION: THE PHOTOSYNTHESIS RATE IN PLANTS
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.9%; Score 34; DB 1; Length 7218; Best Local Similarity 8.1%; Pred. No. 0.77; Matches 19; Conservative 120; Mismatches 95; Indels
                                                                                                                                             ZIP: 22313-0299
COMPUTER READBRIE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                        CLASSIPTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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Patent No. 6245967
GENERAL INFORMATION:
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
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; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
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APPLICANT: Bradford, Kent J.
APPLICANT: Dahal, Peetambar
APPLICANT: Dahal, Peetambar
APPLICANT: Yang, Hong
APPLICANT: Yang, Hong
APPLICANT: Cooley, Michael
APPLICANT: Downie, Bruce
APPLICANT: Downie, Bruce
APPLICANT: Gee, Oilver
APPLICANT: Gee, Oilver
APPLICANT: Gee, Oilver
APPLICANT: Gee, Oilver
APPLICANT: Gee, Oilver
APPLICANT: Gee, Oilver
APPLICANT: Gee, Oilver
APPLICANT: Gee, Oilver
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
TITLE OF INVENTION: Los Stress Conditions in Plants
FILE REFERENCE: 023070-095900US
CURRENT APPLICATION NUMBER: US/09/359,161A
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 AATGGAGCTGGAGAATTTTGGGCTGGCAGTGTTATGGTGATGGCCAGGACGAGATGGGA 285
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56.2%; Pred. No. 0.42;
tive 0; Mismatches 49; Indels 0
                                                                                                                                                                                                                                                            OURTRAING SISTEM: FC-LUGS #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,820
FILING DATE: 04-SEP-1997
CLASSIFICATION NOTA:
APPLICATION NUMBER: US 19502053.7
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: H3-2y, James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: AGREVO-7
TELEPHONE: 212-596-9000
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 1136 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                          1251 Avenue of the Americas
                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 4, Application US/09359161A; Patent No. 6342656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Conservative
                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 30..1121
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Matches 63; Conserva
                                                     New York
New York
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GENERAL INFORMATION:
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US-09-359-161-4/c
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                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 TCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTTAAAAAAGGGCAGCAGAT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 CTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAATTTTGGGCTGGCAGTGT 257
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                            ) OTHER INFORMATION: Lycopersicon esculentum plant homolog of yeast; OTHER INFORMATION: SNF1 kinase subunit of protein kinase (LeSNF1) US-09-359-161-4
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8.8%; Score 33.6; DB 4; Length 1929;
Best Local Similarity 52.9%; Pred. No. 0.54;
Matches 72; Conservative 0; Mismatches 64; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CAPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CUSHMAN DARBY & CUSHMAN ADDRESSEE: Intellectual Property Group of ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTERIAL GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08286870A
Setent No. 6053605
GENERAL INFORMATION:
APPLICANT: ELY, S.
APPLICANT: TALLOR, RH
APPLICANT: TRAILOR, RH
APPLICANT: TREETT, JM
APPLICANT: REBNK, RG
ITTLE OF INTUNTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
TYPE: DNA ORGANISM: Lycopersicon esculentum
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REPERDICE/DOCKET UMBER: 706
TELECOMMUNICATION:
TELEPHONE: (202) 861-3000
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                           FEATURE
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FACENTAL INFORMATION:
APPLICANT: Tirrell, David A
APPLICANT: Tirrell, David A
APPLICANT: Tirrell, David A
APPLICANT: Tirrell, David A
APPLICANT: Tirrell, David A
APPLICANT: Tirrell, David A
TITLE OF INVENTION: Efficient Production of Engineered Proteins Containing
TITLE OF INVENTION: Amino Acid Analogues
TITLE OF INVENTION: Amino Acid Analogues
FILE REFERENCE: 30431.6030, And Analogues
FILE REFERENCE: 2001-01-23
FRICK APPLICATION NUMBER: 60/207,627
PRIOR APPLICATION NUMBER: 60/207,627
PRIOR APPLICATION NUMBER: 2000-05-26
NUMBER: OF EQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
ENGTH: 6501
                                                                                                                                                                                                                                                                                                    2002 TGGTGGTGGTGAACAGGGGGGTGACCTTCTCCTGGGCCTTCTCGAAGTCGTACTCGGCCT 1943
                                                                                                                                                                                                                                                                                                                                                                                                                     1942 GGTAGGTCACCTCCACGGGCACGAACTCGATGCGGTCGATGTACACCTCGTTGCCGCTGC 1883
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Patent No. 6586207
GENERAL INFORMATION:
APPLICANT: Tirrell, David A
PAPLICANT: Kitck, Kristi L
TITLE OF INVENTION: Overexpression of Aminoacyl-tRNA Synthetases for TITLE OF INVENTION: Efficient Production of Engineered Proteins Containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 TGGAGAATTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGGAGGAGTGGGAGTTCGTGGG 293
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                                                                                                                                                                                                                                        228 TGGAGCTGGAGAATTTTGGGCTGGCAGTGTTAATGGTGATGGCCAGGACGAGATGGGAGT 287
                                                                                                                                                                                                                                                                                                                                                                288 CGTGGGTTATTTCCCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAA 347
                                                                                                                                                                                0; Gaps
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US-09-767-515-1
                                                                                                                 Query Match 8.8%; Score 33.6; DB 3; Length 2159; Best Local Similarity 52.1%; Pred. No. 0.57; Matches 75; Conservative 0; Mismatches 69; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1882 reaactriccagececearga 1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 GGAAGTTCCCACCACGGATATTGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/09767515; Patent No. 6586207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                  1..2159
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         SOS
; NAME/KEY:
; LOCATION:
US-08-286-870A-7
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Matches
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COMPUTER READABLE FORM:
WEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
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Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brockes, A. Anders
REGISTRATION NUMBER: 36,373
REFREENCE/FOCKET NUMBER: P9340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-961-527-191/c

Sequence 191, Application US/08961527

Patent No. 6420135

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-889
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CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                RESULT 14
US-09-252-991A-889/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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STATE:
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Best Local (
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APPLICANT: WEL, Ming-thui et al
APPLICANT: WEL, Ming-thui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CLOOIOL8
CURRENT PILING PATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
CURRENT PILING PATE: 2000-12-13
SOFTWARE: FREESOF FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 TGGAGAATTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 ITATTTCCCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGT 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: pQEI5-W305F
US-09-767-515-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

8.5%; Score 32.8; DB 4; Length 6501;
Best Local Similarity 54.0%; Pred. No. 1.8;
Matches 67; Conservative 0; Mismatches 57; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183529 AGrccaggaarcccaargrrgagggggaaaraaaggaagagrrg 183573
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Best Local Similarity 49.7%; Pred. No. 15;
Matches 82; Conservative 0; Mismatches
                            FILE REFERENCE: 30431.6US01
CURRENT APPLICATION NUMBER: US/09/767,515
CURRENT FILING DATE: 2001-01-23
FRIOR APPLICATION NUMBER: 60/207,627
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 6501
TITLE OF INVENTION: Amino Acid Analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 3, Application US/09734674; Patent No. 6498022
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OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Human
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LENGTH: 202001
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US-09-734-674-3
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR RILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 889
LEGGTH: 1944
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TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
WIMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 TATTICCCCAGGAACTIGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTI 354
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| TELEFAX: (301) 309-8512 | INFORMATION FOR SEQ ID NO: 191: | SEQUENCE CHARACTERISTICS: | LANGTH: 10357 base pairs | TYPE: nucleic acid | STRANDENESS: double | TYPE: nucleic acid | TYPE: nucleic acid | TYPE: nucleic acid | TYPE: nucleic acid | STRANDENESS: double | TYPE: nucleic acid | TYPE: nucleic acid | TYPE: nucleic acid | TYPE: nucleic acid | TYPE: nucleic acid | TYPE: nucleic acid | TYPE: nucleic acid | TYPE: nucleic acid | TYPE: TRANDENESS: double | TYPE: nucleic acid | TYPE: TRANDENESS: double | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: No. 7.4; | TYPE: N
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Search completed: December 30, 2003, 06:10:38 Job time : 41.014 secs

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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	BD010805 Novel pol AF243504 Mus muscu BD093126 Novel pol AJ243399 Mus muscu BD093122 Novel pol BD093135 Novel pol BD010817 Novel pol BD010817 Novel pol BD010817 Novel pol BD010817 Novel pol BD010818 Novel pol BD010818 Novel pol BD010818 Novel pol BD010818 Sequence AX35818 Sequence AX362311 Sequence AX362311 Sequence AX362311 Sequence AX491252 Sequence AX491252 Sequence AX491252 Sequence AX491251 Novel pol BD010820 Novel pol BD010820 Novel pol BD093131 Novel pol BD093131 Novel pol BD010818 Novel pol BD010818 Novel pol BD010818 Novel pol BD010818 Novel pol BD010818 Novel pol BD010818 Novel pol BD010818 Novel pol BD010818 Novel pol BD010818 Novel pol BD010818 Novel pol BD010818 Novel pol BD010818 Novel pol BD010818 Novel pol BD010818 Novel pol BD033131 Novel pol BD033131 Novel pol BD033131 Novel pol BD010818 Novel pol BD010818 Novel pol BD03318 Novel pol BD010828 Novel pol BD010828 Novel pol BD0108448 Human DNA AJ253254 Homo sapi AJ253254 Homo sapi AJ253328 Ratusa nove AJ25325 Homo sapi AJ253328 Sequence AX16788 Sequence BT007775 Synthetic AX253435 Sequence	NNA linear PAT 31-JAN-2002 ta; Vertebrata; Euteleostomi; sgnathi; Muridae; Murinae; Mus. Mogi,S., Noguchi,Y.,
DB ID	6 BD010805 6 BD03106 10 AF243504 6 BD010821 6 BD010821 10 AF243333 6 BD010835 6 BD010835 6 BD010835 6 BD010836 6 BD010820 6 BD010816 9 AF233261 9 AF233261 9 AF233261 9 AF233262 9 AF233266 9 BD010836 6 BD010836 6 BD010816 9 BD010816 9 BD010816 9 BD010816 9 BF252326 9 HSA252326 9 HSA252326 9 HSA252326 9 HSA25336 10 MMM1 6 AA2945 6 AA2945 6 AA2945 6 AA283435 6 AX283435 6 AX283435	384 bp I 199178 thereof. 19178 Chordata; Crania 1 Rodentia; Sciurc 191,K., Okubo,S., Ina Rak,H.
% Query Match Length )	100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 10	0805 11 polypeptide 0805.1 GI:186 0805.1 GI:186 001069994-A/6. sp. ryota, Metazoa pla; Eutheria alia; Eutheria alas: T. Nishi, K., imura, K. and I
Result No. Score	C 252.2 28.4 + 1.0 29.4 + 1.0 20.5 + 2.0 20.5 + 2.	RESULT 1 BD010805 LOCUS DEFINITION NOVEL DO VERSION NOVEL DO VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010805 VERSION BD010

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Yoshimura, K. and Tanaka, H.

Novel polypeptide and its DNA
Patent: WO 0102564-A 6 11-3DV-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDENUKI TANAKA
OS Mus sp. (mouse)
PN WO 0102564-A/6
PD II-JAN-2001
PF .29-JUN-2001
PF .29-JUN-2001
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
                                                                                                                                                                                                                                   A61K38/17,
2 A61K39/395,A61K49/16,A61P19/02,A61P19/08,A61K31/7088//(C12P21/
3 02,C12R1:19)
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                       YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
CI2N15/12,CI2N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00,
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100.0%; Pred. No. 1.8e-106;
ive 0; Mismatches 0;
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/organism="Mus sp."
/mol_type="genomic DNA"
/db.xref="taxon:10095"
a 68 c 111 g 107
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                            OS Mus sp. (mouse)
PN JP 201069994-A/6
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHTNICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC CIZNIS/09, A61K38/00, A61K45/00, A61F89/00, A61P9/02,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 384)
Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
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100.0%; Pred. No. 1.8e-106;
ive 0; Mismatches 0;
  Patent: JP 2001069994-A 6 21-MAR-2001;
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/mol_type="genomic DNA"
/db_xref="taxon:10095"
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WO 0102564-A/6.
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PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/08,
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
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                                                                 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 to 94. Nishi, K. 4, 7 Nishi, K., 0gi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H. Povel polypeptide and DNA thereof Patent: JP 2001069994.A 22 21 WAR-2001; TAKEDA CHEMICAL INDUSTRIES LTD
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    .p. (mouse)'.

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/mol_type="genomic DNA"
/db_xref="taxon:10095"
_158 c 221 g 28
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Location/Qualifiers
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JP 2001069994-A/22
21-MAR-2001
BD010821.1 GI:18639194 JP 2001069994-A/22.
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Best Local Similarity 100.
Matches 384; Conservative
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SHINICHI MOGI
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RAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENCAGEFWAGSVYGDHQDEMGIVGYFPS
NLVKEQRVYQEATKEIPTTDIDFFCE"
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                                                                                                                                                             2 (bases 1 to 929)
Cohen-Salmon,M., Frenz,D., Verpy,E., Voegeling,S. and Petit,C.
Direct Submission
Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue
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Cohen-Salmon,M., Frenz,D., Liu,W., Verpy,E., Voegeling,S.
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                                                    Edp, a new fibrocyte-derived protein related to
in vitro effect on the early differentiation of
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                                                                                           J. Biol. Chem. 275 (51), 40036-40041 (2000)
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Novel polypeptide and DNA thereof.
BD010821
                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
                                                                                                                                                                                                                                 du Dr. Roux, Paris 75015, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/chromosome="2"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 947)

S Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,

S Yoshimura, K. and Tanaka, H.

Novel polypeptide and its DNA

L Patent: WO 0102564-A 22 11-JAN-2001;

TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO

OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,

HIDEYUKI TANAKA

OS Mus sp. (mouse)

PN WO 0102564-A/22

PD 11-JAN-2001

PP 29-JUN-2000 WO 2000JP0004278

PR 30-JUN-2009 WO 2000JP0004278

PR 30-JUN-1999 JP 99P 186718

PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
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I YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
CIZUNIS/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC
A61K38/17,
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02,C12R1:19)
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 Novel polypeptide and its DNA.
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BD093122.1 GI:22638710
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RESULT

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958 bp mRNA linear ROD 29-JAN-2001
Mus musculus mRNA for melanoma inhibitory activity-like protein
AJ243939
                                                                                                                                                                                                                                                                                                                                                               Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation
Genomics 71 (1), 40-52 (2001)
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                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 ATGGCAAGGATATTGATTCTTTTGCTTGGGGGCCTTGTGGGTTCTATGTGCCGGGCATGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-JUL-1999) Rendtorff N.D., Department of Medical Genetics, Institute of Medical Biochemistry and Genetics, Blegdamsvej 3, 2200 Copenhagen N, DENMARK Related sequence: AJ242552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                               Rendtorff, N.D., Frodin, M., Attie-Bitach, T., Vekemans, M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 958;
                                                                                                                                         AJ243939.1 GI:12619174
melanoma inhibitory activity-like protein; Mial gene.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="79.4-80 cM"
/tissue_type="whole fetus"
/dev_stage="12.5 pc"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .958
/organism="Mus musculus"
/mol_type="mRNA"
/db xref="taxon:10090"
/chromosome="2"
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/gene="Mial"
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/gene="Mial"
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/gene="Mial"
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Rendtorff, N.D.
Direct Submission
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SHINICHI MOGI,

PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,

PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDBYUKI TANAKA

PC CIZNIS/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,

PC CO7K14/47, CO7K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
                                                                                                                                                                                                                                                                                                                                                        PAT 31-JAN-2002
                                                                                                                                                            CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 360
                                                                                         TITIGGECTGGCAGTGTTATGGTGACCACCAGGATGAGATGGGGAATTGTAGGTTATTTC 300
                                                                                                                                                                                318 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 377
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                      TITIGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGGAATTGTAGGTATTTC
                     AAGAAAGGGCAGCAGCAGTCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG
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1 (bases 1 to 384)

S Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,

Yoshimura,K. and Tanaka,H.

Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 36 21-MAR-2001,

TAKEDA CHEMICAL INDUSTRIES LTD

OS RATTUS SP. (rat)

PN JP 2001069994-A/36

PD 21-MAR-2001

PR 29-JUN-2000 JP 2000195911
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Novel polypeptide and DNA thereof. BD010835

BD010835.1 GI:18639208
JP 2001069994-A/36.
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/organism="Rattus sp."
/mol_type="genomic DNA"
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a 72 c 109 g 105
                                                                                                                                                                                                                              ACGGATATTGACTTCTTCTGTGAA 384
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Location/Qualifiers
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Matches 359
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Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C.
Direct Submission
Submitted (10-FEB-2000) Pathology, Brigham and Women's Hospital, 75
Francis Street, Boston, MA 02115, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  ROD 06-JUL-2000
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/db_xref="G1:8927430"
/db_xref="G1:8927430"
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/db_xref="G1:8927430"
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Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C. and served cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping Genomics 66 (3), 242-248 (2000)
                                                                                   264 TITIGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC 323
                                                                                                                      CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 360
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324 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC
                                                   TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC
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ilarity 100.0%; Pred. No. 2e-106;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                              AF233333 1054 bp mRNA Mus musculus otoraplin mRNA, complete cds. AF2333333
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/product="otoraplin"
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AUTHORS
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AF233333
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PAT 31-JAN-2002
                                                                         121 ATTICTCTGGCAGAGACACAGAAGACTACAATGCCCCGGACTGTAGGTTCATCAATGTC 180
61 ATGTTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGCAGATGAGGAGTGTGTATACC 120
                                                                                                                                                                                         241 TICTGGGCTGGCAGTGTTATGGTGACCACCAGGATGAGATGGGGAATTGTGGGTATTTC 300
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Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H.
Yoshimura,K. and Tanaka,H.
Patent: JP 2001069994 A 18 21-MAR-2001;
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                                                                                                                                         AAGAAAGGGCAGCAGATCTATTTTATTCCAAGCTGGTAACAGAAAATGGAGCTGGGGCA 240
                                                                                                                                                                                                                                  CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCCACCAAGGAGATCCCAACC 360
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CI2N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50,
                                                                                                            AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CATGGTGTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGCGGATGAGGAGTGTGTC
                                                                                                                                                                       TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGGAATTGTAGGTTATTTC
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100.0%; Pred. No. e.
... 0; Mismatches
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BD010817
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Location/Qualifiers
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/db_xref="taxon:10095"
60 c 92 g 8
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JP 2001069994-A/18
21-MAR-2001
29-JUN-2000 JP 2000195911
                                                                                                                                                                                                                                                                                               361 ACGGATATTGACTTCTTCTGTGA 384
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/organism="Mus sp."
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JP 2001069994-A/18.
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Best Local Similarity 100.
Matches 330; Conservative
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Mus sp.
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BD010817
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29-JUN-2000 WO 2000JP004278
30-JUN-1999 JP 99P 186718
YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
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CI2N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC
                                                                                                                                                                                                                                                                                                                                                          PAT 27-AUG-2002
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02,C12R1:19)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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                         AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG
                                                                                                                              TITIGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGGAATTGTAGGTTATTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H.
Novel polypeptide and its DNA
Patent: WO 0102564-A 36 11-JAN-2001;
TAKEBA CHEMICAL INDUSTRIES LTD,YASUAKI ITO,KAZUNORI NISHI, KP
OGI, SHOICHI OKUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,
HIDEYUKI TANAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 344; DB 6; Length 384;
Pred. No. 3.3e-94;
0; Mismatches 25; Indels
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/organism="Rattus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10118"
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WO 0102564-A/36.
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Best Local Similarity 93.5%;
Matches 359; Conservative
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WO 0102564-A/36
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PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
CC FF Key Location/Qualifiers
FT Source 1. .330
FT /organism='Rattus sp. (rat)'.
121 GATGTCAAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAACGGAGCT 180
                                                                                                                                          181 GGAGAGTTTTGGGCTGGCAGTGTTTATGGTGACACCACCAGGATGAGATGTAGGT 240
                                                                                                                                                                                                               241 TATTTCCCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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BI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC CIZNIS/09, A6IK38/00, A6IK45/00, A6IK48/00, A6IP9/00, A6IP9/02, A6IP9/08,
                                                    GATGTCAAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCT
                                                                                                                                                                                            TATITCCCCAGCAACTIGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATC
                                                                                                                         GGAGAGTTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATTGTAGGT
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(bases 1 to 330)

Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H.
Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 37 21-MaR-2001,
TAKEDA CHEMICAL INDUSTRIES LTD
OS Rattus sp. (rat)
PN JP 2001069994-A/37
PD 21-MAR-2001
PP 29-JUN-2000 JP 2000195911
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anism='Rattus sp. (rat)'.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10118"
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JP 2001069994-A/37.
Rattus sp.
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AUTHORS
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BD010836
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Yoshimura, K. and Tanaka, H.
Yoshimura, K. and Tanaka, H.
Novel polypeptide and its DNA
Novel polypeptide and its DNA
L PAREDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA,
OS Mus sp. (mouse)
PN WO 0102564-A/18
PP 11-AN-2000
PP 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
                                                                                                                                                                                                                                                                                                                                                                                                                     PAT 27-AUG-2002
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CIZNI5/12,CIZNS/10,CI2P21/02,C07K14/47,C07K16/18,A61K45/00, PC
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02,C12R1:19)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 330)
                                    TATACTATTTCTCTGGGGAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATC
                                                                                                     GATGTCAAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCT
                                                                                                                                                                            181 GGAGAGTTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGT
                   TATACTATTTCTCTGGCAAGAGACACAGATTACAATGCCCCAGACTGTAGGTTCATC
                                                                                       GATGTCAAGAAAGGGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCT
                                                                                                                                                          GGAGAGTTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGT
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6.4e-90;
0; Indels
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/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"
a 60 c 92 9 87
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I YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
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A61P19/08,
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                    121 AATGTCAAGAAAGGGCAGCAGATCTATGTTTATTCCAAGCTGGTAACAGAAAATGGAGCT 180
                                                                                                                                TATTICCCCAGCAACTIGGIGAAGGAGCAGCGIGIAIACCAGGAGGCCACCAAGGAGAIC 354
                                                                                                                                                     241 TATTICCCCAGCAACTIGGTTAGAGAGCAACGAGTGTACCAGGAGGCCACCAAGGAGATT 300
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. It Chases I to 384.
It (Bases I to 384); K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H. Powel polypeptide and DNA thereof Patent: JP 201069994-A 31-MAR-2001; TAKEDA CHEMICAL INDUSTRIES LTD
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     GATGTCAAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCT
                                                                     GGAGAGTITITGGGCTGGCAGTGTTATGGTGACCACCAGGATGAGATGGGATTGTAGGT
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Pred. No. 9.9e-77;
0; Mismatches 60
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Location/Qualifiers
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Novel polypeptide and DNA thereof.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2001069994-A/3
21-MAR-2001
29-JUN-2000 JP 2000195911
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JP 2001069994-A/3.
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illarity 84.3%;
Conservative 0
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Homo sapiens
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Best Local Simil
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TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO GGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
OS RALTUS SP. (rat)
PN WO 0102564-A/37
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29-JUN-2000 WO 2000JP004278
30-JUN-1999 JP 99P 186718
YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI
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02,C12R1:19)
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                                                                                                                                                           TATITCCCCAGCAACTIGGIGAAGGAGCAGCGIGIAIAACCAGGAGGCCACCAAGGAGAIC 354
                                                                                                                                                                                 TATACCATTTCTCTGGCAAGAGCACAGGAAGACTACAATGCCCCGGACTGTAGGTTCATC 120
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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CIZNI5/12,CIZNS/10,CIZP21/02,C07KI4/47,C07KI6/18,A61K45/00,
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                                                  GGAGAGTTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGT
                                                                                                               GATGTCAAGAAAGGGCAGCAGATCTATTACTCCAAGCTGGTAACAGAAAACGGAGCT
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Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
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/organism="Rattus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10118"
a 62 c 91 g 86
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BD093137
BD093137.1 GI:22638725
WO 0102564-A/37.
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Rattus sp.
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Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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1 (bases I to 384)

1 (by., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,

1 (soshimura, K. and Tanaka,H.

Novel polypeptide and its DNA
Patent: WO 0102564-A 3 11-JAN-2001;

TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
031, SHOICHI OKUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,

HIDEYUKI TANAKA
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WO 0102564-A/3
II.-JAN-2001
29-JUN-1999 JP 99P 186718
YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
                                                                                                                                                                                                                                                                                                                                             PAT 27-AUG-2002
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C12N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC
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02, C12R1:19)
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                                                                                                                              241 TTTTGGGCTGGCAGTGTTATGGTGATGGCCAGACGAGATGGGGAGTCGTGGGTTATTC 300
                                                                                                                                                                                          301 CCCAGGAACTIGGICAAGGAACAGCGTGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 360
                                                AAGAAAGGGCAGCAGATCTATTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG 240
                                                                             AAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAATGGAGCTGGAGAA 240
                                                                                                          TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC 300
                                                                                                                                                                        CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 360
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/organism="Homo sapiens"
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Novel polypeptide and its DNA.
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WO 0102564-A/3.
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Homo sapiens
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Best Local Similarity
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ATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 180
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EST analysis of gene expression in the mouse Organ of Corti at the conset of hearing

AL Unpublished
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kacharpenied(a.ini.gov
Plate: 143 row: b column: 10
Plate: 143 row: b column: 10
Seq primer: M13RP1 reverse primer (ABI).
            BÖ564944 G127909. V
BQ568471 g1108904.
BB611549 BB611549
BC56537 g142903. V
BO565768 g106609. V
BO56578 g106609. V
BO565713 g13909. V
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BC567749 g1124d08. V
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BC56776 g1122a07. V
BC56776 g1125a12. V
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gil43bl0.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gil43bl0 5', mRNA sequence.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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BQ568498 gil09c02.
BQ564134 gilld01.y
                                                                                                         ; Search time 1278.03 Seconds (without alignments) 7302.593 Million cell updates/sec
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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193 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAACGGAGCTGGAGA 552

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301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 360

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source

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/dev stage="Post natal day 5 to 13"
/done lib="Mouse Organ of Corti CDNA pBluescript"
/clone lib="Mouse Organ of Corti CDNA pBluescript"
/note="Organ: Organ of Corti, Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
from P12 and 24 from P3. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
organism="Mus musculus"
                                /db_xref="taxon:10090"
/clone="gi143b10"
                                                         /sex="male and female"
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/sex="male and female"
/sex="male and female"
/dev stage="Post natal day 5 to 13"
/dev stage="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pBluescript"
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organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochhea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
                                          EST 19-JUN-2002
                               PQ564607
gil9h02.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gil9h02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                     EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 488)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kachar,B.
Contact: Kachar,B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Februs 301-402-1369
Email: kacharb@nidcd.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: 19 row: h column: 02
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .488
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="gi19h02"
                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                         BQ564607.1 GI:21467924
                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                       Kachar, B.
                                                                                                                               BQ564607
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                                                                            DEFINITION
                                                                                                                                                                                                                                           ORGANISM
                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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KEYWORDS
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RESULT 2
BQ564607
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Query Match
Best Local Similarity 100.0%; Pred. No. 3.6e-106;
Matches 384; Conservative 0; Mismatches 0; Indels 0

BASE COUNT

ORIGIN

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epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
(catalog # K1591-02; Invitrogen, Catlabad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
Giagapack III Gald Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker-primer severse transcribed using
Moloney murine leukemia virus reverse transcribed using
Moloney murine leukemia virus reverse transcribed using
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
columns to enrich for CDNA spracter than 400bp and 1000 bp
, respectively. The CDNA was then directionally ligated to
the Uni-ZAP XR vector, which had been predigested with
EcoR I and Xho I. The phagemid was packaged with Gial and, upon Itration on XLI Blue MRF' cells, the
yield of the phage library was estimated to be 11,100,000
rescue plasmid DNA from the phages. Upon plating of the
resistance helper phage (E ExAssist Interference
resistance helper phage (Saturated culture with the
grown in 96-well, Z ml growth plate. Plasmid DNA was sinstructed culture. Step
concerts of (TM) plasmid puring reverse penerated with the
the S' end of the cDNA clones were generated with the
tuiversal M13 reverse primer (GAGGAAAGCTMAGCC) and 25%
strandth Rights for EDNA clones were generated with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on M7 Tetrad thermal cyclers (MM Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have I copy; 14.3% 2; 12% 3-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified." 83 c 135 g 127 t
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ö GTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGCGGATGAGGAGTGTGTTATACT 126 181 AAGAAAGGGCAGCAGAATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG 240 ATTTCTCTGGCAAGAGCACAGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 180 TITIGGGCTGGCAGTGTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC 300 TITITGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGAATTGTAGTTTC 306 7 AIGGCAAGGAIAITGAITCITÍTIGCTIGGGGGCCITIGIGGITICTÁIGIGGGCGGGALAGAT 66 AAGAAAGGCCAGCAGATCTATGTTTACTCCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG 1 ATGCCAAGGATATTGATTCTTTTGCCTTGGGGCCTTGTGGTTCTATGTGCCGGGCATGGT 0; Gaps 100.0%; Score 384; DB 13; Length 488; 100.0%; Pred. No. 4e-106; ive 0; Mismatches 0; Indels 0 Query Match
Best Local Similarity 100.
Matches 384; Conservative 121 61 67 127 187 241 247 BASE COUNT ORIGIN 셤 qq g ò à 유 à à

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/ / sex="male and lemale"
/ / sex="male and lemale"
/ / sex="male and lemale"
/ / sex="male and lemale"
/ clone_lib="Mouse Organ of Corti cDNA pBluescript"
/ clone_lib="Mouse Organ of Corti; Vector: pBluescript; The
organ of Corti; (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from PG: 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fastrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
digapack III Gold Cloning kit (catalog # 237212), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo (df) linker-primer
reverse transcribed using a hybrid oligo (df) linker-primer
reverse transcribed using a hybrid oligo (df) linker-primer
                                                                                                                                                                                                                                                                                                                                                                            BQ568498 514 bp mRNA linear EST 19-JUN-2002 gil09c02.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gil09c02 5', mRNA sequence.
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CCCAGCAACTIGGIGAAGGAGCAGCGIGIAIACCAGGAGGCCCACCAAGGAGAICCCAAGC 360
                                     EST analysis of gene expression in the mouse Organ of Corti at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 514)
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Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
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Plate: 109 row: c column: 02
Seg primer: M13RPI reverse primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="gi109c02"
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                                                                                                                                                                                                            367 ACGGATATTGACTTCTTCTGTGAA 390
                                                                                                                                         361 ACGGATATTGACTTCTTCTGTGAA 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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   301
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                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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BQ568498
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Mus musculus (house mouse)

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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                              JOURNAL
COMMENT
                                                                                                                                                                            AUTHORS
TITLE
                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
               over Pharmacia Size Sept00 (Planmacia, Oppsain, Sweden) and Clontecch Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for CDNAs greater than 400pp and 1000 by respectively. The CDNA was then directionally ligated to the Uni-2DP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with digapak III Gold and, upon titration on XII Blue NRF cells, the yield of the phage library was estimated to be 11.00,000 recombinants. Stratagene's Exhasist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the concert96 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTF from the 5' end of the CDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25% strength Baggoye terminator sequencing rematery (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA).

The frequency distribution of the library is as follows: 72% of genes have I copy; 14.3% 2; 12% 3.10; 1.4% 11-50 and 0.1% 51-160. As to gene function, 45% of genes are present in GenBank and have know function; 12% have uncharacterized ESTs and 20% are unidentified."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GTATTTATGGATAAACTTTCTTAAGAAGTTGTGCGGATGAGGAGGAGTGTCTATACT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 CCCAGCAACTIGGIGAAGGAGCAGCGIGIATACCAGGAGGCCACCAAGGAGATCCCAACC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAAACC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 TTTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 Areschadgararrearcrirgerrecedecerreresrargrandrecedecearesr 64
   Uppsala, Sweden)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 GTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGCGGATGAGGAGGAGTGTGTTATACT
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   over Pharmacia Size Sep400 (Pharmacia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 384; DB 13; 100.0%; Pred. No. 4.1e-106;
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Best Local Similarity 100.
Matches 384; Conservative
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gilidol.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gilldol.y. mRNA sequence.
BQ554134
BQ564134.1 GI:21467451
EST.

DEFINITION

RESULT 4 BQ564134

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ACCESSION VERSION KEYWORDS

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Buckaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammaculus

Nammalia; Eutheria; Rodentia, Sciurognathi, Muridae, Murinae; Mus.

1 (Deses 1 to 534)

Rodhar B.

Extransia of gene expression in the mouse Organ of Corti at the Outpublished of gene expression in the mouse Organ of Corti at the Outpublished of gene expression in the mouse Organ of Corti at the Outpublished of Beating

Extransia of gene expression in the mouse Organ of Corti at the Outpublished Colored ```

Location/Qualifiers

FEATURES

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Strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MT Terrad thermal cyclers (MA Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGGAATTGTAGGTTATTTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGAATGTAGTTTC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCAGCAACTTGGTGAAGGAGCAGGGTGTATACCAGGAGGCCACCAAGGAGATCCCAAACC 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 ATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 182
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
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Plate: 135 row: f column: 01
Seg primer: M13RP1 reverse primer (ABI).
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Fax: 301-402-1765
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100.0%; Score 384; DB 13;
Best Local Similarity 100.0%; Pred. No. 4.3e-106;
Matches 384; Conservative 0; Mismatches 0;
organism="Mus musculus"
                                                                                    /db_xref="taxon:10090"
/clone="gi135f01"
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/couse and female...
/dev stage="Post natal day 5 to 13"
/dev stage="Post natal day 5 to 13"
/dev stage="Post natal day 5 to 13"
/dev stage="Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 organ of Corti (OC) was fine dissected from a total of 386 from post-natal (P) day 5; 72 from PS: 18 from PS: 20 from PD: 14 from PT: 46 from PS: 18 from PS: 20 from PD: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 46 from PT: 4
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gi27g09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
Clone gi27g09 5', mRNA sequence.
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Structural Cell Biology
Autional Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
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Plate: 27 row: g column: 09
Seq primer: MI3RP1 reverse primer (ABI).
Location/Qualifiers
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/strain="BALB/c"
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and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total TNA, was extracted using the micro Fastrack kit (catalog # K1593.02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR digapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney mutine leukemia virus reverse transcribed using Moloney mutine leukemia virus reverse transcribed using Moloney mutine leukemia virus reverse transcribed using Moloney mutine leukemia virus reverse transcribed using Moloney mutine leukemia virus reverse transcribed using Moloney mutine leukemia virus reverse transcribed using Moloney mutine leukemia virus reverse transcribed using Moloney mutine leukemia virus reverse transcribed using Moloney mutine leukemia virus reverse transcribed using Moloney mutine leukemia virus reverse transcribed using Moloney mutine leukemia virus reverse transcribed using over Pharmacia Size Sep400 (Bharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for CDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with Gold pot the Uni-ZAP XR vector, which had been predigested virus greater than 400bp and 1000 by respectively. The CDNA was then directionally ligated to the phage library was estimated to be 11,100,000 recombinants: Stratagener's Exatagener's Stratagener's Strat strength BigDye terminator sequencing chemistry (Applied Biosystems). Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ETS and 20% are unidentified."

Gaps ö 100.0%; Score 384; DB 13; Length 608; 100.0%; Pred. No. 4.5e-106; Live 0; Mismatches 0; Indels 0 Matches 384; Conservative Query Match Best Local Similarity ๙

180 121 ATTICICIGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC

73

241 TTTTGGGCTGGCAGTGTTATGGTGACCACCAGGATGAGAATGGGAATTGTAGGTATTTC 300

BQ568471

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SOURCE

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/croute="gat-wought"
//cav="maile and female"
/dev_stage="Post natal day 5 to 13"
/clone lib="Mouse Organ of Corti cDNA pBluescript"
/clone lib="Mouse Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from p8; 18 from p9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            library construction were carried out with the Uni-Zap XR vector kit (catalog # 23721, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 up RRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker. Primer and transcribed using Moloney mutine leukemia virus reverse transcribed wing Moloney mutine leukemia virus reverse transcribeds (MMLV-RT) and 5-methyl dCTP. The second strand was
                                                                                                                                                                                                                                                                                                                                                                                       630 bp mRNA linear EST 19-JUN-2002
gilo8g04.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
Elone gilo8g04 5', mRNA sequence.
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                                                                  CCCAGCAACTIGGIGAAGGAGCAGCGIGIAIACCAGGAGGCCACCAAGGAGAICCCAACC 360
                                                                                                     253 TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST analysis of gene expression in the mouse Organ of Corti at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus muscullus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 630)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: kacharb@nidcd.nih.gov
Plate: 108 row: g column: 04
Seg primer: M13RP1 reverse primer (ABI).
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                                                                                                                                                                                                                                    373 ACGGATATTGACTTCTTCTGTGAA 396
                                                                                                                                                                                                        361 ACGGATATTGACTTCTTCTGTGAA 384
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/strain="BALB/c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301-402-1599
Fax: 301-402-1765
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                                                                      301
                                                                                                                                        313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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VERSION
KEYWORDS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
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with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin.1000 (Clontech, Palo Alto, CA) columns to enrich for cDNA greater than 400hp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the CDNA clones were generated with the universal M13 reverse primer (CAGGAAACGCTARGCC) and 25%
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BB611549.1 GI:15393547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strength Biggy terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing chemistry (Applied Briosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy, 14.3% 2; 12% 3-10, 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of penes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function, 12% are uncharacterized ESTs and 20% are unidentified."
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ilarity 100.0%; Pred. No. 4.6e-106;
Conservative 0; Mismatches 0;
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Best Local Simi
Matches 384;
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ORIGIN
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COMMENT

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/dev_stage="Post natal day 5 to 13"
                                                                                                                                      100.0%; Score 384; DB 10; 100.0%; Pred. No. 4.9e-106;
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Seg primer: M13RP1 reverse primer
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/organism="Mus musculus"
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/clone="gi42g03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 ACGGATATTGACTTCTTCTGTAA 407
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Plate: 42 row: q column: 03
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/strain="BALB/c"
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Mammalia; Eutheria;
1 (bases 1 to 474)
                                                                                                                                                                                          Matches 384; Conservative
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Unpublished
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninoi, P., Shibata, Y., Hayatash.N., Sugahara, Y., Shibata, K., Itoh
W., Komno, H., Okazaki, Y., Hayatash.N., and Hayashizaki, Y.
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wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Lishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
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Konnotter-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. . 11 (2), 281-289 (2001)
Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shihaqawa, A., Aizawa, K., Phukuda, S., Hara, M., Itch, M., Kawai, J., Shibata, X., Aizawa, K., Phuc, Genomics 2 pre, L72-L86 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Bases I to 696)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Komo, H., Kouda
, M., Koya, S., Mateuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Sakai, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takabashi, F., Takeda, Y., Tanaka, T., Toya, T.,
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
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                                              Mus musculus (house mouse)
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474 bp mRNA linear BST 19-JUN-2002 gi42g03.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi42g03 5', mRNA sequence.
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Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Structural Tell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1765
Fax: 301-402-1765
                                                                                                                                              24 ATGGCAAGGATATTGATTCTTTTGCTTGGGGGCCTTGTGGTTCTATGTGCCGGCCATGGT
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Length 696;
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/clone_lib="Mouse Organ of Corti cDNA pBluescript" The force="Organ: Organ of Corti; wector: pBluescript" The organ: Organ of Corti; wector: pBluescript; The organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ: Organ
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74 GTATTTATGGATAAACTTTCTTCTAATAAGTTGTGTGCGGATGAGGAGTGTGTTATTACT 133 121 ATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCCAGACTGTAGGTTCATCGATGTC 180 TGTGGTTCTATGTGCCGGGCATGGT 60 14 Argecaaggararrgarrcrrrrgcrrrggggccrrgrggrrcrargrgccggggarggr 73 DB 13; Length 474; 1; Indels cch 99.6%; Score 382.4; DB 13; al Similarity 99.7%; Pred. No. 1.2e-105; 383; Conservative 0; Mismatches 1; 1 ATGCCAAGGATATTGATTCTTTTGCTTGGGGGCCT 61 Query Match Local BASE COUNT ORIGIN Matches D, à a

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was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fastrack kit (catalog # X159-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR digapack III Gold Cloning kit (catalog # 237512), both from Stratagene (La Jolla, CA, USA), according to
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/dev stage="Post natal day 6 to 13"
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134 ATTICICIGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 193
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 684)
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Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1765
                                                                                                          194 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG
                                                     181 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG
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Plate: 06 row: column: 09
Seq primer: MI3RPL reverse primer (ABI).
Location/Qualifiers
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RESULT 11

BQ566932

ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS TITLE

JOURNAL

FEATURES

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Extremely BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have I copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 43% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
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313 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 372 GTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGCGGATGAGGAGTGTGTTATACT 120 121 ATTICICIGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 180 181 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGA 240 241 TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC 300 253 TITIGGGCIGGCAGIGITIAIGGIGACCACCAGGAIGAGAIGGGAAIIGIAGGIIAIIIC 312 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATGCCAACC 360 72 13 ATGCCAGGGATATTGATTCTTTTGCTTGGGGCCTTGTGGTTCTATGTGCCGGGCATGT 1 ATGCCAAGGATATTGATTCTTTTGCCTTGGGGCCTTGTGGTTCTATGTGCCGGGCATGGT Gaps ; DB 13; Length 684; 1; Indels Query Match 99.6%; Score 382.4; DB 13, Best Local Similarity 99.7%; Pred. No. 1.5e-105; Matches 383; Conservative 0; Mismatches 1; ACGGATATTGACTTCTTCTGTGAA 384 361. 193 61 133 301 BASE COUNT ORIGIN qq ò 유 à à d 8 g ò g ò q

373 ACGGATATTGACTTCTTCTGTGAA 396

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14 from P12 and 24 from P13. After Killing alminals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was cartacted using the micro Fastrack Mit (ctalog # K153-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap KR vector kit (ctalog # 237211, Stratagene) and Uni-Zap KR vector kit (ctalog # 237211, Stratagene) and Uni-Zap KR vector kit (ctalog # 237211, Stratagene) and Uni-Zap KR vector kit (ctalog # 237211, Stratagene) and Uni-Zap KR vector kit (ctalog # 237211, Stratagene) and Uni-Zap KR vector kit (ctalog # 237211, Stratagene) and Uni-Zap KR vector kit (ctalog # 237211, both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 up mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using synthesized with DNA polymerase and RNASE H. Complementary DNA was blunt ended with Ptu DNA polymerase and digested with DNA was blunt ended with Ptu DNA polymerase and digested with Ecox I adapters in the presence of ligase and digested vith Xho I. The CDNA was steader than 400bp and 1000 by columns to enrich for CDNAS greater than 400bp and 1000 by columns to enrich for CDNAS greater than 400bp and 1000 the Uni-ZAP XR vector, which had been predigested with Ecox I and Xho I. The phagemid was packaged with Gagapak III Gold and mon titrafon on XI, Blue MRF, cells, the
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/clone lib="Mouse Organ of Corti cDNA pBluescript,"
/note="Organ: Organ of Corti; Vector: pBluescript, The
organ of Corti (CC) was fine dissected from a total of 386
OC as follows: 10.2 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
BQ566932 409 bp mRNA linear EST 19-JUN-2002 gi73g09.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi73g09 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST analysis of gene expression in the mouse Organ of Corti at the
                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Kachar, B. Structural Cell Biology
National Institute of Deafness and other Communication Disorders 50,4249 South Drive, NIH, Bethesda, MD 20892-8027, USA Tel: 301-402-1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: kacharbenided.nih.gov
Plate: 73 row: g column: 09
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="gi73g09"
/sex="male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db xref="taxon:10090"
                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                         BQ566932.1 GI:21470249
                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 409)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            onset of hearing
Unpublished
                                                                                                                                                                                                                                                                                                                    musculus
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                                                                                                                                                                                                                                    EST.
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JOURNAL

source

FEATURES

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recombinants. Stratagene's Exhssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the concerty6 (TM) plasmid purification kit (Invitrogen, Carlebad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on M1 Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy, 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are unharacterized ESTs and 20% are unidentified."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 19-JUN-2002
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2137bl2:y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gi37bl2 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 TATTICICIGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGA 239
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 490)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 ATGCCAAGGAIAITGAITCTTTTGCTTGGGGCCTTGCGGTTCTATGTGCCGGGCAIGGT 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.4%; Score 366.2; DB 13; Length 409; 99.0%; Pred. No. 9.9e-101; ive 0; Mismatches 3; Indels 1;
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Mus musculus
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Best Local Similarity 99.0°
Marches 379; Conservative
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EST analysis of gonset of hearing
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DEFINITION
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KEYWORDS
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ORIGIN
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BQ565411
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TITLE
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 365)
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BY232622 RIKEN full-length enriched, adult inner ear Mus musculus
cDNA clone F930026J20 5', mRNA sequence.
BY232622
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genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified." 77 c 109 g 112 t 1 others
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                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                13; Length 490;
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Pred. No. 4.6e-95;
0; Mismatches 17; Indels
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al Similarity 95.5%;
358; Conservative (
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
Email: genome-remegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nasamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakaune,N., Sasaki,D., Muramatsu,M. and Hayashizaki,Y. Direct Submission.
,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepare mouse tissues.

Tissues were provided by Kirk W. Beisel ( Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKBN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in Riken
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of 110 g 98 t
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/clone="F930026J20"
                                                                                                                                                                                                                                                                                                                                                    Contact: Yoshihide Hayashizaki
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al Similarity 99.7%;
341; Conservative
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/db xxef="texon:1000"
/clone="gi88608":
/clone="gi88608":
/clone="gi88608":
/clone="gi88608":
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/clone lib="Mouse Organ of Corti; Vector: pBluescript; The
/clone lib="Mouse Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P12 and 24 from P13. After Killing animals by
oervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fastrack kit
(catalog # X1593-02; Invittogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
digapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (Ita Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker- primer and transcribed using
Moloney murine leukemia virus reverse transcribeds
(MMLV-RT) and 5-methyl dCTP. The second strand was
                                                                                                                                                                                                                                                                                                                                                                                                                               BQ567343 604 bp mRNA linear EST 19-JUN-2002 gi88d08.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi88d08 5', mRNA sequence.
                                                                                                                    TITIGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC 300
                                                                                                                                                EST analysis of gene expression in the mouse Organ of Corti at the
AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAACGGAGCTGGAGAG 240
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Mus musculus
Mus musculus
Mukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musi
1 (bases 1 to 604)
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Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
                         CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCC 365
                                                                                                                                                                                                                                         CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCC 342
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Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 301-402-1765
Email: kacharb@nidcd.nih.gov
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KEYWORDS
SOURCE
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AUTHORS
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synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Pala Alto, CA) columns to enrich for CDNA greater than 400bp and 100b by respectively. The CDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Giappak III Gold and, upon Litration on XLI Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 resouce helper phage (catalogue # 21120) was adopted to resistance helper phage (catalogue # 21120) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual CDNA clones were selected and grown in 96-well, and growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the concerts (TM) plasmid purification kit (Invitrogen, Carlabad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal NI3 reverse primer (CAGGAAACAGCTATGACC) and 25 strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA).

Sequencers using POPS polymer (Applied Biosystems, Foster City, CA). Sequencing reactions as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank, but do not have assigned tuction; 12% are unharacterized ESTs and 20% are unidentified.

78 a 108 c 152 g 166 t 280 bp mRNA linear EST 19-JUN-2002 gill4f04.y2 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA BQ568785 204 61 GATTACAATGCCCCAGACTGTAGGTTCATCGATGTCAAGAAAGGGCAGCAGCAGTCTATGTT 120 264 265 GACCACCAGGATGAGAATTGTAGGTTATTTCCCCAGCAACTTGGTGAAGGAGCAG 324 240 325 CGTGTATACCAGGAGGCCACCAAGGAGATCCCAACCACGGATATTGACTTCTTCTGTGAA 384 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 9 1 AAGAAGTTGTGTGCGGATGAGGAGTGTGTCTATACTATTTCTCTGGCAAGGAGCACAGGAA TACTCCAAGCTGGTAACAGAAACGGAGCTGGAGGTTTTTGGGCTGGCAGTGTTTATGGT 85 AAGAAGTTGTGTGCGGATGAGGAGTGTGTCTATACTATTTCTCTGGCAAGAGCACAGGAA 145 GATTACAATGCCCCAGACTGTAGGTTCATCGATGTCAAGAAAGGGCAGCAGATCTATGTT Gaps . 0 78.1%; Score 300; DB 13; Length 604; 100.0%; Pred. No. 2.1e-80; ive 0; Mismatches 0; Indels 0 Mus musculus (house mouse) Mus musculus BQ568785.1 GI:21472102 Query Match
Best Local Similarity 100.0
Matches 300; Conservative 205 VERSION KEYWORDS SOURCE ORGANISM DEFINITION BASE COUNT RESULT 15 ACCESSION BQ568785 LOCUS ORIGIN g 셤 g ò g Š ò à ઠ

REFERENCE AUTHORS TITLE

JOURNAL

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epithelium was carefully dissected out or the modification and rotal RNA was extracted using the micro Fastrack Kit (catalog # K1593-02; Invitrogen, Carlabad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR Gigapack III Gold Cloning Kit (catalog # 23761), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptuse (MMLV-RT) and 5-methyl GTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Aho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The bhagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF' cells, the Yello of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of seturated culture with the Concert of Parcer of Murin Process
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev stage="Post natal day 5 to 13"
/clone lib="Mouse Organ of Corti cDNA pBluescript"
/clone lib="Mouse Organ of Corti cDNA pBluescript; The
/note="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
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                                                                 EST analysis of gene expression in the mouse Organ of Corti at the
                                                                                                                                                                                                               Confact: Kachar,B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4294 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: kacharb@nidcd.nih.gov
Plate: 114 row: f column: 04
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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/mol_type="mRNA"
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clone="gill4f04"
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sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have I copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Mouse MLP nucleoti Mouse MLP nucleotide Rat MLP nucleotide Mouse MLP nucleotide Human MLP nucleotide Human MLP nucleotide Human MLP nucleotide Human Growth regul Description AAF59068 AAF59084 AAF59098 AAF59099 AAF59065 AAF59065 947 338 330 330 384 387 426 Length Query Match 1000.0 1000.0 899.6 85.9 76.8 74.7 384 384 344 330 294.8 287 287 Score Result

WPI; 2001-159271/16.

|          | PR09873  | cDNA encoding huma | Human EST-derived | Human growth regul | Human MLP nucleoti | Human growth regul | Rat MLP nucleotide | Human MLP nucleoti | Rat MLP nucleotide | Sequence encoding | Recombinant human | Sequence encoding |          |          | D.       | Breast cancer rela | Breast cancer rela | Seguence encoding | Amplified fragment | Human gene express | Human protein enco | Human cDNA encodin | Human cDNA encodin | Human PRO19670 cDN | Human cDNA encodin | Human angiogenesis | Human PRO19670 cDN | Human PRO19670 cDN |          |          | (I)      | Human cDNA encodin | Novel human secret | Human secreted/tra |          | Human PRO polynucl |  |
|----------|----------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|----------|----------|----------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|----------|--------------------|--------------------|--------------------|----------|--------------------|--|
| ABL95740 | ABL88251 | ABK33571           | AAH98228          | AAH26342           | AAF59083           | AAH26343           | AAF59093           | AAF59079           | AAF59092           | AAQ84052          | AAH47783          | AAQ84050          | AA170083 | AAD18732 | ABV59229 | ABL63602           | ABL64012           | AAQ84061          | AAQ84055           | AAZ14828           | AAH99775           | AAS22695           | AAS22459           | AAF92140           | ABS74460           | ABL95738           | ABL88249           | ACA57963           | ACA58892 | ACA60445 | ACA63455 | ABX98433           | ABX98935           | ACA05980           | ABX98024 | ABX78808           |  |
| 24       | 24       | 24                 | 22                | 22                 | 22                 | 22                 | 22                 | 22                 | 22                 | 16                | 22                | 16                | 22       | 22       | 23       | 24                 | 24                 | 16                | 16                 | 20                 | 22                 | 22                 | 22                 | 22                 | 24                 | 24                 | 24                 | 25                 | 25       | 25       | 25       | 25                 | 25                 | 25                 | 25       | 25                 |  |
| 521      | 521      | 521                | 891               | 891                | 923                | 1201               | 307                | 330                | 261                | 581               | 433               | 459               | 459      | 459      | 555      | 442                | 442                | 330               | 305                | 300                | 417                | 429                | 884                | 1060               | 1060               | 1060               | 1060               | 1060               | 1060     | 1060     | 1060     | 1060               | 1060               | 1060               | 1060     | 1060               |  |
| 74.7     | 74.7     | 74.7               | 74.7              | 74.7               |                    |                    |                    |                    | 6.09               | 17.2              | 15.7              | U)                | 15.7     | 15.7     | 15.7     | Ŋ                  | 'n                 | 4                 | 13.7               | ď                  | 12.3               | N                  | N                  |                    | 4                  | 12.3               | 4                  | ď                  | ď        | ď        | ά.       | 2                  | ď                  | ď                  | 12.3     | ď                  |  |
| 287      | 287      | 287                | 287               | 287                | 287                | 287                | w                  | u                  | 233.8              | w                 | 60.2              | 60.2              | 60.2     | 60.2     | 60.2     | 8                  | 8                  | LO.               |                    | 2                  |                    | 7                  | ζ.                 | ~                  | •                  | 7                  | 47.2               | 47.2               | 47.2     | •        | •        | •                  | 7                  | 7                  | 7.       | ۲.                 |  |
| 6        | 10       | 11                 | 12                | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                | 20                | 21                |          | c 23     |          |                    | c 26               |                   | 28                 | 29                 | 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38       | 39       | 40       | 41                 | 42                 | 43                 | 44       | 45                 |  |

## ALIGNMENTS

AAF59068 standard; DNA; 384 BP

RESULT 1

AAF59068;

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Noguchi Y, Yoshimura K;
                                                                                    MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter; inhibitor; ds.
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                                                                 Mouse MLP nucleotide sequence SEQ ID NO:10
                                                                                                                                                                                                                                                             Ogi K, Ohkubo S,
                                                                                                                                                                                                 29-JUN-2000; 2000WO-JP04278.
                                                                                                                                                                                                                     99JP-0186718
                                                                                                                                                                                                                                         (TAKE ) TAKEDA CHEM IND LTD.
                                                 23-APR-2001 (first entry)
                                                                                                                                                                                                                                                            Itoh Y, Nishi K,
                                                                                                                                                            WO200102564-A1.
                                                                                                                                                                                                                     30-JUN-1999;
                                                                                                                                        Mus musculus.
                                                                                                                                                                              11-JAN-2001
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joint

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TTTTGGGCTGGCAGTGTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTC 300
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                                                                                                                                   The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
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                    Safe, low-toxicity secretory cell function-regulatory protein and encoded DWA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and diseases
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                                                                                                                                                                                                                                                                                                                     Length 384;
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                                                                                                                                                                                                                                                                                   Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;
                                                                                                                                                                                                                                                                                                                   100.0%; Score 384; DB 22;
100.0%; Pred. No. 1.6e-113;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                      exemplification of the present invention.
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                                                                                                                                                                                                                                                       The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis.

AAF59063 to AAF59099 and AAB69122 to AAB6912 represent sequences used
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                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 384; DB 22;
100.0%; Pred. No. 2.4e-113;
ive 0; Mismatches 0;
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          29-JUN-2000; 2000WO-JP04278
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                                       30-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                 Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint diseases
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MIA; melanoma inhibitory activity; cancer; bone disease; cisease; pathologic angiogenesis; diagnosis; antiinflammatory; ant; gene therapy; secretory cell function regulator; promoter;
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Pred. No. 1.3e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the exemplification of the present invention.
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                                                                                                                                                                                                                                                                          Mogi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Page 105-106; 111pp; Japanese.
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                                                                                                                                                                                                                                                                          Ohkubo S,
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93.5%;
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                                                                                                                                                                             2000WO-JP04278.
                                                                                                                                                                                                            99JP-0186718
                                                                                                                                                                                                                                                                          Ogi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND
                                                                                                                                                                                                                                                                                                                         2001-159271/16
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Best Local Similarity
Matches 359; Conserv
                                                                                                                                                                                                                                                                          Nishi K,
                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAB69130
                                                                                                                 WO200102564-A1
                                                                                                                                                                             29-JUN-2000;
                                                                                                                                                                                                            30-JUN-1999;
    MLP; MIA; me
joint diseas
cardiant; ge
inhibitor; o
                                                                                                                                               11-JAN-2001
                                                                                                                                                                                                                                                                          Itoh Y, N
Tanaka H;
                                                                                    sb.
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                                                                                    Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGAGTTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant extivities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATTTCCCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint diseases
                                                                                                                                                                                                                                                                                                                                                                                                    Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATACTATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATACTATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCCAGACTGTAGGTTCATC
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                                                                                                                         MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                     Noguchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                     Ohkubo S, Mogi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     llarity 100.0%; Pred. No. 3.9
Conservative 0; Mismatches
                                                                                             nucleotide sequence SEQ ID NO:25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 98; 111pp; Japanese.
 BP
                                                                                                                                                                                                                                                                                                          29-JUN-2000; 2000WO-JP04278.
                                                                                                                                                                                                                                                                                                                                        99JP-0186718.
AAF59080 standard; DNA; 330
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                                                                entry)
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Matches 330; Conser
                                                                                                                                                                                                                                                                                                                                                                                                     Nishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAB69127
                                                                                                                                                                                                                                          WO200102564-A1
                                                                                                                                                                                                                                                                                                                                                                       (TAKE ) TAKEDA
                                                                                                                                                                                                            Mus musculus.
                                                                                                                                                                                                                                                                                                                                        30-JUN-1999;
                                                                23-APR-2001
                                                                                                                                                                                                                                                                        11-JAN-2001
                                                                                                                                                                             inhibitor;
                                                                                              Mouse MLP
                                                                                                                                                                                                                                                                                                                                                                                                                        Tanaka H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
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                                 AAF59080;
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The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis.

AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
                                                                                                             TATTICCCCAGCAACTIGGIGAAGGAGCAGCGIGIAIACCAGGAGGCCACCAAGGAGAIC 354
                                                                                                                                  241 TATTTCCCCAGCAACTTGGTTAGAAGCAACGAGTGTACCAGGAGGCCACCAAGGAGATT 300
121 AATGTCAAGAAAGGGCAGCAGCAGTTTATTCCAAGCTGGTAACAGAAAATGGAGCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA
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                                       235 GGAGAGTITTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGAATTGTAGGT
                                                    181 GGGGCATTCTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yoshimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 287; DB 22; Length 384;
Pred. No. 3e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Noguchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , 3e-82;
60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mogi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                              301 CCAACCACGGATATTGACTTCTTCTGTGAA 330
                                                                                                                                                                                           CCAACCACGGATATTGACTTCTTCTGTGAA 384
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human MLP nucleotide sequence SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohkubo S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 91; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                                                                                                                                                                               AAF59065 standard; DNA; 384
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Best Local Similarity 84.33
Matches 323; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-159271,
P-PSDB; AAB69123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200102564-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibitor; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-2001
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                                                                                                                      295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAIGGIGIAITIAIGGAIAAACIITICIAAGAAGIIGIGIGIGGGAIGAGGAGIGIGIC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATACTATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antinflammatory and cardiant extivities, and can be used in gene therapy and as secretory call function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
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             Yoshimura K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Noguchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
76.8%; Score 294.8; DB 22;
Best Local Similarity 93.3%; Pred. No. 8.7e-85;
Matches 308; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ς,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mogi
                                                                                                     CCAACCACGGATATTGACTTCTTCTGTGAA 330
                                                                                                                                                                                                                                                                                                                    Rat MLP nucleotide sequence SEQ ID NO:48.
                                                                          CCAACCACGGATATTGACTTCTTCTGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nishi K, Ogi K, Ohkubo S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 107; 111pp; Japanese.
                                                                                                                                                                                                        BP.
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                                          TTTTGGGCTGGCAGTGTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC
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                 GTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGTGAGGAGTGTGTCTATACT
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The invention relates to an isolated novel secreted polypeptide (I) and polynucleotide (II). (I) and (II) are useful for treating cancer, would healing disorder, infections, haematopoietic disorders, inflections, haematopoietic disorders, inflections, haematopoietic disorders, inflammatory disorders, infections, haematopoietic psychiatric diseases, cardiovascular diseases, respiratory diseases, cardiovascular diseases. These may also be used to treat diseases, abnormalities and disorders caused by abnormal expression, production, function and/or metabolism of the genes, as vaccines for inducing immunological response in a mammal, and in careening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. The polypeptides can be used as immunogens to produce antibodies immunospecific for the polypeptides, and to identify membrane-bound or soluble receptors. The polypurcleotides and to identify membrane-bound or soluble receptors. The polypurcleotides and to identify membrane-bound or soluble receptors. The polypurcleotides and to identify expression studies. The present sequence represents the coding sequence of novel human secreted protein #12.
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                                                                                                                                                                    Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmine disorders, hyperproliferative disorders, coagulation disorders, and nervous system disorders.
                                                                                                                                                                                                                                                                                                                                                                        signature analysis, and Sanger sequencing techniques. This expressed sequence tag was used in the assembly of a full-length copy. Sequence (see AAH26343) encoding a novel human growth regulatory-like polypeptide (GRLP, see AAB82671). The GRLP belongs to the same protein family as growth regulatory proteins, percursor (64% similarity and derived growth regulatory protein precursor (64% similarity and 45% identity over 111 amino acids) or melanoma inhibitory activity, cattle cartilage-derived cretinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid-sensitive proteins. GRLP polypeptides and polymucleotides of the invention can be used in the prophylaxis, treatment (including gene therapy) and diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                production of protein, in the generation of antisense, ribozyme an peptide-nucleic acid molecules, and to produce transgenic animals.
                                                                                                                                                                                                                                                                                                    The present sequence is that of Hyseq clone identification number 1637272, which was obtained from a human thymus cDNA library using standard PCR with primers specific for vector sequences flanking the inserts, sequencing by hybridisation sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 14.7%; Score 287; DB 22; Length 426; al Similarity 84.3%; Pred. No. 3.2e-82; 323; Conservative 0; Mismatches 60; Indels (
                                                                                           Liu
                                                                                           Tang YT,
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                                                                                         Arterburn MC,
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                                                                                                                                                                                                                                                                   Example 1; Page 114; 119pp; English.
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                                                                                             Ford JE,
       25-JAN-2000; 2000US-0491404
02-MAY-2000; 2000US-0563786
                                                                                             Boyle BJ,
                                                                                                                                               WFI; 2001-483233/52.
                                                             (HYSE-) HYSEQ INC.
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                                                                                   Mize NK, Bo)
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Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; gene; ss.
                                                                                                                                                                                       Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.
ACGGATATTGACTTCTTCTGCGA 401
                                                                                               BP.
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25-MAY-2001; 2001US-0866028.
25-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001US-087092.
30-MAY-2001; 2001US-0870574.
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2001US-0854208.
2001US-0854280.
2001US-0866028.
2001US-0866028.
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2001US-0767609.
2001US-0796498.
                                                                                              ABL95740 standard; cDNA; 521
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2001WO-US06666
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28-JUN-2001; 2001WO-US00000
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2000WO-US20710.
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                                                                                                                                                               19-JUL-2002 (first entry)
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GODOWSKI P J.
GURNEY A L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENENTECH INC.
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FERRARA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GERBER H.
                                                                                                                                                                                                                                                                                                                                             WO200208284-A2.
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05-APR-2001; 2
10-MAY-2001; 2
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09-MAR-2001;
14-MAR-2001;
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01-DEC-2000;
20-DEC-2000;
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24-OCT-2000;
08-NOV-2000;
08-NOV-2000;
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17-AUG-2000;
23-AUG-2000;
24-AUG-2000;
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                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                 ABL95740;
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(BAKE/)
(FERR/)
(GERB/)
(GERR/)
(GODD/)
(GODO/)
(GURN/)
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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
                                 Human; angiogenesis, cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerctic; PRO agnosist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; themazoiad arthritis; myccardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SA, Pan J,
WI, Ye W;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Stephan JF, Watanabe CK, Williams PM, Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerritsen ME,
            Human PRO9873 cDNA sequence SEQ ID NO:359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerber H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 359; 565pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       2000WO-US23522.
2000WO-US23328.
2000US-230978P.
2000US-0664510.
2000US-242922P.
2000US-242922P.
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2001US-0767609.
2001US-0796498.
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2001WO-US06666.
2001US-0802706.
2001US-0808689.
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2001US-0828366.
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2000WO-US32678.
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2001US-0854280.
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2000US-0643657.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-090516/12.
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                                                                                                                                                                                                    WO200200690-A2
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01-DEC-2000;
                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTICICICGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 180
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                                                                                                                                                                                                                                                                                                                                                            hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 ATATITATIGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGGTGTGTCTATACT 157
                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 Argecaagaararrerrerrerrerecedegeerrergeergreergeergeaga 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 ATTICTICGÉCTAGTÉCTCAAGAAGATTATAATÉCCCCGGACTGTAGATTCATTAACGTT
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                                                                                                                                            Paoni NF;
                                                                                                                                                                                                                             One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       nealing. The present sequence is a coding sequence of the invention
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                                                                                                                           Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J,
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
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                                                                                                                                                                                                                                                                                          Claim 1; Fig 359; 567pp; English.
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                              PAN J.
PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
   HILLAN K J.
MARSTERS S A.
                                                                                                                                                                                         WPI; 2002-171999/22.
P-PSDB; ABB95602.
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Matches 323; Conserv
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                                             (PAON/)
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The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polymucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation of chondrocyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tismulating the proliferation of normal human dermal thorough markers and for tismulating use as hybridisation probes, and in chromosome and gene mapping. ABR33536_ABR33567 represent human
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Smith V, Stephan JF, Watanabe CK, Wood WI;
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                                                                                                                 2000US-22063BP.
2000US-220664P.
2000US-220666P.
2000US-220893P.
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28-FEB-2001; 2001WO-US06520.
10-MAY-2001; 2001US-0854280.
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2000WO-US23522.
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01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000US-0747259.
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15-SEP-2000;
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28-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 74.7%; Score 287; DB 24; Length 521;
Best Local Similarity 84.3%; Pred. No. 3.5e-82;
Matches 323; Conservative 0; Mismatches הוי דיילירו
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
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ATTICTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 180
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                                                                                                                                                                                                                                  CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 360
             ATTTCTCTGGCTAGTGCTCAAGAAGATTATAAATGCCCCGGACTGTAGATTCATTAAACGTT
                                                                                                                                       CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC
GTATTTATGGATAAACTTTCTTAAGAAGTTGTGCGGATGAGGAGTGTCTATACT
                                                                                                                AAGAAAGGGCAGCAGCAGTCTATGTTTACTCCAAGCTGGTAACAGAAAACGCAGCTGGAGAG
                                                                                                                                                                                                     TTTTGGGCTGGCAGTGTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of a novel nucleic acid that was sasembled from human thymns cDNA library-derived Hyseq clone identification number 16372272 (see AAH26341). A recursive algorithm was used to extend the clone by pulling additional sequences from different databases. A full-length sequence (see AAH26343) encoding novel human growth regulatory-like polypeptide (GRLP, see AAB2671) was subsequently obtained. Human GRLP belongs to the same protein family as growth regulatory proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Growth regulatory-like polypeptide; human; cartilage; melanoma; neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human growth regulatory-like polypeptide partial cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arterburn MC,
                                                                                                                                                                                                                                                                                            383
                                                                                                                                                                                                                                                                                                                         401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 115; 119pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                                                                                                                                              AAH26342 standard; cDNA; 891
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02-MAY-2000; 2000US-0563786
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                            361
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61
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                                                                                   397
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300
                CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            novel
TITIGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC
                                                                          1 ATGCCAAGGATATTGATTCTTTGCTTGGGGGCCTTTGTGGTTCTATGTGCCGGGCATGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases, diagnostics, raising
                                                                                                                                                                                                                                                                                                                                  Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; toanto; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of
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llarity 84.3%; Pred. No. 4.4e-82;
Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen
                                                                                                                                                                                                                                                                                                        Human EST-derived coding sequence SEQ ID NO: 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              z,
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Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polypeptide for treatment of antibodies and research use -
                                                                                                                                            420
                                                                                                                ACGGATATTGACTTCTTCTGTGA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 236; 1275pp; English.
                                                                                                                                 ACGGATATTGACTTCTTCTGCGA
                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0613451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                     AAH98228 standard; cDNA; 891
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                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Liu C, Zh
Drmanac RA,
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Best Local Simil
Matches 323; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                       78
         precursor (64% similarity and 45% identity over 111 amino acids) or melanoma inhibitory activity, cattle cartilage-derived or melanoma inhibitory activity, cattle cartilage-derived crimic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid-sensitive proteins. GRLP polypeptides and polymucleotides of the invention can be used in the prophylaxis, treatment (including gene therapy) and diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma cell growth and tumours, including neuroectodermal tumours such as and primars. The polymucleotides can also be used to design probes and primars, for chromosome and gene mapping, in the recombinant production of protein, in the generation of antisense, ribozyme and peptide-nucleic acid molecules, and to produce transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTCCCGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATCATTAACGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>aaaaaagggcagcagarcrargrargracrcaaagcrggraaaagaaaargaagcrggagaa</u>
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                                                                                                                                                                                                                                                                                                                                                 Gaps
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growth factors, human melanoma derived growth regulatory protein
                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                         Score 287; DB 22; Length 891;
Pred. No. 4.4e-82;
0; Mismatches 60; Indels (
                                                                                                                                                                                                                                                                      Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGGATATTGACTTCTGTGA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 ACGGATATTGACTTCTTCTGCGA 401
                                                                                                                                                                                                                                                                                                           cch 74.7%;
al Similarity 84.3%;
323; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WC200102564-A1
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Best Local S
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                                                                                                                                                                                                                        The present invention describes novel MLP proteins and their encoding DNAS. The MLP proteins and DNAS have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAS can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis.

AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                       Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                     Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTATTTATGGATAAACTTTCTTATGAAGTTGTGCGGATGAGGAGTGTCTATACT
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0
                                                                                                                                                                                                                                                                                                                                                                                      Length 923;
                                                     Noguchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                         Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                  603
                                                                                                                                                                                                                                                                                                                                                                                   Score 287; DB 22;
Pred. No. 4.5e-82;
0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                in the exemplification of the present invention.
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                                                        Mogi
                                                                                                                                                                                                 Example 1; Page 99-100; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGGATATTGACTTCTTCTGCGA 416
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                                                        Ohkubo S,
                                                                                                                                                                                                                                                                                                                                                                          74.7%; Scc.
84.3%; Pred
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                            (TAKE ) TAKEDA CHEM IND LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 323; Conservative
                                                        gi
                                                                                                 WPI; 2001-159271/16.
                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                        Nishi K,
30-JUN-1999;
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Query Match 74.7
Best Local Similarity 84.3
Matches 323; Conservative
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  Homo sapiens
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The sequence was assembled using human thymus CDNA library-derived Hyseq clone identification number 1637272 (see AAH26341) as seed, using software programs to pull additional sequences from Hyseq's proprietary database containing expressed sequences from Hyseq's proprietary database containing expressed sequences from Hyseq's proprietary database containing expressed sequences from Hyseq's proprietary database containing expressed sequences from Hyseq's proprietary activity, cof 14 kDa unglycosylated. GRLP belongs to the same protein family as growth regulatory proteins, procursor (64% similarity and 16% identify as growth regulatory proteins or melanoma inhibitory activity, cattle cartilage-derived cretinoic acid sensitive protein (CD-RAP, 44% identify and 64% similarity polypeptides and polynucleotides of the invention or melanoma in the prophylaxis, treatment (including gene therapy) and diagnosis of disorders and polynucleotides of the invention and diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma cell growth and tumours, including neuroeccodermal tumours such as gliomas. The polynucleotides can also be used to design probes and primers, for chromosome and gene mapping, in the recombinant production of protein, in the generation of antisense, ribozyme and peptide-mucleic acid molecules, and to produce transgenic animals. They may also have cytokine and cell growth factor activity, mannosuppressive or immunosuppressive or immunostimulant activity, activity, activity, and activity, use in cancer diagnosis and therapy, when acreating activity, use in cancer diagnosis and therapy, when acreating activity, we in cancer diagnosis and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    screening, receptor/ligand activity, antiinflammatory ity, and treatment of leukaemia, nervous system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 115-116; 119pp; English.
                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ford JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2001; 2001WO-US02455.
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02-MAY-2000; 2000US-0563786.
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                                                      33..419 /*tag= a 33..101 /*tag= b 102..416 /*tag= c
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P-PSDB; AAB82671.
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74.7%; Score 287; DB 22; Length 1201; 84.3%; Pred. No. 5.1e-82; ive 0; Mismatches 60; Indels 0;

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                                 AIGCCAAGAATATTGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGA
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Search completed: December 30, 2003, 02:14:32 Job time : 128.462 secs

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December 30, 2003, 04:08:13; Search time 315.339 Seconds (without alignments) 4172.254 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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384
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|---------------|-------|---------------------|------------------------------------|----|------------------|-------------------|---------------|
| Result<br>No. | Score | %<br>Query<br>Match | %<br>Query<br>core Match Length DB | DB | ID               | Description       |               |
| 1             | 287   | 74.7                | 426                                | 15 | US-10-216-038-1  | Sequence 1, Appli | ·r-1          |
| 7             | 287   | 74.7                |                                    | 13 | US-10-216-163-71 | Sequence 71, App  | _             |
| ĸ             | 287   | 74.7                |                                    | 13 | US-10-218-765-71 | Sequence 71, App  | <del></del> 1 |
| 4             | 287   | 74.7                |                                    | 13 | US-10-219-063-71 |                   | _             |
| ß             | 287   | 74.7                |                                    | 13 | US-10-219-066-71 |                   | 7             |
| 9             | 287   | 74.7                |                                    | 13 | US-10-219-067-71 |                   | _             |
| 7             | 287   | 74.7                | 521                                | 13 | US-10-219-068-71 | Sequence 71, Appl | _             |
| 80            | 287   | 74.7                |                                    | 13 | US-10-219-069-71 |                   | _             |
| σ             | 287   | 74.7                |                                    | 13 | US-10-219-073-71 | 71,               | _             |
| 10            | 287   | 74.7                |                                    | 13 | US-10-219-475-71 | 71,               | _             |
| 11            | 287   | 74.7                |                                    | 13 | US-10-219-480-71 | 71,               | -             |
| 12            | 287   | 74.7                |                                    | 13 | US-10-219-483-71 |                   |               |
| 13            | 287   | 74.7                |                                    | 13 | US-10-219-525-71 |                   | _             |
| 14            | 287   | 74.7                |                                    | 13 | US-10-219-526-71 |                   | _             |
| 15            | 287   | 74.7                |                                    | 13 | US-10-219-530-71 |                   | _             |

| 1                                                                                                                                                                                                                                                                                                       | Sequence 71, Appl<br>Sequence 71, Appl<br>Sequence 71, Appl<br>Sequence 71, Appl         |
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| 10-219-531<br>10-219-532<br>10-223-0833<br>10-223-0833<br>10-223-0832<br>10-223-8882<br>10-223-8882<br>10-230-163<br>10-230-163<br>10-219-076<br>10-219-076<br>10-219-076<br>10-219-676<br>10-219-676<br>10-219-676<br>10-219-676<br>10-219-676<br>10-219-676<br>10-219-676<br>10-219-676<br>10-219-676 | .5 US-10-232-233-71<br>.5 US-10-216-165-71<br>.5 US-10-218-956-71<br>.5 US-10-219-468-71 |
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## ALIGNMENTS

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APPLICANT: Macy K
APPLICANT: Macy K
APPLICANT: Macy K
APPLICANT: Boyle, Bryan J
APPLICANT: Aterburn, Matthew C
APPLICANT: Tang, Y Tom
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Song, Yong
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74.7%; Score 287; DB 15;
Best Local Similarity 84.3%; Pred. No. 7.1e-87;
Matches 323; Conservative 0; Mismatches 60;
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| LOCATION: (425)..(426)
| OTHER INFORMATION: n = A, T, G, or C
US-10-216-038-1
                                              Sequence 1, Application US/10216038 Publication No. US20030124573A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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APPLICANT: BAKELY, Kevin P.
APPLICANT: Besnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wacd, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
ATGCCAAGGATATTGATTCTTTTGCCTTGGGGCCTTGTGGTTTTTGTGCCGGGCATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
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CURRENT APPLICATION NUMBER: US/10/216,163
CURRENT APPLICATION NUMBER: US/10/216,163
PRIOR PLING DATE: 2002-08-09
PRIOR PELING DATE: 2002-08-09
PRIOR PELING DATE: 10/11,480
PRIOR PLING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-28
PRIOR PELING DATE: 1997-10-31
PRIOR PELING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/06873
PRIOR FILING DATE: 1997-12-17
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; Sequence 71, Application US/10216163
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APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: US/10/218,765
CURRENT APPLICATION NUMBER: US/10/19,480
PRIOR APPLICATION NUMBER: 60/06313
PRIOR PILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-0-17
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR PILING DATE: 1997-10-38
PRIOR PILING DATE: 1997-10-38
PRIOR PILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/06913
PRIOR APPLICATION NUMBER: 60/06913
PRIOR PILING DATE: 1997-12-17
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PRIOR APPLICATION NUMBER: 60/06913
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                                                                                                                                                                              Query Match 74.7%; Score 287; DB 13; Length 521; Best Local Similarity 84.3%; Pred. No. 7.9e-87; Matches 323; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Baker, Kevin P.
APPLICANT: Benoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 ACGGATATTGACTTCTTCTGTGA 383
361 ACGGATATTGACTTCTTCTGCGA 420
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; Publication No. US20030187201A1
                                                           TYPE: DNA
GORGANISM: Homo Sapien
US-10-216-163-71
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SEQ ID NO 71
LENGTH: 521
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| 3-20<br>60/079294<br>3-25<br>60/079656<br>60/079728                | 8 4 4 4 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9                                                                                                                                        | 6-17<br>60/08990<br>60/08047<br>6-24<br>60/09055<br>60/09069<br>60/09069<br>60/09198<br>60/09198<br>60/09198<br>60/09530<br>60/09530<br>60/09531<br>60/09531<br>60/09531                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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| 1998-0<br>NUMBER:<br>1998-0<br>NUMBER:<br>1998-0                   | 1998<br>NUMBER<br>1998<br>NUMBER<br>NUMBER<br>1998<br>NUMBER<br>NUMBER<br>1998<br>1998<br>1998<br>NUMBER<br>NUMBER<br>NUMBER<br>NUMBER<br>NUMBER<br>NUMBER<br>NUMBER<br>NUMBER | NUMBER 11998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 (1998 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PRIOR APPLICATION NUMBER: 60/10137
PRIOR APPLICATION NUMBER: 60/101477
PRIOR PILING DATE: 1998-09-17
PRIOR PLING DATE: 1998-09-23
PRIOR PILING DATE: 1998-09-24
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SEQ ID NO 71
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84.3%; Pred. No. 7.9e-87;
iive 0; Mismatches 60;
                                                            FILE REFERENCATION NUMBER: US/10/219,063
CURRENT PELING DATE: 2002-08-13
PRIOR FULING DATE: 2002-08-13
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/063549
PRIOR PILING DATE: 1997-10-31
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PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1998-03-20
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TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3530P1C24
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Sequence 71, Application US/10219066
Publication No. US20030187203A1
GENERAL INFORMATION:
APPLICAMT: Basker, Kevin P.
APPLICAMT: Gerritsen, Mary
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Best Local Similarity 84.3
Matches 323; Conservative
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ORGANISM: Homo Sapien
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APPLICANT: Besnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddweki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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84.3%; Pred. No. 7.9e-87;
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                PRIOR FILING DATE: 1999-07-20
PRIOR PAPPLICATION NUMBER: 60/146598
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-08-28
PRIOR FILING DATE: 1999-08-03
PRIOR PILING DATE: 1999-08-03
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PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-11-09
PRIOR PILING DATE: 1999-11-09
PRIOR PILING DATE: 1999-11-09
PRIOR PAPLICATION NUMBER: 60/16445
PRIOR PILING DATE: 1999-12-07
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Best Local Similarity
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APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE SEPREMENT SPLICATION NUMBER: US/10/219,067
CURRENT PILING DATE: 2002-08-14
FRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-01-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/06387
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-12-17
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PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-26
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PRIOR FILING DATE: 1998-03-26
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Pred. No. 7.9e-87;
0; Mismatches 60;
                                                                                                                                                                                                                                                                                                        Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
                                                          Sequence 71, Application US/10219067
Publication No. US20030187204A1
GENERAL INFORMATION:
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Best Local Similarity 84.3%;
Matches 323; Conservative (
                                                                                                                                                                                       APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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US-10-219-067-71
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                              APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC27
CURRENT APPLICATION NUMBER: US/10/219,066
CURRENT FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR PRILING DATE: 1997-10-17
PRIOR PRILING DATE: 1997-10-17
PRIOR PRILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-12-17
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SEQ ID NO 71
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Pred. No. 7.9e-87;
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
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PRIOR PELING DATE: 1907-00-17
PRIOR APPLICATION NUMBER: 60/05913
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/063549
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/069913
PRIOR PILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/07934
PRIOR PILING DATE: 1998-03-20
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                                                                       181 AAGAAAGGCCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG 240
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158 ATTICICIGGCIAGIGCICAAGAATIAIAAIGCCCCGGACIGIAGAITCAITAACGIT 217
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84.3%; Pred. No. 7.9e-87;
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Publication No. US20030187206A1
GENERAL INFORMATION:
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Gerritsen, Mary
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
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APPLICANT: Watenabe, Colin L.
APPLICANT: Watenabe, Colin L.
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APPLICANT: WATENABE, B350PLTA BAD THANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: 06/06213
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06349
PRIOR FILING DATE: 1997-10-28
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                                                               CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 360
                                                                                                                            CCCAGGAACTIGGICAAGGAACAGCGIGIGIA IACCAGGAAGCIACCAAGGAAGIICCCACC
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Pred. No. 7.9e-87;
0; Mismatches 60; Indels
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                                                                                                                                                                                                              ACGGATATTGACTTCTTGTGA 383
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Publication No. US20030187205A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.7%;
84.3%;
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Best Local Similarity 84.3
Matches 323; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Sapien
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Gaps 0;

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APPLICANT: Desnoyers, Inc.
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Santh, Victoria
APPLICANT: Matanabe, Colin L.
APPLICANT: Wacd, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC49
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: 19350PLC49
FRIOR REPLICATION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 60/06313
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063973
PRIOR PLILNG DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/069873
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/078910
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                                                                                                    Length 521;
                                                                                                                                                         60; Indels
                                                                                                 Query Match 74.7%; Score 287; DB 13; Best Local Similarity 84.3%; Pred. No. 7.9e-87; Matches 323; Conservative 0; Mismatches 60;
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  ; TYPE: DNA
; ORGANISM: Homo Sapien
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APPLICANT: Goddwaff, Audrey
APPLICANT: Goddwaff, Audrey
APPLICANT: Goddwaff, Audrey
APPLICANT: Godwaff, Authoria
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
APPLICANT: Wood, Milliam I.
APPLICANT: WOOD ENGINE STORE OF 10/119, 480
PRIOR FILING DATE: 2002-04-09-17
PRIOR APPLICATION NUMBER: 60/06313
PRIOR APPLICATION NUMBER: 60/06387
PRIOR APPLICATION NUMBER: 60/06389
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06389
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06389
PRIOR FILING DATE: 1997-10-10-17
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/07928
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/07928
PRIOR PILING DATE: 1998-03-26
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ATGGCAAGAATATTGTTACTTTTCTCCCCGGGTCTTTGTGGCTGTATGTGCTGTAGGA 97
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Gerritsen, Mary
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US-10-219-480-71
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Best Local Similarity
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US-10-219-483-71
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US-10-219-480-71
US-10-219-480-71
Sequence 71, Application US/10219480
publication No. US2003018720941
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Generate, Mary
APPLICANT: Generate, Mary
APPLICANT: Gondard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
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APPLICANT: Stephan, Jean-Philippe
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PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
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                                                                                                                                                                                                                                                                                                                                                          Length 521;
                                                                                                                                                                                                                                                                                                                                                          Query Match

74.7%; Score 287; DB 13; Length 5
Best Local Similarity 84.3%; Pred. No. 7.9e-87;
Matches 323; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo Sapien
US-10-219-475-71
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APPLICANT: Desnoyers, Luc
APPLICANT: Gordate, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
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PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/664103
PRIOR APPLICATION NUMBER: 60/66813
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR PRILING DATE: 1998-03-26
PRIOR PLILNG DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 246
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Pred. No. 7.9e-87;
0; Mismatches 60;
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APPLICANT: Grimali, victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3530PLC29
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3530PLC29
CURRENT PAPLICATION NUMBER: U5/10/219,525
CURRENT PAPLICATION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 60/65287
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-13
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-12-37
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PRIOR FILING DATE: 1998-03-37
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84.3%; Pred. No. 7.9e-87;
live 0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGGATATICACTICITCTGTGA 383
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Matches 323; Conservative
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US-10-219-525-71
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CURRENT APPLICATION NUMBER: US/10/219,483
CURRENT FILING DATE: 2002-08-13
FRIOR PAPLICATION NUMBER: US/10/19,480
FRIOR PELING DATE: 2002-08-03
FRIOR PELING DATE: 1997-09-17
FRIOR PELING DATE: 1997-09-17
FRIOR PELING DATE: 1997-10-17
FRIOR PELING DATE: 1997-10-17
FRIOR PELING DATE: 1997-10-17
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FRIOR PELING DATE: 1997-10-31
FRIOR PELING DATE: 1997-10-31
FRIOR PELING DATE: 1997-10-17
FRIOR PELING DATE: 1997-10-17
FRIOR PELING DATE: 1998-10-20
FRIOR PELING DATE: 1998-03-20
FRIOR PELING DATE: 1998-03-25
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FRIOR FILING DATE: 1998-03-27
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FRIOR FILING DATE: 1998-03-27
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Publication No. US20030187211A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin F.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 84.3%;
Matches 323; Conservative
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ORGANISM: Homo Sapien
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                                                                                                                                                               ACGGATATTGACTTCTTCTGCGA 420
                                                                                                                                   ACGGATATTGACTTCTTCTGTGA 383
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CORGANISM: Homo Sapien
US-10-219-530-71
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APPLICANT: STEADAR, JELOZIA L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE SEPREMENT E: 2302-08-13
CURRENT APPLICATION NUMBER: US/10/219,526
CURRENT PILING DATE: 2002-04-09
PRIOR PILING DATE: 2002-04-09
PRIOR PLILNG DATE: 1997-09-17
PRIOR PLILNG DATE: 1997-09-17
PRIOR PLILNG DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06387
PRIOR PLILNG DATE: 1997-10-28
PRIOR PLILNG DATE: 1997-12-17
PRIOR PLILNG DATE: 1997-12-17
PRIOR PLILNG DATE: 1997-12-17
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PRIOR PLILNG DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/069873
PRIOR PLILNG DATE: 1997-12-17
PRIOR PLILNG DATE: 1998-03-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 287; DB 13;
Pred. No. 7.9e-87;
0; Mismatches 60;
                                                                                                                                                                                                               Desnoyers, Luc
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
                                                                                         ; Sequence 71, Application US/10219526; Publication No. US20030187212A1
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ORGANISM: Homo Sapien
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Best Local Similarity
Matches 323; Conserv
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APPLICANT:
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        Qy
        181 AAGAAAGGCCAGCAGATCTATGTTTACTCCAAGCTGGAAAACGGAAAACGGAGAGG
        240

        Db
        218 AAAAAGGCCAGCAGCATCTATGTGTACTCCAAAGCTGGTAAAGAAAATGGAGCTGGAGAA
        277

        Qy
        241 TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGGGAATTGTAGGTTATTTC
        300

        Db
        278 TTTTGGGCTGCAGTGTTTATGGTGACCAGGAGGCCACCAGGAGTGTGGTTATTTC
        310

        CCACCAACTTGGTGAAGAGCAGCAGCAGGAGCCACCAGGAGGTCGTAGGTTATTTC
        300

        Db
        331 CCCACCAACTTGGTGAAGAGCAGCAGGAGCCACCAGGAGGCCCCCACGAGAGATCCCAACC
        360

        Db
        338 CCCAGGAACTTGGTCAAGGAACAGGAGTGTAACCAGGAAGCTACCACGAAGGAATCCCACC
        397

        Qy
        361 ACGGATATTGACTTCTTCTTGGA
        383

        Db
        398 ACGGATATTGACTTCTTCTTGGA
        383

        CCACCACTTCTTCTTCTTCTTGGA
        30

        Bb
        398 ACGGATATTGACTTCTTCTTCTTGGA
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Search completed: December 30, 2003, 10:03:01 Job time : 316.339 secs

Sequence 3, Appli Sequence 55, Appl Sequence 55, Appl Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 48, Appl Sequence 105, App Sequence 105, App Sequence 48, Appl Sequence 4920, Appl Sequence 4920, Appl

Sequence Sequence

Sequence 3,

Sequence

us-10-019-455a-10.rni

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COUNTER:
ZIP: 10022
COMPUTER REALDABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
medium TYPE: 1 inch 1.45 mb storage diskette
medium TYPE: 1 or-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IRM PS/2

COMPUTER: IRM PS/2

COMPUTER: Wordperfect

CONTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/578,649

FILING DATE: 29-011y-1994

CLASSIFICATION DATA:

APPLICATION NUMBER: US PE 43 24 247.2

FILING DATE: 20-011y-1993

ATTORNEY/ACENT INFORMATION:

NAME: Andrew L. Tiajoloff

REGISTRATION INFORMATION:

TELEPAX: (212) 838-384

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 581 base pairs

TYPE: MUCHEN SEG ID NO: 4:

STRANDENNESS: Single
                                                                                                                                                                                                                                                                                                     APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Reighte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                      US-08-311-731A-132
US-09-252-991A-4920
US-09-252-991A-4922
                                     US-08-433-522A-55
US-09-135-166-55
US-08-92-046-55
US-08-416-870C-3
US-08-328-254-5
US-08-353-700-2
                                                                                                    PCT-US95-16216-2
US-08-961-527-48
US-08-687-080-105
                                                                                                                                                                      US-08-714-918-35
US-09-265-315-35
                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                    ; Sequence 4, Application US/08578649; Patent No. 5770366; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
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NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
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57, Appl
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1, Appli
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8, Appli
                                                                        December 30, 2003, 01:34:27 ; Search time 31.014 Seconds (without alignments) 5464.987 Million cell updates/sec
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Sequence 3, Ag
Sequence 35, P
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Sequence 14, P
Sequence 4, Ap
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Sequence 6
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Sequence 1
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                                                                                                                                                                                                                                                                                                                 Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
             GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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US-08-578-649-18

US-08-578-649-24

US-08-578-649-24

US-09-399-913-35

US-09-299-913-35

US-09-298-711-35

US-09-899-595-4

US-08-899-595-4

US-09-08-651-1

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                                                                                                                                                                                                569978 seqs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                  IDENTITY NUC Gapoxt 1.0
                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                     US-10-019-455A-10
384
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Match Length DB
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3565
2644
7218
5822
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111109
111110
11212
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                                                                                                                                     Perfect score:
                                                                                                                                                 Sequence:
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No.
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TATTTCCCCAGCAACTTGGTGAAGGAGCAGC 325
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Best Local Similarity 56.8%; Pred. No. 5e-
Matches 154; Conservative 0; Mismatches
                                                                                                                                                                                                 mat_peptide
112..432
                                                                                                                                       sig_peptide
40..111
                   TOPOLOGY: linear
MOLECULE TYPE: CDNA
FRATURE: NAME/KEY: CDS
LOCATION: 40..432
FRATURE: NAME/KEY: sig_pepti
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: New York
RY: USA
STRANDEDNESS:
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                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-578-649-1
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                                                                                                                           Gaps
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                                                                                  Score 66.2; DB 1; Length 581;
Pred. No. 6.2e-12;
0; Mismatches 143; Indels
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APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brighte Kaluza
TITLE OF INVENTION: MELANOWA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felie & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5 INCH 1.44 PD SCOLAGE GLASHELLE COMPUTER: BM PS/2
OPERATING SYSTEM: PC-DOS
SOCTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-011y-1994
CLASSIFICATION DATA:
APPLICATION DATA:
TELEPHONE: 20-011y-193
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFP/ALT
TELECOMMUNICATION NUMBER: BOER 1035-PFP/ALT
TELEPHONE: (212) 888-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: LASP Dase pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 GGAGATCCCAACCACGGATATTGACTTCTTG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               463 TGATATGAAGACCGATCAATGGGATTTCTACTG 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08578649
Patent No. 5770366
                                                                                    Query Match 17.2%;
Best Local Similarity 54.4%;
Matches 181; Conservative
          mat_peptide
179..499
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          ; NAME/KEY:
; LOCATION:
US-08-578-649-4
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US-08-578-649-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 crcifichédeaaddcháceifichedaharhárhardeadhreidecrecredec 342
                                                                                                                 58 GGTGTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGCGGATGAGGAGTGTCTAT
                                                                                                                                                                                                                                                                                                                                                        178 GTCAAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGA
                                                                Gaps
                                                             6
Length 459;
                                    Pred. No. 5e-10;
0; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New YOLK
COUNTRY: USA
ZIP: New YOLK
COUNTRY: USA
ZIP: 10.022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2.
COMPUTER: IBM PS/2.
COMPUTER: DA PS. 10.0
COMPUTER: DA PELICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
FILING DATE: 20-July-1994
ATORNEY AGENT INFORMATION:
NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BER 1575
REFERENCE/DOCKET NUMBER: BER 1575
REFERENCE/DOCKET NUMBER: BER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brighter Kaluza
; TITLE OF INVENTION: MELANOWA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
      DB 1;
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6
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Sequence 24, Application US/08578649

Sequence 24, Application US/08578649

Patent No. 5770366

GENERAL INFORMATION:

APPLICANT: Wisher Baigite Kaluza

APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner

APPLICANT: Reinhard Buttner

APPLICANT: Weighte Kaluza

TTTLE OF INVENTION: MELANOMA-INHIBITING PROTEIN

NUMBER OF SEQUENCES: 24

CORRESPONDENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

COUNTRY: USA

ITY: New York

COUNTRY: USA

ITY: New York

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette

COMPUTER: IBM PS/2.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRICA APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
MAME/KEY: misc RNA
LOCATION: join(1..29, 277..305)
OTHER INFORMATION: /function= "Primer"
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                                                                                                                                                                                                                                                               LENGTH: 305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 cacccharcrecardecreredecerreadacracaredecedacideceariecea 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 330;
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14.4%; Score 55.2; DB 1; Length 3:
Best Local Similarity 55.5%; Pred. No. 1.8e-08;
Matches 152; Conservative 0; Mismatches 113; Indels
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COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
^MPUTER: PEM PS/2
^MPUTER: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brightte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COCATION: 4 .. 6

LOCATION: 4 .. 6

OTHER INFORMATION: /function= "Startcodon Met"
US-08-578-649-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 GGTTATTTCCCCAGCAACTTGGTGAAGGAGCAGC 325
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APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASCIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
(212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                             TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                     LENGTH: 330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                 mat peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc RNA
                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-08-578-649-8
                                                                                                                                                                                                                                                                                                                   FEATURE
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NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31,575
REPERENCE/DOCKET NUBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-384
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
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1378..1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
1378..1504
                                                                                                                                                                                                                                                                                                                          nucleic acid
EDNESS: single
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1586..1719
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2804..2914
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3232..3252
                                                                                                                                                                                                                                                                                                                             TYPE: nucleic
STRANDEDNESS:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY:
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FEATURE:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-578-649-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 ciritertecarigicargicetreagaciraciaegecececariceragacea 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: one-of(194, 369, 527)

OTHER INFORMATION: /note= "N in positions 194, 369

OTHER INFORMATION: and 527 denotes an indefinite number and sequence OTHER INFORMATION: of nucleotides "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.3%; Score 35.6; DB 1; Length 596; 60.2%; Pred. No. 0.058; tive 0; Mismatches 39; Indels
                                                                                                                                                                                                                                            join(40..111, 40..166, 214..347, 393..503, 549
..569)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Neinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
TITLE OF INVENTION: MELANOWA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 TCAAGAAAGGGCAGATCTATGTTTACTCCAAGCTG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 TTCACCGGGCCAAGTGGTGTATGTCTTCTCCAAGCTG 314
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
                  REGISTRATION NUMBER: 31,575
REGISTRATION NUMBER: 31,575
REPERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 888-9804
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 base pairs
TERNOTH: 596 base pairs
TYRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08578649
Patent No. 5770366
                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.29
Matches 59; Conservative
           ATTORNEY/AGENT INFORMATION
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549..569
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LOCATION:
FEATURE:
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LOCATION:
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OCREATION STREET, PC-DOS
SOFTWARE, MOSTGREECT
CURRENT APPLICATION DAYS.
PRICE PROJECTION 133-1394

APPLICATION NUMBER: De 143 42 47.2

TREADMOND DATE: 20-011y-1933

APPLICATION NUMBER: DE 15 142 47.2

PRICE PROJECTION: 133-1364

APPLICATION NUMBER: DE 15 142 47.2

TELEPHONE: (12) 688-920

TELEPHONE: (12) 688-920

TELEPHONE: (12) 688-920

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2000 CCAGGCAACAGGTCAGCAGACCTCAGGAGAGAGA-GAGAGCTGTTCCTGCCTCCCCAGGC 2058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 GATTACAATGCCCCAGACTGTAGGTTCATCGATGTCAAGAAAGGGCAGCAGATCTATGTT 204
247 GCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTCCCCAGC 306
                                                                                                   307 AACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACCACGAT 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22313-0299
ZIP: 22313-0299
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.0%; Score 34.4; DB 1;
2.9%; Pred. No. 0.43;
                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICALL...
FILING DATE:
CLASSIFICATION: 435
PRICASIFICATION DATA:
APPLICATION NUMBER: US/07/935,313
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORREY/ASENT INFORMATION:
NAME: BENT, 5tephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30472/114 IP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300

TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                            2119 GTACATTCCATC 2130
                                                                                                                                                                                                           367 ATTGACTTCTTC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; ; IMMEDIATE SOURCE: ; CLONE: pTZgpt-F1s US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-08-232-463-14/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 GGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAGTTTTGG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 GGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGATTTTGG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 GCTGGCAGTGTTTATGGTGACCACCAGGATGAGATTGTAGGTTATTTCCCCAGC 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35, Application US/09298731
Sequence 35, Application US/09298731
Sequence 35, Application US/09298731
Patent No. 6369197
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMY: RENNETH HODES, MARIA BETTY, HUAI-PING LING, AND FRANK AN TITLE OF INVENTION: POOTASSIUM CHANNEL INTERACTORS AND USES THEREFOR FILE REFERENCE: MNI-070 SSIUM CHANNEL INTERACTORS AND USES THEREFOR FILE REFERENCE: MNI-070 SSIUM NUMBER: US/09/298,731
CURRENT APPLICATION NUMBER: 1999-04-23
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 35
LENGTH: 2644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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9.0%; Score 34.4; DB 4; Length 2644;
Best Local Similarity 52.1%; Pred. No. 0.28;
Matches 100; Conservative 0; Mismatches 91; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2644;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
9.0%; Score 34.4; DB 4;
Best Local Similarity 52.1%; Pred. No. 0.28;
Matches 100; Conservative 0; Mismatches 91;
               EARLIER APPLICATION NUMBER: USSN 60/110,277
EARLIER FILING DATE: 1998-11-30
EARLIER FILING DATE: 1998-11-25
EARLIER FILING DATE: 1998-11-25
EARLIER FILING DATE: 1998-11-25
EARLIER FILING DATE: 1998-11-20
EARLIER FILING DATE: 1999-04-23
EARLIER FILING DATE: 1999-04-23
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
SERIER FILING DATE: 1999-07-09
SOFTWARE: PATCHING NATE: 2.0
SOFTWARE: PATCHING NATE: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; JOCATION: (49)..(816)
US-0:-298-731-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (49)..(816)
US-09-399-913-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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168 GITCATCGATGICAAGAAAGGGCAGCAGATCTATGITIACTCCAAGCTGGTAACAGAAAA 227
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                                                                                                                                                                                                               1886 GGA 1884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: YES
ORIGINAL SOURCE:
                                                                                                                                                                             GGA 350
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                                                                                                                                                                                                                                                                      RESULT 11
US-08-899-595-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                             348
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                                                                                              265 GACCACCAGGATGAGAATTGTAGGTTATTTCCCCAGCAACTTGGTGAAGGAGCAG 324
205 TACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAGTTTTGGGCTGGCAGTGTTTATGGT 264
                                                                                                                                                                                                                                                         Sequence 4, Application US/08899595

Patent No. 6111072
GENERAL INFORMATION:
APPLICANT: Narumiya, Shuh
APPLICANT: Narumiya, Shuh
APPLICANT: Narumiya, Shuh
APPLICANT: Narumiya, Shuh
APPLICANT: Narumiya, Shuh
APPLICANT: Narumiya, No. 6111072uaki
TITLE OF INVENTION: BROODING SAME
NUMBER OF SEQUENCES: 14
CORRESSEE: Foley & Lardner
APPRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: DO.
STATE: DO.
COUNTRY: USA
ZITP: 1007-5109
COUNTRY: USA
ZITP: PREADALE FORM:
MEDIUM TYPE: Floppy disk
COUNTRY: BM PC COMPAINED
COMPUTER: IBM PC COMPAINED
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,595
FILING DATE: 24-UUL-1997
CILASSIFICATION NUMBER: US/08/899,595
FILING DATE: 24-UUL-1997
CILASSIFICATION NUMBER: US/08/899,595
FILING DATE: 25-UG-196
FILING DATE: 25-UG-196
FILING DATE: 25-UG-196
FILING DATE: 25-UKR-1997
ATTORNEY/AGRY INFORMATION:
NAME: Stephen A. Bent
TELEPONE: (202)672-5399
TELEFRAX: QAA174
TELEPONE: QAA174
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                                                                                                                                                                        325 CGTGTATACCAGGAGGCCACCAAGGAGATCCCAACCAC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89; Conservative
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Best Local Similarity
Matches 89; Conserv
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                   RESULT 10
US-08-899-595-4/c
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2066 GTACCTCCAGGTAAAGAAGGGGGTGAGGAGTGCAAACGCCCCCAGGCAAAGGAGGTGGA 2007
                                                                          228 CGGAGCTGGAGGTTTTGGGCTGGCAGTGTTATGGTGACCACCAGGATGAGATGGGAAT 287
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8.5%; Score 32.6; DB 3; Length 5822;
Best Local Similarity 48.6%; Pred. No. 1.5;
Matches 89; Conservative 0; Mismatches 94; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Narumiya, Shuh
APPLICANT: Takahashi, No. 6111072uaki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
TITLE OF INVENTION: ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IMN PC Compatible

COMPUTER: IMN PC Compatible

COMPUTER: DATENIN PC-DOS/MS-DOS

SOFTWARE: PATENIN PC-DOS/MS-DOS

SOFTWARE: PATENIN DATA:

APPLICATION NUMBER: US/08/899,595

FILING DATE: 24-JUL-1997

CLASSIFFCATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 9-20170

FILING DATE: 26-AUG-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 9-90170

FILING DATE: 25-AUG-1997

ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Stephen A. Bent
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 0494
TELECOMMUNICATION INFORMATION:
TELEFONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5822 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08899595
Patent No. 6111072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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                                                                                                                                                                           252 CAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTCCCCAGCAACTT
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8.3%; Score 31.8; DB 3; Length 683;
Best Local Similarity 59.3%; Pred. No. 1.1;
Matches 54; Conservative 0; Mismatches 37; Indels
                                                                                     Length 654;
                                                                                                                                Indels
                                                                                   Score 31.8; DB 4;
Pred. No. 1;
0; Mismatches 37;
                   OTHER INFORMATION: trypsin-like serine proteases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOSS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         312 GGTGAAGGAGCAGCGTGTATACCAGGAGGCC 342
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APPLICATION NUMBER: GB9712088.5
FILING DATE: 10-UNRE-1997
APPLICATION NUMBER: EP 97308295.1
FILING DATE: 17-OCT-1997
APPLICATION NUMBER: GB 9803650.2
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F.
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09088651;
Patent No. 6165771
GENERAL INFORMATION:
APPLICANT: GLINEENSARD, HELEN E.
APPLICANT: CLINEENSARD, HELEN E.
APPLICANT: SOUTHAN, CHRISTOPHER D.
TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/088,651
FILING DATE: JUNE 1, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GH30358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                     8.3%;
ilarity 59.3%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 946169
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 683 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
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                                                                                                                Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                             US-09-280-116-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-088-651-3
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                                                                                          Query Match
  FEATURE:
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APPLICANT: WEI, Ming-Hui et al
APPLICANT: WEI, Ming-Hui et al
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFRENENCE: CLO01018
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT APPLICATION NUMBER: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOUTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 202001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183409 CTAGAACTCAGGAGAGAGAGCTAAGGCAGAGACGTAGGTCCCGTGAATCATTAGCAAGTCTGT 183468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183469 GAAAGTCAAAGCCATGGGTATGGATGAACTATTCCAGGAAAAGAAAAGAAACAGAAATGAG 183528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 57, Application US/09280116A
Sequence 57, Application US/09280116A
Parent No. 6331427
GENERAL INFORMATION:
APPLICANT: RObison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57
LERGTH: 654
3817 GGAGGAGGAGGAGGAGGAGGAGGAGGAGTGGTACTÁTCCCCAGGAGCÁGGTGGTGGT 3876
                                                                                                                                                                                                      3877 GGAATAATAGTGCCAGAGTCACCAGGTAAAGGAGGGGCAGGAGGAACAGGAGGACTA 3936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 CTATTICTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATG 178
                                                                          CGGAGCTGGAGAGTTTTGGGCTGGCAGTGTTATGGTGACCACCAGGATGAGATGGGAAT 287
                                                                                                                                                                288 TGTAGGTTATTTCCCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 TCAAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.4%; Score 32.2; DB 4; Length 202001;
49.7%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183529 AGTCCAGGAATCCCAATGTTGAGGGCCAAATAAAGGAAGAAGATTG 183573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 AGTTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGG 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature; LOCATION: (1)...(202001); OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09734674
Patent No. 6498022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 82; Conserva
                                                                                                                                                                                                                                                                                                          3937 GGA 3939
                                                                                                                                                                                                                                                               348 GGA 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-280-116-57/c
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252 CAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTCCCCAGCAACTT 311
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369 CGGTGTCTTTGCTGTAGAGCAGGTTGCACTTGGGTGTGGATGATGGGCACAGCGAGTT 310
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                                                                                                                                                                                                                                                                   RESULT 15
US-09-023-942A-30/C
US-09-023-942A-30/C
US-09-023-942A-30/C
Sequence 30, Application US/09023942A
Fetent No. 6479274
GENERAL INFORMATION:
APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
APPLICANT: (US only) ANTALIS Toni Marie and HOOPER JOHN CONTESPONDENCES: 30
CORRESPONDENCE ADDRESS: 30
CORRESPONDENCE ADDRESS: 30
CORPTER: VOR GARDEN CITY PLAZA
STRATE: NEW YORK
COUNTY: USA
COUPTINE NEADABLE FORM:
MEDIUM TYDE: Floppy disk
COMPTINE READABLE FORM:
MEDIUM TYDE: Floppy disk
COMPTINE NEADABLE FORM:
MEDIUM TYDE: Floppy disk
COMPTINE PALICATION DATA:
APPLICATION NUMBER: US/09/023,942A
FILING DATE: 13-FEB-1998
CLASSIFICATION NUMBER: POSIO1/97
FILING DATE: 13-FEB-1998
FILING DATE: 13-FEB-1998
FILING DATE: 13-FEB-1998
FILING DATE: 13-FEB-1998
APPLICATION NUMBER: POSIO1/97
FILING DATE: 13-FEB-1998
ATTORNEY ADDREST: 18-FEB-1998
ATTORNEY APPLICATION DATA:
APPLICATION NUMBER: POSIO1/97
FILING DATE: 13-FEB-1998
ATTORNEY APPLICATION NUMBER: 11168
FILING DATE: 13-FEB-1998
ATTORNEY APPLICATION NUMBER: 113-FEB-1998
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8.3%; Score 31.8; DB 4; Length 980;
Best Local Similarity 59.3%; Pred. No. 1.2;
Matches 54; Conservative 0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 GGTGAAGGAGCAGCGTGTATACCAGGAGGCC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465 rerigeaddarecederreegedadderc 435
                                                                                  312 GGTGAAGGAGCAGCGTGTATACCAGGAGGCC 342
                                                                                                                                                 309 rciccadatcacacricadadadatc 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: December 30, 2003, 06:10:40 Job time : 33.014 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 980 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-023-942A-30
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
               Copyright
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OM protein - protein search, using sw model

; Search time 13.2661 Seconds (without alignments) 927.898 Million cell updates/sec December 29, 2003, 16:03:18 on:

Run

US-10-019-455A-12

676 1 MARILILLLGGLVVLCAGHG.....RVYQEATKEIPTTDIDFFCE 128 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues

283308 Total number of hits satisfying chosen parameters: Searched:

seq length: 0 seq length: 200000000 0B 0B Minimum Maximum Maximum Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| SOMMARIES | Description    | melanoma-derived | transforming prote | ğ      | O      | myosin-IA - Acanth | hypothetical prote | cell division cor | protein-glutamine | hypothetical prote | _      | _      | _      | _      | _      |        | _      |        | copper ABC transpo | ATP-dependent RNA | receptor kinase ho | ribunucleotide red | mixed-lineage prot | yceG protein precu | >-     | dTMP kinase (EC 2 | VHS domain contain |        |        |   |
|-----------|----------------|------------------|--------------------|--------|--------|--------------------|--------------------|-------------------|-------------------|--------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|-------------------|--------------------|--------|--------|---|
| AND S     | ID             | I38019           | TVMSVV             | TVHUVV | 151940 | T32734             | G86746             | RGBYC5            | <b>S66662</b>     | T18921             | C64427 | S07164 | T31504 | T04200 | C81920 | T21356 | F84138 | T48525 | E81183             | G96995            | T06793             | T12925             | A53800             | F64853             | C90813 | G85672            | T39655             | A47299 | A84055 | 4 |
|           | DB             | 1 8              | Н                  | Н      | 7      | 7                  | ~                  | Н                 | 7                 | 7                  | ~      |        |        |        |        | ~      | ~      | ~      | N                  | ~                 |                    |                    |                    |                    |        |                   | C\$                | Н      | ~      |   |
|           | Length         | 131              | 844                | 839    | 878    | 1215               | 722                | 1589              | 695               | 176                | 259    | 406    | 1097   | 332    | 344    | 994    | 93     | 308    | 344                | 585               | 636                | 1084               | 847                | 340                | 340    | 340               | 373                | 946    | 333    |   |
| d         | Query<br>Match | 41.1             | 13.5               | 13.2   | 12.5   | 12.1               | 11.7               | 11.6              | 11.4              | 11.3               | 11.2   | 11.1   | 11.0   | 10.9   | 10.8   | 10.8   | 10.7   | 10.7   | 10.7               | 10.7              | 10.7               | 10.7               | 10.6               | 10.5               | 10.5   | 10.5              | •                  | 10.5   | 10.4   |   |
|           | Score          | 277.5            | 91.5               | 89.5   | 84.5   | 81.5               | 79                 | 78.5              | 77                | 76.5               | 16     | 75     | 74.5   | 74     | 73     | 73     | 72.5   | 72     | 72                 | 72                | 72                 | 72                 | 71.5               | 71                 | 71     | 71                | 71                 | 71     | 70.5   |   |
|           | Result<br>No.  |                  | 10                 | m      | 4      | ഹ                  | φ                  | 7                 | Φ                 | σ                  | 10     | 11     | 12     | 13     | 14     | 15     | 16     | 17     | 18                 | 19                | 20                 | 21                 | 22                 | 23                 | 24     | 25                | 26                 | 27     | 28     |   |

| protein-tyrosine k | hypothetical proce | hypothetical prote | probable chromomet | 3',5'-cyclic-GMP p | cell division cycl | alliin lyase (EC 4 | connexin 45 - mous | S-receptor kinase | ribonucleoside-dip | hypothetical prote | hypothetical prote | probable peroxisom | probable signal tr | hypothetical prote | Snf2 family protei |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| \$24553            | T02310             | T29580             | G96719             | S13030             | F90113             | S29302             | \$23589            | T02693            | D65047             | B91071             | E85915             | T38696             | S67383             | T17257             | D95177             |
| ٦                  | N                  | N                  | ~                  | 2                  | 7                  | 8                  | ~                  | ~                 | 7                  | ~                  | ~                  | N                  | N                  | 0                  | 7                  |
| 506                | 718                | 780                | 839                | 859                | 295                | 486                | 396                | 413               | 714                | 714                | 714                | 288                | 670                | 816                | 1032               |
| 10.4               | 10.4               | 10.4               | 10.4               | 10.4               | 10.4               | 10.4               | 10.3               | 10.3              | 10.3               | 10.3               | 10.3               | 10.2               | 10.2               | 10.2               | 10.2               |
| 70.5               | 70.5               | 70.5               | 70.5               | 70.5               | 70                 | 70                 | 69.5               | 69.5              | 69.5               | 69.5               | 69.5               | 69                 | 69                 | 69                 | 69                 |
| 30                 | 31                 | 32                 | 33                 | 3.4                | 35                 | 36                 | 37                 | 38                | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

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|-------|-----|---------------|
|       |     | growth        |
| ULT 1 | 019 | anoma-derived |

atory protein MIA - human

Useracionar Jerukun Leguratory protein min - numman.
C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 04-Mar-2000
C;Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 04-Mar-2000
C;Accession: 138019; AKC; Apfel, R.; Behl, C.; Hessdoerfer, B.; Schmitt, A.; Jac
Cancer Res. 54, S695-5701, 1994
A;Title: Cloning of a novel malignant melanoma-derived growth-regulatory protein, MIA.
A;Reference number: 138019; MUID:95007612; PMID:7923218
A;Accession: 138019
A;Accession: 138019
A;Accession: type: mRNA
A;Residues: 1-131 cREs>
A;Gross-references: EMBL:X75450; NID:9438057; PIDN:CAA53203.1; PID:9438058
C;Genetics:
A;Genetics:

9 Gaps 13; DB 2; Length 131; Indels th 41.1%; Score 277.5; DB 2; Similarity 43.4%; Pred. No. 6.6e-21; 59; Conservative 29; Mismatches 35; Local Similarity Query Match Best Loca Matches

54 1 MARILILLIGGLVVLC---AGHGVF---MDKLSSKKLCADEECVYTISLARAQEDYNAPD ò g CRFIDVKKGQQIYVYSKLVTENGAGE-FWAGSVYGDHQDEMGI-VGYFPSNLVKEQRVYQ 112 22 ò

59 CRFLTIHRGQVVYVFSKL---KGRGRLFWGGSVQGDYYGDIAARLGXFPSSIVRBDQTLK 115 g

EATKEIPTTDIDFFCE 128 116 PGKVDVKTDKWDFYCQ 131 113 ð g

transforming protein vav - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: Mus-1994 #sequence revision 16-Feb-1996 #text\_change 18-Jun-1999 C;Accession: A61187, A39576, Z36941; S23669 R;Coppola, J.; Bryant, S.; Koda, T.; Conway, D.; Barbacid, M. Cell Growth Differ. 2, 95-105, 1991 A;Title: Mechanism of activation of the vav protooncogene. A;Reference number: A61187; MulD:91299578; PMID:2069873

ď A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-844 <COP. Sr;Retzav, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, Mol. Cell. Biol. 11, 1912-1920, 1991

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A,Crose-references: GDB:127112; OMIM:164875
A,Grose-references: GDB:127112; OMIM:164875
A,Grose-references: GDB:127112; OMIM:164875
A,Grose-references: GDB:13.3-19913.3
C,Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding C,Superfamily: vav transforming protein; zinc finger
F;126-170/Region: acidic
F;188-452/Domain: CDC24 homology <CD24>
F;188-452/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F;525-542/Region: zinc finger CCC motif
F;547-560/Region: zinc finger CCC motif
F;547-560/Region: SH3 homology <SH3A>
F;589-648/Domain: SH3 homology <SH3A>
F;664-756/Domain: SH3 homology <SH3B>
F;664-756/Domain: SH3 homology <SH3B>
F;433/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
                          A;Cross-references: EMBL:X16316
R;Adama, J.M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.
Gnogene 7, 611-618, 1992
A;Tile: The hematopoietically expressed vav proto-oncogene shares homology with the dayritle: The hematopoietically expressed vav proto-oncogene shares homology with the dayrence number: $23669; MUID:92228488; PMID:1565462
A;Contents: annotation
A;Note: in the sequence from mouse the authors find three additional nucleotides that occurred in the published human sequences
C;Comment: In comparing these sequences with the mouse (see PIR:TVMSVV), there appear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 ARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.2%; Score 89.5; DE 32.9%; Pred. No. 0.6; ative 14; Mismatches
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                     A; Residues: 62-839 < KAT2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB: VAV1; VAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: VAV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
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Best Local &
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A,Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene ad A,Reference number: A39576; MUID:91172176; PMID:2005887
A,Accession: A39576
A,Accession: A39576
A,Accession: A39576
A,Accession: A39576
A,Residues: 1.28, 'E',30-32 «KAT
A,Residues: 1.28, 'E',30-32 «KAT
A,Residues: 1.28, 'E',30-32 «KAT
A,Residues: 1.28, 'E',30-32 «KAT
A,Redames, J.M.
Submitted to the EMBL Data Library, January 1992
A,Accession: S36941
A,Accession: S36941
A,Residues: 1.23, 'DLMWPWRVLKHLLDGELVW', 346-347, 'QDAT', 352, 'K', 354,'N', 355-453,'R', 45
A,Cossion: S36941
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A,Cossion: S36941
A,Reference number: S2669, MUID:92228488; PMID:156462
A,Cossion: S36941
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Liansforming protein vav - human (fragments)

LyAlternate names: finger protein vav

CiSpecies: Homo sapiens (man)

CiDate: 31-Mar-1991 #sequence_revision 03-May-1996 #text_change 18-Jun-1999

CiAccession: 839576; S05382

Rikatzav, S.; Cleveland, Jl.; Heslop, H.E.; Pulido, D.

Mol. Cell. Biol. 11, 1912-1920, 1991 Helix-loop-helix domain of the vav proto-oncogene active number: A39576; MUID:91172176; PMID:2005887

A;Mccession: B39576

A;Mccession: B39576

A;Mccession: Clerk amino-terminal helix-loop-helix domain of the vav proto-oncogene active number: A39576; MUID:91172176; PMID:2005887

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A;Note: the authors translated the codon CAA for residue 6 as Glu, CAG for residue 13 as R;Katzav, S.; Martin-Zanca, D.; Barbacid, M.
EMBO (8, 2283-2290, 1989
A;Title: vav, a novel human oncogene derived from a locus ubiquitously expressed in hem: A;Reference number: S05382; MUID:90005432; PMID:2477241
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F;670-761/Domain: SH2 homology <SH2>
F;788-836/Domain: SH3 homology <SH3B>
F;439/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          834
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Best Local Similarity 32.9%; Pred. No. 0.38;
Matches 23; Conservative 14; Mismatches 20; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    835 YVEED--YSE 842
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A; Molecule type: mRNA
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20; DB 1;

Length 839; Indels

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A, Map position: 9434-9434
C; Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding
F;198-462/Domain: CDC24 homology <CD24>
F;524-572/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F;673-764/Domain: SH2 homology <SH2>
F;823-872/Domain: SH3 homology <SH3>
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                                            C;Accession: 151940
R;Henske, B.P.; Short, M.P.; Jozwiak, S.; Bovey, C.M.; Ramlakhan, S.; Haines, J.L.;
Ann. Hum. Genet. 59, 25-37, 1995
A;Title: Identification of VAV2 on 9q34 and its exclusion as the tuberous sclerosis A;Reference number: 151940; MUID:95283235; PMID:7762982
A;Reference number: 151940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 VYT---ISLARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEM 94
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                              A,Cross-references: GB:S76992; NID:g913345; PIDN:AAB34377.1; PID:g913346
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-878 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:370880; OMIM:600428
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protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - red sea bream N;Alternate names: transglutaminase (Species et chrysphrys major (red sea bream) C;Species: Chryspophrys major (red sea bream) C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999 C;Accession: S6662 K;Nanazawa, Y.; Nagase, K.; Motoki, M.; Matsui, H. Bur. J. Blochem. 232, 411-419, 1995 A;Title: Tissue-type transglutaminase from red sea bream (Pagrus major). Sequence anal; A;Reference number: S66662; MUID: 96035874; PMID: 7556189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Curr. Genet. 10, 879-885, 1986
A,Title: The CDC25 "Start" gene of Saccharomyces cerevisiae: sequencing of the active A,Reference number: S43051; MUID:88194639; PMID:3329037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: positive control of level of cellular cAMP at the stage at which the ce C; Superfamily: budding yeast CDC25; CDC25-type guanine nucleotide exchange activator ha C; Reywords: cell cycle control; transmembrane protein
F;65-123/Domain: SH3 homology <SH3>
F;1301-1542/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Molecule type: DNA
A, Residues: 1-1589 - PAU>
A, Residues: 1-1589 - PAU>
A, Cross-references: ENEL:U17247; NID:g577216; PIDN:AAB67360.1; PID:g577222; GSPDB:GN00
R, Cross-references: ENEL:U17247; NID:g577216; PIDN:AAB67360.1; PID:g577222; GSPDB:GN00
R, Cross-references: ENEL:U17247; NID:g577216; PIDN:AAB67360.1; PID:g577222; GSPDB:GN00
R, Cross-reference in a Sequence analysis of the CDC25 gene which contra A; Reference number: A23444; MUID:86220116; PMID:3011405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: A23444
A;Motecule type: DNA
A;Residues: 1-496,'Y', 498-953,'LSVIMNLSR',964-1589 <CAM>
A;Residues: EMBL:X03579; NID:g3483; PIDN:CAA27259.1; PID:g3484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Indels 11;
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11.6%; Score 78.5; DE
Best Local Similarity 27.0%; Pred. No. 16;
Matches 24; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 FWAGSVYGDHQDEMGIVGYFPSNLVKEQR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 WWDGLVIDDSNGKVN-RGWFPQNFGRPLR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: SGD:CDC25; CTN1; MIPS:YLR310c
A;Cross-references: SGD:S0004301; MIPS:YLR310c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: X03579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S43051
A; Molecule type: DNA
A; Residues: 877-1589 < DAN>
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myosin-17
myosin-18 - Acanthamoeba castellanii
Cispecies: Acanthamoeba castellanii
Cispecies: Acanthamoeba castellanii
Cispecies: Acanthamoeba castellanii
Cispecies: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 08-Sep-2000
CiAccession: T32734
Ribec, W.L.; Ostap, E.M.; Zot, H.G.; Pollard, T.D.
submitted to the EMBL Data Library, August 1998
A;Pescription: Hydrodynamic and ligand binding properties of Acanthamoeba myosin-IA GPA/
A;Reference number: Z21216
A;Accession: T32734
A;Accession: T32734
A;Accession: T32734
A;Rolecule type: DNA
A;Residues: 1-1215 < LEE>
A;Residues: 1-1215 < LEE>
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A;Re
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C;Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homolo
F;14-674/Domain: myosin motor domain homology <MMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 GLVVLCAGHGVFMDKLSSKKLCADEEC-VYTISLARAQEDYNAPDCRFIDVKKGQQIYVY 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 12.1%; Score 81.5; DB 2; Length 1215; 1 Similarity 30.0%; Pred. No. 5.9; 21; Conservative 13; Mismatches 23; Indels 13.
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11.7%; Score 79; DB 2; Length 722;
Best Local Similarity 29.0%; Pred. No. 5.9;
Matches 31; Conservative 17; Mismatches 53; Indels
          | :|:||| | :|: : GRIGWFPSTYVEEEGI 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ||:| |::
GVFPANYVED 1214
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Best Local Similarity
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                                                      862
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A;Gene: nrdE
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A;Residues: 1-406 <ROUS
A;Cross-references: EMBL;X05005; NID:gl1525; PID:gl1526
A;Cross-references: EMBL;X05005; NID:gl1525; PID:gl1526
A;Cross-references: EMBL;X05005; NID:gl1525; PID:gl1526
B;Agxporimental gource: strain 2, 753
R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielm Nucleic Acids Res. 21, 3537-3544, 1993
Nucleic Acids Res. 21, 3537-3544, 1993
A;Fitle: Complete sequence of Euglena gracilis chloroplast DNA.
A;Fitle: Complete sequence of Euglena gracilis chloroplast DNA.
A;Reference number: S34862; MuID:9347989; PNID:8346031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: chloroplast Euglena gracilis
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
C;Accession: S07164; S34923; S34556
K;Roux, B.; Stutz, E.
Curr. Genet: 9, 221-227, 1985
A;Title: The chloroplast genome of Euglena gracilis: the mosaic structure of a DNA seg
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C;Superfamily: Euglena gracilis chloroplast hypothetical protein 406 (s16S rRNA 3' reg
C;Keywords: chloroplast
A;Molecule type: DNA
A;Residues: 1-259 <BUL>
A;Cross-references: GB:U67544; GB:L77117; NID:g1591671; PIDN:AAB99024.1; PID:g1591678;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X70810; NID:9415327; PIDN:CAA50139.1; PID:9415795
A;Experimental source: strain Pringsheim Z
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GQQIYVYSKLVTENGAGEF-----WAGSVYGDHQDEMGIVGYFPSNLVKE--QRVYQ 112
                                                                                                                                                                                                                                                                                                                                                                                163 VIAVADGIDMIKGRSRIPICKKCYDIHSVSAASIER------VEIKEGDEKPIQ 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 RVVIFLICLTMVLCAGGGFFSCKRHSNK-------KRSKASYTPP-----VPD 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 NYAIF------NDLGKYKAKVPVFEWQNA----HAHSLGIMP-LPPNLVNEMSSEEIK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                        14 VLCAGHGVFMDKLSSK----KLCADEECVYTISLARAQEDYNAPDCRFIDVKKGQQIYVY 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein 406 (s16S rRNA 3' region) - Buglena gracilis chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Y116ABC.36 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31504
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                                                                                                                                                                                                                                                                    18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 SKLVTENGAGEFWAGSVYGDHQDEMGIVGYFP--SNLVKEQRVYQEAT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Status: nucleic acid sequence not shown; translation not shown
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Pred. No. 8;
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                                                                                                                                                                                                        Length 259;
                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                45;
                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                     11.2%; Score 76; DB 2 ilarity 25.0%; Pred. No. 3.9; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 26.0%;
Matches 33; Conservative 14
                                                                                                                                             A; Map position: FOR950420-951199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 EATKEIP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 EAILEVP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-406 < HAL>
                                                                                                                                                                                                                                         Local Similarity
nes 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: S07164
A;Molecule type: DNA
                                                                                                                                                                                                                  Query Match
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T31504
                                                                                                                                                                                                                                                Best Loca
Matches
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R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, P. Bilt, C.J.; White, O.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; reich, C.I.; Overbeek, R.J.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; reich, C.I.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID: 96337999; PMID: 8688087

A;Accession: C64427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T18921

Typothetical protein C04G2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18921
R;Hembry, C.
Submitted to the EMBL Data Library, April 1996
A;Reference number: Z19045
A;Reference number: Z19045
A;Reference number: Z19045
A;Reference number: Z19045
A;Reference number: Z19045
A;Ccession: T18921
A;Ccession: T18921
A;Ccession: T18921
A;Ccoss-references: EMBL:Z70718; PIDN:CAA94673.1; GSPDB:GN00022; CESP:C04G2.1
A;Experimental source: clone C04G2
C;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 AIGRKQAVGVKGKLMCGGRPVRNATVKLWDNDMFD-------PDDLIAETHVNED 101
                                                                                                                                                                                                                                                                                                                                                                                                       49 DYNAPDCRFIDVKKGQQIYVXSKLVTENGAG---EFWAGSVYGDHQDEMGIVGYFPSNLV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 EVNADTIYWIVQKDGQR-----RKITEDHASVGKNISTKSVYGNHREDVTLHYKYPEGSQ 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KVLIVLLFATILLTFSNASNLDEINANASETDE----VIELIATQK----PPVRFIDKVR 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                          A,Accession: S66662
A,Accession: S66662
A,Golocule type: may S48>
A,Residues: 1-695 < YAS>
A,Residues: 1-695 < YAS>
A,Cross-references: GB:S79761; NID:g1176434; PIDN:AAB35370.1; PID:g1176435
C,Superfamily: procein-glutamine gamma-glutamyltransferase
C,Superfamily: procein-glutamine gamma-glutamyltransferase
F;272/Active site: Cys #status predicted
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                                                                                                                                                                                                                                                                                       Length 695;
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                                                                                                                                                                                                                                                                                                                                                   28; Indels
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22.4%; Pred. No. 2.3;
:ive 24; Mismatches
                                                                                                                                                                                                                                                                                    ch 11.4%; Score 77; DB 1 Similarity 27.5%; Pred. No. 9.1; 22; Conservative 20; Mismatches
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448 KEREVYKKAGRRVTEPSNEI 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 KEQRVYQEATKEI--PTTDI 123
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Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                 Query Match
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A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84045.1; PID:g7379
A;Experimental source: serogroup A, strain 22491
C;Genetics:
A;Gene: NMA0762
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A;Introns: 129/2; 177/1; 206/2; 349/3; 436/3; 506/2; 626/3; 689/3; 772/3; 845/3; 903/3
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-994 <WIL>
A,FCross-references: EMBL:Z79754; PIDN:CAB02102.1; GSPDB:GN00019; CESP:F25H2.13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 AGKCVFAYNANYDKLSANHFENCQIGIHFTAAIEGTSLHDNSFIN-NESOVKYVSTRFLD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:283224; PIDN:CAB05720.1; GSPDB:GA00019; CESP:F25H2.13
A;Experimental source: clone F29C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 MDKLFGSSQLKSVPPLSGKASDGE-ILLETLAKAGFDANSVE-RLVDVLRDAISYLLSKN 396
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                                                                                                                                                                                                                                                                                                                                                                                                                              73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T21356; T21540
R;Wilkinson, J:
Submitted to the EMBL Data Library, September 1996
A;Reference number: 219411
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                                                                                                                                                                                                                                                                                                                                                                                                                           17 AGHGVFMDKLSSKKLCAD--EECVYTISLARAQEDYNAPDCRFIDVKKGQQIYVYSKLV-
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Pred. No. 34;
                                                                                                                                                                                                                                                                                             Length 344;
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                                                                                                                                                                                                                                                                                                                                                                46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 -TENGAGEFWA-GSVYGDHQDEMGIVGYFPSNLVKE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F25H2.13 - Caenorhabditis elegans
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A,Molecule type: DNA
                                                                                                                                                                                                                                                                                             Score 73; DB 2;
Pred, No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: clone F25H2
R;Wilkinson, J.
Submitted to the EMBL Data Library, December 1996
A;Reference number: Z19437
A;Accession: T21540
                                                                                                                                                                                                                                                                                                                                                                17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: December 29, 2003, 16:10:39 Job time : 14.2661 secs
                                                                                                                                                                                                                                                                                                 10.8%;
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Best Local Similarity 28.1%;
Marches 27; Conservative
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Best Local Similarity 27.6*
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-994 <WI2>
                                                           A; Molecule type: DNA
A; Residues: 1-344 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Genetics:
A,Gene: CESP:F25H2.13
                                      A; Status: preliminary
A;Accession: C81920
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C.Species: Arabidopsis thaliana (Mouse-ear cress)
C.Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C.Bate: 30-Apr-1999 #sequence_revision 30-Apr-1999
R.Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, March 1999
A.Reference number: Z15260
A.Reference number: Z15260
A.Residue: 170200
A.Residues: 1-32 < kebr.
A.Residues: 1-32 < kebr.
A.Residues: 1-32 < kebr.
A.Residues: L.Bate: Alley = A.References = EMBL: Alley = A.References = Columbia; BAC clone T4F9
A.Reperimental source: cultivar Columbia; BAC clone T4F9
A.Reperimental source: cultivar Columbia; BAC solone T4F9
A.References: EMBL: A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.References = A.Re
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A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491. A;Reference number: A81775; MUID: 20222556; PMID:10761919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 BECVYIISLARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEM 94
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                    R;McMurray, A.

submitted to the EMBL Data Library, October 1999
A;Reference number: 221041
A;Reference number: 221044
A;Rocession: T31504
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule 'type: DNA
A;Residues: 1-1097 'wHL>
A;Residues: 1-1097 'wHL>
A;Cross-references: EMBL:AL117204; PIDN:CAB55138.1; CESP:Y116A8C.36
A;Experimental source: clone Y116A8C
C;Genetics: CESP:Y116A8C.36
A;Gene: CESP:Y116A8C.36
A;Introns: 50/3; 245/3; 411/3; 486/3; 697/1; 820/3; 926/2
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Best Local Similarity 20.8%; Pred. No. 8.1;
Matches 27; Conservative 22; Mismatches 59; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 11.0%; Score 74.5; D
Best Local Similarity 29.7%; Pred. No. 27;
Matches 22; Conservative 10; Mismatches
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1084 SKSGLFPSNYVQQQ 1097
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 29, 2003, 16:03:18 ; Search time 5.01961 Seconds (without alignments) 1199.181 Million cell updates/sec Run on:

US-10-019-455A-12
676
1 MARILILLEGGLVVLCAGHG.....RVYQBATKEIPTTDIDFFCE 128 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | SUMMAKIES | no i tri i tri i tri |        | Q9jie3 | IUMAN Q9nrc9 | OTOR_CHICK Q9i8p6 gallus gall | VANCA Q918p5 rana | Q16674 | RAT Q62946 rattu |      | SE   | P54100 ratt |      | ш    | P15498 homo | Q9ukw4 | MOUSE Q60992 mus r |      | P04821 | PAGMA | 097566      | Q58426 |      | N Q9nzm3 | Q9wv48        |      | TBG ENTHI P54401 entamoeba |     | MOUSE | HUMAN | RAT Q9jlu4 | SPOLA P42686 | SPOLA P42690 | MOUSE P27664 |    |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------|----------------------|--------|--------|--------------|-------------------------------|-------------------|--------|------------------|------|------|-------------|------|------|-------------|--------|--------------------|------|--------|-------|-------------|--------|------|----------|---------------|------|----------------------------|-----|-------|-------|------------|--------------|--------------|--------------|----|
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| m   нанананананананананананананананананан                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |           | 1                    | nengen | 128    | 128          | 132                           | 133               | 131    | 130              | 130  | 130  | 843         | 845  | 847  | 845         | 847    | 868                | 878  | 1589   | 695   | 2161        | 259    | 406  | 1696     | 2167          | 1217 | 451                        | 340 | 1714  | 1721  | 1815       | 505          | 206          | 858          | ,  |
| Length 128 1328 1338 1339 1330 1330 1330 1330 1330 1330 1330                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |           | Query                | March  | 100.0  | 89.1         | 69.3                          | 6.09              | 41.1   | 39.6             | 39.5 | 37.1 | 13.5        | 13.5 | 13.5 | 13.2        | 13.2   | 12.6               | 12.5 | 11.6   | 11.4  | 11.4        | 11.2   | 11.1 | 11.1     | 11.1          | 10.9 | 0                          | 0   | 0     | 10.5  | 10.5       | 10.4         | 10.4         | 10.4         |    |
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| Ouery Core Match Length 676 100.0 128 6602 89.1 128 660.3 39.6 130.2 251 37.1 13.5 84.5 39.5 13.5 84.5 39.5 13.5 84.5 39.5 13.5 84.5 39.5 13.5 84.5 39.5 13.5 84.5 39.5 13.5 84.5 39.5 13.5 84.5 39.5 13.5 84.5 34.5 11.4 2.5 34.5 11.1 10.5 11.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 17.1 10.5 |           | Result               | 0<br>0 | 1      | 7            | m                             | 4                 | ഗ      | φ                | 7    | 80   | σ           | 10   | 11   | 12          | 13     | 14                 | 15   | 16     | 17    | 18          | 19     | 20   | 21       | 22            | 23   | 24                         | 25  | 26    | 27    | 28         | 29           | 30           | 31           | cc |

| P39452 escherichia (10199 schizosacch P51544 nordotis ma P1633 homo sapien 009165 mus musculu (28p0h1 streptococc (29283 streptococc (29779 homo sapien (286887 c genome po P08292 c genome po P08292 c genome po Q12554 aspergillus |   |
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| RIR3 ECOLI<br>YBYZ_SCHPO<br>KRAEG NORMA<br>NCXL_HUMAN<br>CAQ1_MOUSE<br>AROA_STRP9<br>AROA_STRP9<br>AROA_STRP9<br>VINE MOUSE<br>M3XA_HUMAN<br>POLIG_CXB4E<br>POLIG_CXB4E<br>POLIG_CXB4J                                               | 1 |
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| 713<br>670<br>358<br>377<br>399<br>427<br>427<br>430<br>733<br>954<br>2183<br>2183                                                                                                                                                   |   |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew;
MIM; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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                                                                                                                                                                                                                                                                              61 KKGÇÇİYVYSKLVTENGAĞEFWAĞSVYGDHQDEMGIVGYFPSNLVKEQRVYQEATKEIPT 120
                                                                                                                                                                                                                                                                                                      61 KKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEWGIVGYFFSNLVKEQRVYQEATKEIPT 120
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TISSUB-Brain, and Cochlea;
MEDLINE-21100875; PubMed-11161796;
MEDLINE-21100875; PubMed-11161796;
Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;
"Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation.";
Genomics 71:40-52(2001).
                                                                                                                                                                                                               1 MARILILLIGGLVVLCAGHGVFMDKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE-216387P. PubNed=11780052;
Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Deloukas P., Matthews L.H., Ashurst J., Bubton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbes A.K., Bagguley C.L., Bailey J., Barlow K.F., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark L.N., Clark S.Y., Clee C.M., Cleppen S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Ellington A.G., Frankland J.A., French L., Garner P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDDARD 10998416; MEDLINE-20568254; PubMed=10998416; Cohen-Salmon M., Frenz D., Liu W., Verpy E., Voegeling S., Petit C.; Cohen-Salmon M., Frenz D., Liu W., Verpy E., Voegeling S., Petit C.; Fide, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Otoraplin precursor (Fibrocyte-derived protein) (Melanoma inhibitory ortor of FDP OR MIAL.
Homo sapiens (Human)
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20334619; PubMed=10873378; Resendes B.L., Weremowicz S., Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S., Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.; Anovel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping."; Genomics 66:242-248(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                           100.0%; Score 676; DB 1; Length 128; 100.0%; Pred. No. 3.3e-59; tive 0; Mismatches 0; Indels 0
       BY SIMILARITY.
BY SIMILARITY.
3DD47D4C77C4A7FD CRC64;
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            32 37 B
55 127 B
128 AA; 14328 MW;
                                                                                                                                                   Matches 128; Conservative
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                                                                                                       Query Match
Best Local Similarity
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            DISULFID
DISULFID
SEQUENCE
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Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
By Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
Kay M.P., Kimberlay A.M., King A., Knights A., Laird G.K., Lawlor S.,
Lehvaselaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMirray A.A.,
Mille S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
A. Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
Tracey A., Tromans A.C., Vaudin M., Wall M., Walliam S.A.,
Milming L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
Rogers J., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBCELLULAR LOCATION: Secreted (Potential).
-:- TISSUB SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
-:- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-:- SIMILARITY: Contains 1 SH3 domain.
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BY SIMILARITY.
BY SIMILARITY.
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EMBL; AAF24555; CAC27443.1; --
EMBL; AAJ25234; CAC27443.1; --
EMBL; AAJ25234; CAC28085.1; --
EMBL; AAJ25325; CAC28085.1; JOINED.
EMBL; AAJ52327; CAC28085.1; JOINED.
EMBL; AAJ34428; CAC3885.1; JOINED.
EMBL; AAJ34428; CAC16848.1; --
HSSP; Q16674; 111J.
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Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
SIGNAL; SH3 dmain.; FALSE_NEG.
Signal; SH3 dmain.
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39 110 SH
32 127 BY
55 127 BY
128 AA; 14332 MW;
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Matches 111; Conservative
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catesbeiana (Bull frog).
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                                 NCBI_TaxID=8400;
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Q16674;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 VLFLCFGLANPFATGIFMDKLASKKLCADDDCVYTISLVRAEEDYNAPDCRFINIKKGQL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 LVVLCAG-----HGVFMDKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKKGQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=2034619; PubMed=10873378;

Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S., Denis C.S., Heller S., Lin J.S., Morton C.C.;

Denis C.S., and chromosomal mapping.";

Genomics 66:242-248(200).

-: SUBCELLULAR LOCATION: Secreted (Potential).

-: TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.

-: SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.

-: SIMILARITY: Contains 1 SH3 domain.
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9D1CB07FD353CE1C CRC64;
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71.0%; Pred. No. 6.2e-39;
iive 14; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
OCOraplin precursor.
                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                132 AA
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Pro; IPR001452; SH3.
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                 STANDARD;
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132
114
40
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35
58 1
132 AA;
                                                                    Otoraplin precursor.
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                                                                                                                             NCBI_TaxID=9031;
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Q918P5;
                 CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 LVVLCAG-----HGVFMDKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKKGQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 IYVYSKLVTEN-GAGEFWAGSVYGD-HQDEMGIVGYFPSNLVKEQRVYQEATKEIPTTDI
                                                                                                                                                                                                                                                                            MEDLINE=20334619; PubMed=10873378; Resendes B.L., Weremowicz S., Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S., Denis C.S., Bell A.M., Hudspeth A.G., Morton C.C.; A. Bell A.M., A.M., Pudspeth A.G., Morton C.C.; A. A.M., Anyel conserved cochlear gene, OTOR: identification, expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
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MEDLINE=95007612; PubMed=7923218;
Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Melanoma derived growth regulatory protein precursor (Melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.9%; Score 412; DB 1; Length 133; 57.6%; Pred. No. 2.1e-33; ive 28; Mismatches 17; Indels
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BY SIMILARITY.
BY SIMILARITY.
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35 40 BY
58 132 BY
133 AA; 15243 MW;
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HSSP; Q16674; 111J.
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Best Local Similarity 57.00
Test T2; Conservative
-4GV
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINB=2219825); FULDWEGELAW, JOSCHE, Shermen C.M., Schuler G.D., Ratausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Lischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Adolfor M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Scapleton M.J., Uddin T.B., Toshlywis S., Carninci P., Prange C., Rapleton M.J., Uddin T.B., Toshlywis S., Carninci P., Prange C., Asha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Rochards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Alilalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A., A. Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Willialon D.K., Mulawan J.W., Green E.D., Dickson M.C., A. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., A. Schnetz A.C., Grimwood J., Schmutz J., Marra M.A., Schnetz J., Mones C.D., Shering M.A., Green E.D., Dickson M.C., A. Schnetz J., Marra M.A., Green E.D., Marra M.A., Green E.D., Marra M.A., Green E.D., Dickson M.C., A. Schnetz J., Jones S.J.M., Marra M.A., Green E.D., Marra M.A., Green E.D., Marra M.A., Green E.D., Marra M.A., Green E.D., Marra M.A., Green E.D., Marra M.A., Green E.D., Marra M.A., Green E.D., Marra M.A., Green E.D., Marra M.A., Green E.D., Marra M.A., Green E.D., Marra M.A., Human and mouse cDNA sequences.; Green E.D., Marra M.A., Human and mouse cDNA sequences.; Green E.D., Marra M.A., Human and mouse cDNA sequences.; Green E.D., Green E.D., Green E.D., Green E.D., Dickson W.C., Human and mouse cDNA sequences.; Green E.D., Marra M.A.; E.D., Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21244635; PubMed=11331761;
MEDLINE=21246535; PubMed=11331761;
Lougheed J.C., Holton J.M., Alber T., Bazan J.F., Handel T.M.;
Lougheed J.C., Holton J.M., Alber T., Bazan J.F., Handel T.M.;
In structure of melanoma inhibitory activity protein, a member of a "structure of melanoma inhibitory activity protein, a member of a recently identified family of secreted proteins.";
Proc. Natl. Acad. Sci. U.S.A. 98:5515-5520(2001).
-!- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO. AS WELL AS SONE OTHER NEUROSCIODERMAL TUMORS, INCLUDING GLIOMAS.
-!- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND INSERPOUNDERLY IN GLIOMA CELL LINES.
-!- FIM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
-!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-!- SIMILARITY: Contains 1 SH3 domain.
Schmitt A., Jachimczak P., Lottspeich F., Buettner R., Bogdahn U.;
"Cloning of a novel malignant melanoma-derived growth-regulatory
                                                                                                                                                                                  TISSUE=Placenta;
MEDLINE=96132947; PubMed=9550608;
Bosserhoff A.-K., Hein R., Bogdahn U., Buettner R.;
"Structure and promoter analysis of the gene encoding the human melanoma-inhibiting protein MIA.";
J. Biol. Chem. 271:490-495(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22388257; PubMed=12477932;
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                                                                                            Cancer Res. 54:5695-5701(1994).
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MIM; 601340; -
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CRFIDVKKGQQIYVYSKLVTENGAGE-FWAGSVYGDHQDEMGI-VGYFPSNLVKEQRVYQ 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIA RAT (2029-6; P97591; MIA RAT (2020-6); MIA RAT (2020-6); MIA RAT (2020-201); MIA Rel. 35, Created) MIA COCT-2001 (Rel. 40, Last sequence update) (Rel. 40, Last annotation update) (Rel. 41, Last annotation update) (Rel. 41, Last annotation update) (Rel. 41, Last annotation update) (Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinoic acid-sensitive carein) (CD-RAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene expression changes associated with chemically-induced rat
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                                                                MELANOMA DERIVED GROWTH REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mammary carcinogenesis.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
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                              domain; 3D-structure.
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43.4%; Pred. No. 2.8e-20;
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SH3.
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TISSUE=Cartilage;
MEDLINE=96216414; PubMed=8621736;
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116 PGKVDVKTDKWDFYCQ 131
                 PROSITE; PS50002; SH3; 1.
Growth factor; Signal; SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity 43.47
Matches 59; Conservative
                                                                                                                                                                                 SMART; SM00326; SH3; 1.
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                                                                                                                         STRAND
HELIX
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                     Dietz U.H., Sandell L.J.;
"Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MIA MOUSE STANCE.

06.1865; CO09086; P97495;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 41, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartilage-derived retinoic acid-sensitive inhibitory activity) (Cartil
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                                                                                              J. BiÓl. Chem. 271:3311-3316 (1996).
-i- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND
                                                                                                                                                                       -:- SUBCELLULAR LOCATION: Secreted.
-:- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.
-:- INDUCTION: Repressed by retinoic acid.
-:- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
-:- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-:- SIMILARITY: Contains 1 SH3 domain.
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BY SIMILARITY.
BY SIMILARITY.
95D153161C78E02A CRC64;
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; Pred. No. 2.9e-19;
26; Mismatches 38;
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STRAIN-BALB/c;
MEDLINE=95007612; PubMed=7923218;
MEDLINE=96216414; PubMed=8621736;
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58 129 E
130 AA; 14353 MW;
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Growth factor; Signal; SH3
SIGNAL 1 22
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InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
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     U.B., Sandell L.J.; ing of a retinoic acid-sensitive mRNA expressed in cartilage and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinoic acid-sensitive protein) (CD-RAP).
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                                           "Cloning of a retinoic acid-sensitive mRNA expressed in cari
during chondrogenesis.";
J. Biol. Chem. 271:3311-3316(1996).
-!- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND
                                                                                                                                                                 SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: CARTILAGE RIMORDIA AND CARTILAGE.
TISSUE SPECIFICITY: CARTILAGE RIMORDIA AND CARTILAGE.
TANDUCTION: Repressed by retinoic acid.
PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
SIMILARITY: Contains 1 SH3 domain.
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43.0%; Pred. No. 2.3e-19;
iive 27; Mismatches 36; Indels
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5F99149AECF74501 CRC64;
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EMBL; U67884; AAB40659.1; --
HSSP; Q16674; 1117.
ILLE-PRO; IPRO01452; SH3.
Pfam; PF0018; SH3; 1.
SMART; SMO326; SH3; 1.
PROSITE; PS50002; SH3; FALSE NEG.
Growth factor; Signal; SH3 domain.
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123 DEWDFYCQ 130
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SEQUENCE FROM N.A.
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proliferation.
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                                                                                                                                                                                                              MEDLINE=97251341; PubMed=9097023;
MEDLINE=97251341; PubMed=9097023;
A Gilbert D.J. Jenkins N.A., Buettner R., Sandell L.J.;
A Gilbert D.J. Jenkins N.A., Buettner R., Sandell L.J.;
Theorem D.J. Jenkins N.A., Buettner R., Sandell L.J.;
Theorem CD-Rap/MIA gene: structure, chromosomal localization, and cartilage and chondrosarcoma.";
Theor. Dyn. 208:516-525 (1997).
Theor. Dyn. 208:516-525 (1997).
Theor. Dyn. 208:516-525 (1997).
Theor. Dyn. 208:516-525 (1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 LLGGLVVLCAGHGV-----FMDKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO, GO:0007160; P:cell-matrix adhesion; IMP.
GO; GO:0030198; P:extracellular matrix organization and bioge. . .; IMP.
InterPro; IPR001452; SH3.
Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hessdoerfer B., Schmitt A., Jachimczak P., Lottspeich F., Buettner R., Bogdahn U.; "Cloning of a novel malignant melanoma-derived growth-regulatory protein, MIA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
MELANOMA DERIVED GROWTH REGULATORY
PROTEIN.
SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.1%; Score 251; DB 1; Length 130; 43.0%; Pred. No. 1.1e-17; tive 23; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.

BY SIMILARITY.

TL -> NS (IN REF. 1).

16C957459C5BB5F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE, PS50002; SH3; FALSE NEG.
Growth factor; Signal; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 112 SH
35 40 BY
58 129 BY
112 113 TL
130 AA; 14593 MW;
                                                                                                                     Cancer Res. 54:5695-5701(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, X94322; CAA63983.1; --
EMBL, U85612; AAB42082.1; --
EMBL, X9795; CAA66608.1; --
HASP, Q16674; 111J.
MGD; MGI:109615; Mia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 43.0 Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TDIDFFCE 128
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                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00326;
                                                                                                                                                                                                           STRAIN=129/Sv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
CONFLICT
SEQUENCE
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Æ. 843

PRT;

STANDARD;

VAV RAT

RESULT 9
VAV RAT
ID VAV R

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                                                                                                                                                                   Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                    -I. SUBUNIT: Interacts with SLA (By similarity).
-I. PTM: Phosphorylated on tyrosine residues.
-I. SIMILARITY: Contains 1 calponin-homology (CH) domain.
-I. SIMILARITY: Contains 1 PH domain.
-I. SIMILARITY: Contains 1 PH domain.
-I. SIMILARITY: Contains 1 PH domain.
-I. SIMILARITY: Contains 1 zing-dependent phorbol-ester and DAG
         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --
                                                                                                                                                                                                                                                                                                                                                                                                binding domain.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 2 SH3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HASEF, F2934; LOKI.

INTERPRO, 1PR001715; Calponin-like.

INTERPRO; IPR001247; CH type.

INTERPRO; IPR001219; DAG_PR-bind.

INTERPRO; IPR00131; GDS_CDC24.

INTERPRO; IPR001849; PH.

INTERPRO; IPR00189; SH2.

INTERPRO; IPR00189; SH2.

INTERPRO; IPR0019096; SM2_Calponin.

PÉam; PF00107; CH; 1.

PÉam; PF00107; CH; 1.

PÉam; PF00169; PH; 1.

PÉam; PF00169; RH; 1.

PÉam; PF00169; RH; 1.

PÉam; PF00117; SH2; 1.

PÉam; PF00117; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSG021; CH; I.
PROSITE; PSG0479; DAG PE BIND DOM 1;
PROSITE; PSG0419; DAG PE BIND_DOM_2;
PROSITE; PSG010; DH Z; I.
PROSITE; PSG0741; DH_1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodom; P0001527; CH LYPE; 1.
Prodom; P000093; SH2; 1.
Prodom; P0000066; SH3; 1.
SMART; SM00109; CI; 1.
SMART; SM00033; CH; 1.
SMART; SM00233; PH; 1.
SMART; SM00252; RhoGEF; 1.
SMART; SM00252; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PRO0452; SH3DOMAIN.
PRINTS; PRO0888; SM22CALPONIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U39476; AAA98606.1; -. HSSP; P29354; 1GRI.
                                                      Vav proto-oncogene (p95).
                                                                                 Rattus norvegicus (Rat)
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-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 2 SH3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.5%;
                                                                                                                              EMBL; X64361; CAA45713.1; -. EMBL; M59833; AAA63402.1; -. PIR; A61187; TVMSVV.
                                                                                                                                                                                                                                                                            InterPro; IPR001849; PH. ThrerPro; IPR000219; RhoGEF.
                                                                                                                                                                                                                                                                                                  InterPro; IPR000980; SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1119
3373
504
564
660
765
                                                                                                                                                               1F5X; 15-SEP-00.
1GCP; 28-JAN-03.
1GCQ; 28-JAN-03.
1K1Z; 18-DEC-02.
                                                                                                                                                                                      PDB; 1GCO; 28-JAN-03
PDB; 1K1Z; 18-DEC-02
IRANSFAC; T01230; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29
845 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
 44 ARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSN 103
                                                                                                                                                                                                             NEGUENCE OF 1-93 FROM N.A.
MEDLINE=91172176; PubMed=2005887;
Katzav S., Cleveland J.L., Heslop H.E., Pulido D.;
"Loss of the amino-terminal helix-loop-helix domain of the vav proto-
oncogene activates its transforming potential.";
Mol. Cell. Biol. 11:1912-1920(1991).
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Exp. Med. 191:463.474(2000).
- FUNCTION: Couples tyrosine kinase signals with the activation of the Rho/Rac GTPases, thus leading to cell differentiation and/or
 PROSITE; PS50003; PH_DOMAIN; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 2.
PROSITE; PS55002; SH3; 2.
Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams J.A., Houston H., Allen J., Lints T., Harvey R.;
"The hematopoietically expressed vav proto-oncogene shares homology with the dbl GDP-GTP exchange factor, the bcr gene and a yeast gene (CDC24) involved in cytoskeletal organization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20130290; PubMed=10662792;
Sosinowski T., Pandey A., Dixit V.M., Weiss A.;
"Src-like adaptor protein (SLAP) is a negative regulator of T cell
                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBDIT: Interacts with SLA.
TISSUE SPECIFICITY: Widely expressed in hematopoietic cells land in other cell types.
FTM: Phosphorylated on tyrosine residues (By similarity).
SIMILARITY: Contains 1 calponin-homology (CH) domain.
SIMILARITY: Contains 1 DBL-homology (DH) domain.
SIMILARITY: Contains 1 PB domain.
SIMILARITY: Contains 1 PH domain.
                                                                                                                                                                             13;
                                                                                                                                                     13.5%; Score 91.5; DB 1; Length 843; ilarity 32.9%; Pred. No. 0.28; Conservative 14; Mismatches 20; Indels 13
                                                                                         PHORBOL-ESTER AND DAG BINDING.
SH3 1.
                                                                                                                       940 SH3 2.
97953 MW; C4A5CACD45FCB80E CRC64;
                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                         845 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92228488; PubMed=1565462;
                                                         \Xi
                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                104 LVKEQRVYQE 113
                                                                                                                                                                                                                                                                      834 YVEED -- YSE 841
                                                                               504
564
658
763
840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERACTION WITH SLA.
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor signaling.
                                                                                                                                                                                                                                                                                                                                                                                 Vav proto-oncogene.
VAV1 OR VAV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proliferation.
                                                                                                                                      843 AA;
                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                     194
402
516
615
669
780
                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                     RESULT 10
VAV MOUSE
ID VAV MOUSE
AC P27870;
                                                                                                                                       SEQUENCE
                                                                                                                                                            Query Match
                                                                                                                                                                        Local
                                                                      DOMAIN
                                                                                  DOMAIN
                                                                                                                  DOMAIN
                                                                                                                            DOMAIN
                                                             DOMAIN
                                                                                            DOMAIN
                                                                                                        DOMAIN
                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Guanine-nucleotide releasing factor; Repeat; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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DH.
PH.
PHORBOL-ESTER AND DAG BINDING.
SH3 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 SH3 2.
29 Q -> E (IN REF. 2).
98136 MW; 3666DCCDIC5229DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 91.5; DB 1;
Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001452; SH3.
InterPro; IPR003096; SM22_calponin.
                                                                                                                                                                                                                                                                                                                                    Calponin-like.
                                                                                                                                                                                                                                                                                                          MGD; MGI:99923; Vavi.
InterPro; IPR001715; Calponin-lik.
InterPro; IPR002247; CH type.
InterPro; IPR002219; DAG PE-bind.
InterPro; IPR001331; GDS_CDC24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00688; SM2CALPONIN.
ProDom; PD01527; CH type; 1.
ProDom; PD000093; SH2; 1.
ProDom; P0000066; SH3; 1.
SWART; SM0109; C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00307; CH; 1.
Pfam; PF00130; DAG PE-bind; 1.
Pfam; PF001621; RhoGEF; 1.
Pfam; PF00017; SH2: 1.
Pfam; PF00018; SH3; 2.
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PR00452; SH3DOMAIN.
PR00888; SM22CALPONIN.
                                                                                                                                                                                                                                                                                                                                                                                              101 PSNLVKE 107
                                                                                                                                                                                                                                                                                                                                                                                                                   839 PSTYVEE 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vav proto-oncogene.
VAV1 OR VAV.
                                                                                                                                                                                                                                                                                          847 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                              192
400
514
592
672
788
                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                              Query Match
  PRINTS; 1
                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                ARAQEDYNAPDCRFIDVKKGQQIYVYSXLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSN 103
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=20179693; PubMed=10713454;
Trenkle T., McClelland M., Adlkofer K., Welsh J.;
"Major transcript variants of VAV3, a new member of the VAV family of guanine nucleotide exchange factors.";
                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                  ISOId_90ROC8-2; Sequence=Not described;
-!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
-!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
-!- SIMILARITY: Contains 1 PH domain.
-!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG binding domain.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 2 SH3 domains.
                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                           16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9R0C8-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1888518; Vav3.
InterPro; IPR001715; Calponin-like.
InterPro; IPR001715; Calponin-like.
InterPro; IPR00131; CH type.
InterPro; IPR00131; GDS_CDC24.
InterPro; IPR001849; PH.
InterPro; IPR001889; SH2.
InterPro; IPR001889; SH2.
InterPro; IPR001895; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF067816; AAF09171.1; -.
HSSP; P29355; 1SEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00307; CH; 1.
Pfam; PF00130; DAG PE-bind; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00401; SH2DOMAIN.
                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
                                                                      836 YVEED--YSE 843
                                                 104 LVKEQRVYQE 113
                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                              Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                 Name=Beta;
                                                                                                                                                                          Vav-3 protein.
                                                                                                                        MOUSE
            44
                                                                                                                                  Q9R0C8
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MOUSE
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41 ISLARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYF 100
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MEDLINE=91172176; Pubmed=2005887;
Katzav S., Cleveland J., Heslop H.E., Pulido D.;
"Loss of the amino-terminal helix-loop-helix domain of the vav proto-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Denkinger D.R., Shaw C.L., Cushman A.M., Kawahara R.S.; Denkinger D.J., Borges C.R., Shaw C.L., Cushman A.M., Kawahara R.S.; Submitted regulation of the vav proto-oncogene."; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Katzav S., Martin-Zanca D., Barbacid M.;
"vav, a novel human oncogene derived from a locus ubiquitously
expressed in hematopoietic cells.";
EMBO J. 8:2283-2290(1989).
                                                                                                                                                                                                                                                               PROSITE; PS50021; CH; 1.
PROSITE; PS50021; CH; 1.
PROSITE; PS00479; DAG PE BIND DOM 1; 1.
PROSITE; PS50010; DH 2; 1.
PROSITE; PS50010; DH 2; 1.
PROSITE; PS50001; PH 1; 1.
PROSITE; PS50001; PH 1; 1.
PROSITE; PS50001; SH 2; 1.
PROSITE; PS50001; SH 3; 2.
PROSITE; PS50001; SH 3; 2.
PROSITE; PS50001; SH 3; 2.
PROSITE; PS50001; SH 3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHORBOL-ESTER AND DAG BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9A6B63F0D9E60F8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 13.5%; Score 91.5; DB 1; Local Similarity 32.8%; Pred. No. 0.28; les 22; Conservative 13; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAV HUMAN STANDARD; PRT; 845 AA. P15498; Q15860; 01-APR-1990 (Rel. 14, Created) 16-CTT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 62-845 FROM N.A.
MEDLINE=90005432; PubMed=2477241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97946 MW;
PD001527; CH type; 1.
PD000093; SHZ; 1.
PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guanine-nucleotide releasing
   Probom, PD001527; CH type; 1
Probom, PD000093; SH2; 1.
Probom, PD000066; SH3; 1.
SWART; SW00109; C1; 1.
SWART; SW0033; CH; 1.
SWART; SW0023; PH; 1.
SWART; SW00225; RhoGEF; 1.
SWART; SW00225; SH2; 1.
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44 ARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSN 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proto-oncogene, Phorbol-ester binding, Zinc, SH2 domain, SH3 domain, Guanine-nucleotide releasing factor, Repeat, Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.2%; Score 89.5; DB 1; Length 845; 32.9%; Pred. No. 0.44; ative 14; Mismatches 20; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            564 PHORBOL-ESTER AND DAG BINDING.
660 SH3 1.
765 SH2.
842 SH3.
244 A -> P (IN REF. 2).
718 I -> TV (IN REF. 2).
98313 MW, AC3BC9736FD2F138 CRC64;
                                                                                                                                                                                                         MIM; 164875; -
GO; GO: 0003700; F: transcription factor activity; TAS.
GO; GO: 000748; P: oncogenesis; TAS.
GO; GO: 0007048; P: oncogenesis; TAS.
InterPro; IPR001247; CH type.
InterPro; IPR001247; CH type.
InterPro; IPR001341; GDS_CDC24.
InterPro; IPR001349; PH.
InterPro; IPR000349; RhoGBF.
InterPro; IPR000459; SH3.
InterPro; IPR001969; SH2.
InterPro; IPR001969; SM2_calponin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSS0021; CH; 1.
PROSITE; PSS00479; DAG PB BIND DOM 1; 1.
PROSITE; PSS0010; DAG PB BIND DOM 2; 1.
PROSITE; PSS0010; DH 2; 1.
PROSITE; PSS00014; DH 1; 1.
PROSITE; PSS0001; SH2; 1.
PROSITE; PSS0001; SH2; 1.
PROSITE; PSS0001; SH3; 2.
EMBL; AF030224; AAC25011.1; JOINED.
EMBL; AF030225; AAC25011.1; JOINED.
EMBL; AF030225; AAC25011.1; JOINED.
EMBL; X16316; CAA34383.1; ALT_FRAME.
EMBL; RS3331; AAA63267.1; -
PIR; B39576; TVHUVV.
HSSP; P29354; IGRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD001527; CH type; 1.
ProDom; PD000093; SH2; 1.
ProDom; PD000066; SH3; 1.
SMART; SM00109; CL; 1.
SMART; SM00233; CH; 1.
SMART; SM00233; PH; 1.
SMART; SM00252; SH2; 1.
SMART; SM00252; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00307; CH; 1.
Pfam; PF00130; DAG PE-bind; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF; 1.
Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                    TRANSFAC; T00880; -. Genew; HGNC:12657; VAV1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 LVKEORVYOF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    836 YVEED--YSE 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        718 7
845 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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            ਨੇ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 2 SH3 domains.
-!- CAUTION: Ref.2 sequence differs from that shown due to frameshifts in position 322 and 355.
                                                                                                                                                               MEDLINE=9603895; PubMed=7478592; MEDLINE=9603895; PubMed=7478592; Ramos-Morales F., Romero F., Schweighoffer F., Bismuth G., Camonis J., Tortolero M., Fischer S., "The proline-rich region of Vav binds to Grb2 and Grb3-3."; Oncogene 11:1665-1669(1995).
                                                                                                                                                                                                                                                                                                            AEDLINE-92228488; PubMed=1565462; Addams J.M., Houston H., Allen J., Lints T., Harvey R., Addams J.M., Houston H., Allen J., Lints T., Harvey R., Houston H., Allen J., Lints T., Harvey R., Houston H., Houston H., Allen J., Lints T., Harvey R., Manch Congene Started Languages and a yeast gene with the dbl GDP-GTP exchange factor, the bor gene and a yeast gene (CDC24) involved in cytoskeletal organization."; Oncogene 7:611-618 (1992).

-I- FUNCTION: Couples tyrosine kinase signals with the activation of the Rho/Rac GTPases, thus leading to cell differentiation and/or proliferation.

-I- SUBUNIT: Interacts with SLA (By similarity). Interacts with Grb2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Grb3.
TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT
NOT IN OTHER CELL IYPES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- PTM: Phosphorylated on tyrosine residues.
-i- MISCELLANEOUS: 'Vav' stands for the sixth letter of the Hebrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 1 calponin-homology (CH) domain. SIMILARITY: Contains 1 DBL-homology (DH) domain. SIMILARITY: Contains 1 PH domain. SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG binding domain.
                                                                                                       Romero F.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases
        oncogene activates its transforming potential."; Mol. Cell. Biol. 11:1912-1920(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF030227; AAC25011.1; --
EMBL, AF030201; AAC25011.1; JOINED.
EMBL, AF030202; AAC25011.1; JOINED.
EMBL, AF030203; AAC25011.1; JOINED.
EMBL, AF030204; AAC25011.1; JOINED.
EMBL, AF030206; AAC25011.1; JOINED.
EMBL, AF030206; AAC25011.1; JOINED.
EMBL, AF030209; AAC25011.1; JOINED.
EMBL, AF030209; AAC25011.1; JOINED.
EMBL, AF030209; AAC25011.1; JOINED.
EMBL, AF030201; AAC25011.1; JOINED.
EMBL, AF030211; AAC25011.1; JOINED.
EMBL, AF030211; AAC25011.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOINED.
JOINED.
JOINED.
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                                                                           SEQUENCE OF 299-837 FROM N.A.
                                                                                                                                                           SEQUENCE OF 299-334 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC25011.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC25011.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC25011.1;
AAC25011.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC25011.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC25011.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC25011.1;
                                                                                                                                                                                                                                                                                                      SIMILARITY TO CDC24 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF030219;
AF030220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF030222;
AF030223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF030212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF030213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF030215;
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alphabet

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EMBL; EMBL; EMBL; EMBL;

EMBL; EMBL; EMBL; EMBL;

EMBL; EMBL;

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                                                                                                                                                                                                                                                                                                                  MIM; 605541; -.. GYPase activator activity; TAS.

R GO; GO:0005070; F:SH3/SH2 adaptor protein activity; TAS.

R GO; GO:0005070; F:SH3/SH2 adaptor protein activity; TAS.

R GO; GO:0007264; P:Small GTPase mediated signal transduction; TAS.

R InterPro; IPR001215; Calponin-like.

R InterPro; IPR001219; CH Lype.

R InterPro; IPR001219; DAG PE-bind.

R InterPro; IPR001819; PH.

R InterPro; IPR001819; Ph.

R InterPro; IPR00189; SH2.

R InterPro; IPR001890; SH2.

R InterPro; IPR001980; SH2.

R InterPro; IPR001980; SH2.
                                                                                                                                                                                                                SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=99455043; .PubMed=10523675;
Movilla N., Bustelo X.R.;
"Biological and regulatory properties of Vav-3, a new member of the Vav family of oncoprotains.";
Mol. Cell. Biol. 19:7870-7885(1999).
                                                                                                                                                    Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
-!- SIMILARITY: Contains 1 DBL-bomology (DH) domain.
-!- SIMILARITY: Contains 1 PH domain.
-!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG binding domain.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 2 SH3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event * Alternative splicing; Named isoforms = 2;
                                       Q9UKM4, O95230; Q9Y5X8;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isold=Q9UKW4-2; Sequence=VSP_001820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isold=Q9UKW4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF118887; AAD20349.1; -.
EMBL; AF118886; AAD20348.1; -.
EMBL; AF067817; AAC79695.1; -.
HSSP; P29355; JSBM.
Genew; HGNC:12659; VAV3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00307; CH; 1.
Pfam; PF00130; DAG_PE-bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- ALTERNATIVE PRODUCTS:
                             STANDARD;
                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                        Vav-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Beta;
                             VAV3 HUMAN
RESULT 13
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41 ISLARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLCQLLNNLRAHSINLKEINLRPQMSQFLCLKNIRTFLTAC
CETFGMRKSELFEAFDLFDVRDFGK -> MQLPDCFCRAHL
P (in isoform Beta).
FTId=USP 001820.

107 K -> B (IN REF. 2).
217 Y -> H (IN REF. 1; AAD20348).
229 T -> S (IN REF. 1), AAD20348.
3429 V -> A (IN REF. 1; AAD20348).
97775 MW; CLE29F0B094CB721 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH3 2.
MEPWKQCAQWLIHCKVLPTWHRVTWDSAQVFDLAQTLRDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.44;
ches 21; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.2%; Score 89.5; DB 1; Length 847; Best Local Similarity 32.8%; Pred. No. 0.44; Matches 22; Conservative 13; Mismatches 21; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSS0002; SH3; 2.
Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHORBOL-ESTER AND DAG BINDING.
SH3 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guanine-nucleotide releasing factor; Alternative splicing.
DOMAIN
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                       SWART; SW0023; PH; I.
SWART; SW0023; Ph; II.
SWART; SW00252; SH2; I.
SWART; SW00326; SH3; I.
PROSITE; PSG0021; CH; I.
PROSITE; PSG00479; DAG PE BIND_DOM_1; I.
PROSITE; PSG0010; DAG PE BIND_DOM_2; I.
PROSITE; PSG0010; DAG PE BIND_DOM_2; I.
PROSITE; PSG0010; PH DAMAIN; I.
PROSITE; PSG0003; PH DOMAIN; I.
                                              Pram; Pro0017; SH2; 1.
Pram; Pro0018; SH3; 1.
PRINTS; PR00418; SH3DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00458; SH3DOMAIN.
ProDom; P0001527; CH type; 1.
ProDom; P0000093; SH2; 1.
SMART; SM00109; C1; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGBF; 1.
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217
298
429
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PROSITE; PS50001;
PROSITE; PS50002;
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SEQUENCE FROM N.A.
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VAV2 HUMAN
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                       SEQUENCE
MOD_RES
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                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                Schuebel K.E., Bustelo X.R., Nielsen D.A., Song B.J., Barbacid M., Goldman D., Lee I.J.;
"Isolation and characterization of murine vav2, a member of the vav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH2 domain; SH3 domain;
factor; Repeat; Phosphorylation.
CH.
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PHOSPHORYLATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
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PROSITE; PSS00419; DAG PE_BIND_DOM_1; 1.
PROSITE; PSS0081; DAG PE_BIND_DOM_2; 1.
PROSITE; PSS0010; DH Z; 1.
PROSITE; PSS00041; DH 1; 1.
PROSITE; PSS0003; PH DOMIN; 1.
PROSITE; PSS0001; SHZ; 1.
                                                                                                                                                                                                                                                                                                              MGD; MGT:102718; Vav2.
Interpro; IRR001715; Calponin-like.
Interpro; IRR001215; Calponin-like.
Interpro; IRR002219; DAG PE-bind.
Interpro; IRR001311; GDS_CDC24.
Interpro; IRR001319; PH.
Interpro; IRR001919; RhoGEF.
Interpro; IRR000800; SH2.
Interpro; IRR001452; SH3.
    MEDLINE=96313271; PubMed=8710375;
                                                                                                                                                                                                                                                                                                                                                                                                                     Pram; Pr00307; CH; 1.
Pram; Pr001307; DAG PE-bind; 1.
Pram; Pr00130; DAG PE-bind; 1.
Pram; Pr00130; PH; 1.
Pram; Pr00141; RhoGBF; 1.
Pram; Pr00017; SH2; 1.
Pram; Pr00181; SH3; 2.
RINTS; PR00401; SH3DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRODOM; PD0010527; CH_YPP; 1.
ProDom; PD000093; SH3DOMAIN.
ProDom; PD000093; SH2; 1.
SWART; SW00133; CH; 1.
SWART; SW00233; PH; 1.
SWART; SW00252; RhoGBF; 1.
SWART; SW00252; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50002; SH3; 2.
Phorbol-ester binding; Zinc;
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                                                                                                                                                                                                                                                                                        EMBL; U37017; AAC52761.1; -.
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502
562
642
757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50001;
PROSITE; PS50002;
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                                                                                                                                                                               38 VYT---ISLARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEM 94
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION OF TYR-142; TYR-159 AND TYR-172.

PHOSPHORYLATION OF TYR-142; TYR-159 AND TYR-172.

PHOSPHORYLATION OF TYR-142; TUBES A., Sipeki S., Bauer A.,

Tamas P., Solti Z., Bauer P., Illes A., Sipeki S., Bauer A.,

Parago A., Downward J., Buday L.;

Parago A., Downward J., Buday L.;

Perago A., Downward J., Buday L.;

Prochanism of epidermal growth factor regulation of Vav2, a guanine nucleotide exchange factor for Rac.";

J. Blol., Chem. 278:5163-5171(2003).

-I. FUNCTION: Guanine nucleotide exchange factor for the Rho family of Ras-related GTPases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hencke E.D., Short M.D., Jozwiak S., Bovey C.M., Ramlakhan S., Hencke E.D., Short M.D.;
Haines J.L., Kwiatkowski D.J.;
Haines J.L., Kwiatkowski D.J.;
Haines J.L., Kwiatkowski D.J.;
Haines J.L., Kwiatkowski D.J.;
Haines J.L., Kwiatkowski D.J.;
Andentification of VAV2 on 9q34 and its exclusion as the tuberous sclerosis gene TSC1.",
Ann. Hum. Genet. 59:25-37(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: Widely expressed.
-!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
-!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
-!- SIMILARITY: Contains 1 PH domain.
-!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG binding domain.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 2 SH3 domains.
                                                                                                                    13;
                                                                                Length 868;
PHOSPHORYLATION (BY EGFR) (BY
                                                                                                                    22; Indels
                       SIMILARITY).
D18581E7EEB2DBC2 CRC64;
                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Vav-2 protein.
                                                                              12.6%; Score 85.5; DE
28.9%; Pred. No. 1.1;
tive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 600428; -.
InterPro; IPR001715; Calponin-like.
InterPro; IPR003247; CH_type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95283235; PubMed=7762982;
                                          99915 MW;
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852 GRIGWFPSTYVEEEGV 867
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PIR; I51940; I51940.
                                                                         Query Match
Best Local Similarity 28.99
Matches 22, Conservative
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Genew; HGNC:12658; VAV2.
                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
    172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                            868 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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    172
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RESILT.T
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Q8bje9 mus musculu
Q8bje9 mus musculu
Q8c899 mus musculu
Q921x3 mus musculu
Q950xf1 tetraodon n
Q9for5 homo sapien
Q91zv0 mus musculu
Q8r076 mus musculu
Q8r076 mus musculu
Q8vdu4 mus musculu
Q8vdu4 mus musculu
Q8vdu4 mus musculu
Q8vma6 gallus gall
Q9vma6 drosophila
Q9vma7 drosophila
Q9vma7 drosophila
                                                                                                                                                             December 29, 2003, 16:03:18; Search time 19.7199 Seconds (without alignments) 1674.996 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                      1 MARILILLEGGLVVLCAGHG.....RVYQEATKEIPTTDIDFFCE 128
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
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091X0
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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| Q8uux5 gallus gall Q8rzz8 oryza sativ Q8uwe6 tetraodon n Q9h0h homo sapien Q77202 acanthamoeb Q94e20 oryza sativ | Q9fu07 oryza sativ<br>Q9th04 oryza sativ<br>Q9sh16 oryza sativ<br>Q28616 oryctolagus<br>Q9atq5 triticum ae<br>Q9atq5 triticum ae<br>Q9aty7 actococcus | Q9fu01 oryza sativ<br>Q17629 caenorhabdi<br>Q94ek2 allium asca<br>Q94ek5 allium wake<br>Q94366 allium cepa<br>Q9syv1 allium cepa<br>Q9syv1 allium cepa | Q9/7/11 iuwwan aweno<br>Q9h803 homo sapien<br>Q8s003 oryza sativ<br>Q9xd63 corynebacte<br>Q9hdz9 schizosacch<br>Q94f88 arabidopsis<br>Q9u2t9 caenorhabdi |
|------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|
| Q8UUX5<br>Q8RZZ8<br>Q8UWE6<br>Q9H0H2<br>Q8N157<br>Q77202<br>Q94E30                                               | Q9FU07<br>Q9FU04<br>Q9AYH5<br>Q2B616<br>Q9ATQ5<br>Q9CGW7                                                                                              | Q17629<br>Q94EK2<br>Q94EK5<br>Q44EK5<br>Q43366<br>Q9SYV1                                                                                               | Q67711<br>Q9H803<br>Q8S003<br>Q9XD63<br>Q9HZ9<br>Q9HZ9<br>Q9HZ9                                                                                          |
| 110<br>110<br>110<br>110                                                                                         | 100000000000000000000000000000000000000                                                                                                               | 100000000000000000000000000000000000000                                                                                                                | 3401010101010101010101010101010101010101                                                                                                                 |
| 839<br>259<br>1196<br>1196<br>1215<br>615                                                                        | 344<br>6444<br>655<br>722<br>722                                                                                                                      | 0.00<br>0.00<br>0.00<br>0.00<br>0.00<br>0.00<br>0.00<br>0.0                                                                                            | 353<br>498<br>514<br>707<br>346<br>839<br>1097                                                                                                           |
| 27777778<br>277777777777777777777777777777                                                                       | 11.8                                                                                                                                                  | 1111222332                                                                                                                                             | 11.22.11.12.2.11.00.11.1                                                                                                                                 |
| 86.5<br>82.5<br>81.5<br>81.5<br>81.5<br>81.5                                                                     | 7777888                                                                                                                                               | 77 75 76 .5 76 76 76 76 76 76 76 76 76 76 76 76 76                                                                                                     | 75.5<br>75.5<br>75.5<br>74.5<br>74.5                                                                                                                     |
| 11<br>11<br>20<br>21<br>22<br>23                                                                                 | 0 0 0 8 4 6 5                                                                                                                                         | 1 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3                                                                                                                | 8 4 4 4 4 4 4<br>9 0 1 2 2 4 4 5                                                                                                                         |
|                                                                                                                  |                                                                                                                                                       |                                                                                                                                                        |                                                                                                                                                          |

## ALIGNMENTS

|        |        |              |                        |                       |                         |                              |                      |                                     |                                    |              |                          |                    |                                                                    |             |                                                                 |                   |                                                          |                        |                             |                     |                      |                       |                         |                        |        |         |         |                         |                                | ~                     | ī              | 84                                                              | 57      |
|--------|--------|--------------|------------------------|-----------------------|-------------------------|------------------------------|----------------------|-------------------------------------|------------------------------------|--------------|--------------------------|--------------------|--------------------------------------------------------------------|-------------|-----------------------------------------------------------------|-------------------|----------------------------------------------------------|------------------------|-----------------------------|---------------------|----------------------|-----------------------|-------------------------|------------------------|--------|---------|---------|-------------------------|--------------------------------|-----------------------|----------------|-----------------------------------------------------------------|---------|
|        |        |              |                        |                       |                         |                              |                      | i;                                  |                                    |              |                          |                    | R.,                                                                | •           | A-me13                                                          |                   |                                                          |                        |                             |                     |                      |                       |                         |                        |        |         |         |                         |                                | מני                   | 20,00          | 26 LSSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGE-FWAG |         |
|        |        |              |                        |                       |                         |                              |                      | OBTOM                               | tinae                              |              |                          |                    | tner                                                               |             | is of                                                           |                   |                                                          |                        |                             |                     |                      |                       |                         |                        |        |         |         |                         | 96;                            | ď                     | ñ              | ENGAG                                                           | KGRG    |
|        |        |              |                        |                       |                         |                              |                      | Eutele                              | Crice                              |              |                          |                    | ., Buet                                                            |             | stastae                                                         |                   | seg.                                                     |                        |                             |                     |                      |                       |                         |                        |        |         |         | ••                      | ength                          | Tagolo                | aran           | YSKLVI                                                          | FSKL    |
|        |        |              |                        | ite)                  | Last annotation update) | ·                            |                      | Craniata; Vertebrata; Euteleostomi; | Sciurognathi; Muridae; Cricetinae; |              |                          |                    | Guba M., Bosserhoff A.K., Steinbauer M., Anthuber M., Buettner R., |             | "Overexpression of MIA enhances extravasation and metastasis of |                   | Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. |                        |                             |                     |                      |                       |                         |                        |        |         |         | E7B466C3B5505BFB CRC64; | Score 231.5; DB 11; Length 96; |                       |                | KGOOIY                                                          | SGQVVY1 |
|        |        | į            |                        | apan                  | in uc                   | gment                        |                      | ertek                               | i; Mu                              |              |                          |                    | Anthu                                                              |             | tion                                                            |                   | DDBJ                                                     |                        |                             |                     |                      |                       |                         |                        |        |         |         | 05BFE                   | DB                             |                       |                | IDVKI                                                           | LTIH    |
|        |        | 96 AA.       |                        | ence                  | tati                    | (Fra                         |                      | a: V                                | math                               |              |                          |                    | Σ.                                                                 |             | wasa                                                            |                   | ank/                                                     | ÷                      |                             |                     |                      |                       |                         |                        |        |         |         | 3855                    | 11.5;                          | , 8<br>, 8            |                | PDCRF                                                           | DCRF    |
|        |        | PRT;         | 100)                   | Last sequence update) | anno                    | protein (Fragment).          | (Golden hamster).    | aniat                               | iuro                               |              |                          |                    | auer                                                               |             | extra                                                           |                   | /GenE                                                    | CONTAINS 1 SH3 DOMAIN. |                             |                     |                      |                       |                         |                        |        |         |         | B466(                   | re 23                          | Pred. No. 8.3e-17;    | 22; Mismacches | DYNA                                                            | DYMA    |
|        |        | PR           | Created                | Last                  | Last                    | / pro                        | 무                    |                                     |                                    |              |                          |                    | ceinb                                                              |             | ces                                                             |                   | EMBL                                                     | SH3 D                  | ;                           |                     |                      |                       |                         |                        |        |         |         |                         | SGO                            | Pre                   | . 77           | ARAQE                                                           | AVALC   |
|        |        |              | ď                      | 15,                   | 23,                     | ivity                        | older                | Chordata;                           | entia                              |              |                          |                    | S                                                                  |             | enha                                                            |                   | the                                                      | IS 1                   | 0.1;                        |                     |                      |                       |                         | <del>ا</del>           |        |         |         | 10756 MW;               | 34.2%;                         | æ                     |                | TISL                                                            | PISM    |
|        |        | INARY        | 4                      | Lrel                  | rel.                    | / act                        | ns (G                | cho                                 | , Rod                              |              |                          |                    | f A.K                                                              |             | MIA                                                             |                   | 0) to                                                    | NTAIN                  | F7622                       |                     | 2; SH3               | Ξ.                    | 3; 1.                   | SH3;                   |        | 7       | 96      | 1075                    |                                | - 1                   | vacıv          | EECVY                                                           | OECSE   |
|        |        | PRELIMINARY; | /TYEMBI.rol            | TrEMBLrel.            | (TrEMBLrel.             | Melanoma inhibitory activity | Mesocricetus auratus | Eukaryota; Metazoa;                 | Mammalia; Eutheria; Rodentia;      |              | 36;                      | N.A.               | erhof                                                              |             | on of                                                           |                   | Y-200                                                    | K: C                   | EMBL; AF271694; AAF76220.1; | HSSP; Q16674; 111J. | InterPro; IPR001452; | Pfam; PF00018; SH3; 1 | SMART; SM00326; SH3; 1. | PROSITE; PS50002; SH3; |        | н       | 96      | 96 AA;                  |                                | Best Local Similarity | Conservative   | KLCAD                                                           | KLCAD   |
|        |        | ŭ            |                        | ~                     | -                       | inhi                         | tus                  | ; Me                                | But]                               | tus.         | D=10                     | FROM               | Bossi                                                              | .:          | essi                                                            | cell              | (MA)                                                     | ARIT                   | 7169                        | 674;                | IPR                  | 0018                  | 10032                   | PS50                   | i.     |         |         | 96                      |                                | imi                   | . 44<br>       | LSSK                                                            |         |
|        |        | 60           | 290109;<br>01-005-2000 | 01-001-2000           | 01-MAR-2003             | noma                         | crice                | ryota                               | alia;                              | Mesocricetus | NCBI_TaxID=10036;<br>[1] | SEQUENCE FROM N.A. | Μ.                                                                 | Jauch K.W.; | rexpr                                                           | melanoma cells."; | itted                                                    | -1- SIMILARITY:        | ; AF2                       | , 016               | rPro;                | ; PFC                 | T; SN                   | ITE;                   | domain | TER     | TER     | SEQUENCE                | atch                           | cal 5                 |                | 26                                                              | н       |
| л<br>Б | 6      | 097109       | 120109;                |                       | 01-M                    | Mela                         | Meso                 | Euka                                | Mamm                               | Meso         | NCBI<br>[1]              | SEOU               | Guba                                                               | Janc        | "Ove                                                            | mela              | Subm                                                     |                        | EMBL                        | HSSP                | Inte                 | Pfam                  | SMAR                    | PROS                   | SH3    | NON TER | NON TER | SEQU                    | Query Match                    | st Lo                 | Matches        |                                                                 |         |
| RESULT | 09JI09 | 8            | ۲<br>ا                 | <u> </u>              | Ė                       | DE                           | SO                   | ပ္ပ                                 | ဗ                                  | ဗ            | N S                      | RP                 | RA                                                                 | RA          | RT                                                              | RT                | RL                                                       | ပ္ပ                    | DR                          | DR                  | DR                   | DR                    | S,                      | DR                     | Š      | FI      | F       | Ö,                      | g                              | Be                    | Ma             | ò                                                               | Ωp      |

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QBBJE9; Q8BJE9

RESULT 2

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28 HG---RRFSDLKVCGDEECSMLMYRGKALEDFTGPDCRFVNFKKGDDVVYYXKLA--GGS 82
                                                        79 GEFWAGSVYGDHQDEMGIVGYFPSNLVKEQRVYQEATKEIPTTDIDFFC 127
                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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STRAIN-SESTBL/6J, TISSUE-Head;
MEDLINE-22354663; PubMed-12466851;
The FANTOM COMSOLTIUM,
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(TrEMBLrel. 23, I
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/61; TISSUE=Retina;
MEDINDE=22354633; PubWed=12466851;
The FANTOM Consortium.
The FANTOM Consortium.
The RANTOM Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDMAs.";
Nature 420:563-573(2002).
EMBL; AK044449; BAC32064-1; -.
SEQUENCE 1239 AA; 136350 MW; 6E16F9D42ECEFF05 CRC64;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/64; TISSUB=Eye;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The FINTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
BMBL: AKO84444; BAC316431;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 HGVFMDKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 HG---RRFSDLKVCGDEBCGMLMYRGKALEDFTGPDCRFVNFKKGDDVYVYYKLA--GGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.2%; Score 218; DB 11; Length 268;
42.2%; Pred. No. 7.6e-15;
.ive 13; Mismatches 38; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.2%; Score 218; DB 11; Length 1239; 42.2%; Pred. No. 4.8e-14; ive 13; Mismatches 38; Indels 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2003 (TrEMBLrel. 23, Last sequence update) 01-WAR-2003 (TrEMBLrel. 23, Last annotation update) Weakly similar to NPIP-like protein.
                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Weakly similar to NPIP-like protein (Fragment).
                                   SVYGDHQDEMGI-VGYFPSNLVKEQRVYQEATKEIPT 120
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cONAs.";
Nature 420:563-573 (2002).
EMBL; AKO47965; BAC33202.1; -.
SEQUENCE 68 AA; 7431 MW; 3CBE75527D3CBF7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                 Mus mūsculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to cartilage derived retinoic acid sensitive protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009915; AAH09815.1; -.
MGD; MGI:109615; Cdrap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
SEQUENCE 137 AA; 15441 MW; 971415552E6FD536 CRC64;
                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
29.0%; Score 196; DB 11;
Best Local Similarity 64.6%; Pred. No. 3.1e-13;
Matches 42; Conservative 5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 AA.
68 AA
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Matches

24; Gaps

45; Indels

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63 GQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSNLVKEQRVYQEATKEIPTTD 122
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                                                                                                                                                                                60 VKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSNLVKEQRVYQEATKEIP 119
                                                                                                                                                                                                                         60 FTKGEEISVYVKLAGER--EDLWAGSKGKE-----FGYFFRDAVQIEEVFISEEIQMS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RILILLIGGLVVLÇAGHGVFMDKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKK 62
                                                                                                                9 ILLLAISLIKC-----LESTKLLADLKKCGDLECEALINRVSAMRDYRGPDCRYLN 59
                                                   6 ILLLGGLVVLCAGHGVFMDKLSSKKL-----CADEECVYTISLARAQEDYNAPDCRFID 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.1%; Score 156; DB 11; Length 119; ilarity 33.6%; Pred. No. 1e-08; Conservative 20; Mismatches 49; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ddy; TISSUB=Testis;
STRAIN=ddy; TISSUB=10313;
MEDLINE=91190224; PubMed=9038379;
MCDLINE=9118, X., Kaneko Y., Nonogushi K., Nishiyama H., Yokoi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISGUE-Embryo;
Bosscribdf A.K., Buettner R.;
Bosscribdf A.K., Buettner R.;
Characterization of the MIA gene family.";
submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF390177; AAL26992.1; -.
InterPro; IPR001452; SH3.
SMART; SM00326; SH3; 1.
SEQUENCE 119 AA; 13397 MW; S89F390C0B49D1C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         091ZV0 PRELIMINARY; PRT; 119 AA.
091ZV0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 AA
16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 04, (TrEMBLrel. 04, (TrEMBLrel. 23,
   43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         111 TKESDFLC 118
                                                                                                                                                                                                                                                                                                                               120 TIDIDFFC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 42; Conserva
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          Matches
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00912V0

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                                            41 ISLARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAG-EFWAGSV----YGDHQDEMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MB-2003 (TrEMBLrel. 23, Last amnotation update)
MB-2003 (TrEMBLrel. 23, Last amnotation update)
MB-2003 (Green puffer)
MB-2004 inhibitory activity protein (Fragment).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterrygii; Neoperrygii; Teleostei; Buteleostei; Neoteleostei;
Actinopterrygii; Decomorpha; Actanthopterrygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
NEBI_TAXID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Melanoma inhibitory activity protein 2.
Melanoma inhibitory activity protein 2.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.6%; Score 179.5; DB 13; Length 88; 42.4%; Pred. No. 2.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 165; DB 4; Length 119;
Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Indels
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Bosserhoff A.K., Buettner R.;
Bosserhoff A.K., Buettner R.;
Characterization of the MIA gene family.";
Submitted (UUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR390175; AAL26990.1; -.
InterPro; IPR001452; SH3.
SMART; SM00336; SH3; 1.
SRQUENCE 119 AA; 13535 NW; AEF529762D880AC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Bosserhoff A.K., Buettner R.;

Bosserthoff A.K., Buettner R.;

Bosserhoff A.K., Buettner R.;

Bosserhoff A.K., Buettner R.;

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF390176; AAL26991.1; -.

InterPro. 1 PR001452; SH3.

Pfam; PF00018; SH3; 1.

SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 AA; 10080 MW; C355C1FE04DA22EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 IVGYFPSNLVKEQRVYQEATKEIPTTDIDFFC 127
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                                                                                                                                                     98
                                                                                                                                                                                                            GOVVÝVFSKL - - - KGRGRLFWGGSV 87
                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                     63 GQQIYVYSKLVTENGAGE-FWAGSV
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SEQUENCE
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Q90XF1
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14; Gaps

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279 PSTYVEE 285
                                                        101 PSNLVKE 107
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Higuchi T., Itoh K., Yoshida O., Miki T., Fujita J.;

"Expression of a novel isoform of Vav, Vav-T, containing a single
Srchomology 3 demain in murine testicular germ cells.";

11. Orcogene 14:713-720(1997)
12. -- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

13. REMBL: D83266 BAA18950.1;
14. SIMILARITY: CONTAINS 1 SH3 DOMAIN.

15. REMBL: D83266 BAA18950.1;
16. SIMILARITY: CONTAINS 1 SH3 DOMAIN.

16. REMBL: D83261 SH2.

17. REMBL: PRO0017 SH2;
17. REMBL: PRO0017 SH2;
18. REMBL: REMBL: RH3; 1.

18. REMBL: RH00152; SH3; 1.

18. REMBL: SH000065; SH3; 1.

18. RAMRT: SM00126; SH3; 1.

18. SMART: SM00126; SH3; 1.

18. RROSITE; PSS0001; SH2; 1.

18. RROSITE; PSS0002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.5%; Score 91.5; DB 11; Length 166;
32.9%; Pred. No. 0.099;
Live 14; Mismatches 20; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.5%; Score 91.5; DB 11; Length 287; 32.8%; Pred. No. 0.19; tive 13; Mismatches 21; Indels 11;
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SEQUENCE 287 AA; 32662 MW; BF2850B8F921F048 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 AA; 19434 MW; 2C3AF1FF07A5018F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical 32.7 kDa protein.
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InterPro; IPR000452; SH3.
Prom; PP00017; SH2, 1.
Probom; PD000069; SH3; 1.
Probom; PD000066; SH3; 1.
SWART; SW00252; SH3; 2.
PROSITE; PS50001; SH3; 2.
PROSITE; PS50001; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 32.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 LVKEQRVYQE 113
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Q8R076
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44 ARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSN 103
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Strausberg R.; Strausberg R.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. SIMILARITY: CONTAINS 1 PH DOMAIN. EMBL; BC020487; AAH20487.1; -.
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                                                                                  01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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PROSITE; PS50021; CH; 1.
PROSITE; PS00479; DAG PE BIND DOM 1; 1.
PROSITE; PS00741; DAG PE BIND DOM 2; 1.
PROSITE; PS50010; DH 1; 1.
PROSITE; PS50010; DH 2; 1.
PROSITE; PS50010; SH2; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50001; SH3; 2.
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| InterPro; | IRR001715; | Calponin-like. |
| InterPro; | IRR001715; | CH Lype. |
| InterPro; | IRR001219; | DAG PE-bind. |
| InterPro; | IRR001313; | GDS_CDC24. |
| InterPro; | IRR001313; | PH. |
| InterPro; | IRR001319; | PH. |
| InterPro; | IRR001999; | PH. |
| InterPro; | IRR001999; | SH2. |
| InterPro; | IRR001999; | SH3. |
| InterPro; | IRR001999; | SH3. |
| InterPro; | IRR001999; | SH3. |
| InterPro; | IRR001999; | IR. |
| InterPro; | IRR001999; | IR. |
| InterPro; | IRR00199; | IRR1; |
| InterPro; | IRR00199; | IRR1; |
| InterPro; | IRR00199; | IRR1; |
| InterPro; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IRR00199; | IR
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SMART; SM00325; RhGGEF; 1.
SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 2.
PRELIMINARY;
                                                                                                                                                                                                                                                  Similar to vav oncogene.
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                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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Q8VDU4
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44 ARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSN 103
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STRAIN=NOD; TISSUE-Thymus;
STRAIN=NOD; TISSUE-Thymus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM COnsortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Explorations pased on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK088586; BA240436.1;
EMBL; AK088586; BA240436.1;
EMBL; AK088586; BA240436.1;
FRIENTENCE 845 AA; 98093 MW; 5D0DE0D9311DFB8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1921_TaxID=10090;
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Kurosaki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                         13.5%; Score 91.5; DB 11; Length 845; 32.9%; Pred. No. 0.7; tive 14; Mismatches 20; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The way a Modulates B Cell Receptor Responses by Regulating Phosphonositide 3-Kinase Activation.";

L. Exp. Med. 195:189-200(2002).

J. Exp. Med. 195:189-200(2002).

- -- SIMILARITY: CONTAINS 1 PH DOMAIN.

EMBL; AY046915; AAL06249.1; -- RIBLIS AY046915; AAL06249.1; -- RIBLIS AY046915; AAL06249.1; -- RIBLIS AY046915; AAL06249.1; -- RIBLIS AY046915; AAL06249.1; -- RIBLIS AY046915; AAL06249.1; -- RIBLIS AY046915; AAL06249.1; -- RIBLIS AY046915; AAL06249.1; -- RIBLIS AY046915; AAL0625.1 RR001391; AAR0465.1 RR001391; AAR0465.1 RR0014951; SH3.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
GDP/GTP exchange factor VAV3.
                                                                                                       WAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 32.9%
Marches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken)
                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 LVKEQRVYQE 113
797 YVEED--YSE 804
                                                                                                                                                             VAV proto-oncogene.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=11805146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08UUX6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus
                                                                                08BTV7
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Gaps

13;

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41 ISLARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYF 100
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STRAIN=Berkeley;

MEDLINE=20196006;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., In P.W., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

A dams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

A dams M.D., Candre S.E., Li P.W., Hoskins R.A., Galle R.F.,

A sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,

Ballew R.M., Bason R.Y., Bouck J., Brokstein P., Bottier P.,

Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CG11098 protein.
CG31635 OR CG13768 OR CG13769.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bobyera, Endopterrygota; Diptera, Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 34.3%; Pred. No. 0.7;
Matches 23; Conservative 12; Mismatches 21; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         846 AA; 97815 MW; C47EE949D873821B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 13, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1257 AA.
                                                                                                               PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR000889; SH3DOMAIN.
ProDom; PD0010527; CH type; 1.
ProDom; PD000066; SH3; 1.
SMART; SM000033; SH2; 1.
SMART; SM00023; PH; 1.
SMART; SM00223; PH; 1.
SMART; SM00223; PH; 1.
SMART; SM00223; PH; 1.
SMART; SM00223; PH; 1.
SMART; SM00225; SH2; 1.
SMART; SM00225; SH2; 1.
PROSITE; PS50013; PH; 1.
PROSITE; PS50010; DH_2; 1.
PROSITE; PS50010; DH_2; 1.
PROSITE; PS50001; DH_2; 1.
PROSITE; PS50001; DH_2; 1.
PROSITE; PS50001; SH3; 2.
SM3 Admain.
InterPro; IPR003096; SM22_calponin.
          Pfam; PF00307; CH; 1.
Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF00169; PH; 1.
                                                                Pfam; PF00621; RhoGBF; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 PSNLVKE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             838 PSTYVEE 844
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RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Robert C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris D., Houston K.A., Howland T.J., Wel M.-H., Ibegwam C.,
RA Jali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Markulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., May M., Murphy E., Murphy L., Marzy D.M., Nelson D.L.,
RA Reinert K., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Saunders R.D.C., Scheeler F., Shen H.,
RA Svieska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.A.,
RA Zhens X.H., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zhens X.H., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zhens X.H., Zhong W., Rubhin G.M., Venter J.C.,
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RA Zhens X.H., Shong W., Zhon W., Zhu S., Zhu X., Smith H.O.,
RA Zhence 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
A Cocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Barzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A Dodsom T.C., Moy M., Murphy B., Nelson C., Moshon K.A., Nunco J.,
A Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
A Stapleton M., Strong K., Svirskas R., Tector C., Tyler D.,
A Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
R. Sequencing of Drosophila melanogaster genome.;
Cubmitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smithias F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.3%; Score 90; DB 5; Length 1257; 25.6%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AE003614; AAF52413.2; -.
Flybase; FBgn0051635; CG31635.
SEQUENCE 1257 AA; 139136 MW; 5843F0540EEA9511 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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ILLIGGLVVLCAGHGVFMDKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKKGQQ 65 : |: ||:: | : | : | |:|||| : | | |:|| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Gaps

56; Indels

19; Mismatches

30; Conservative Similarity

Query Match Best Local &

Best Loca Matches

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RX MEDLINE=20196006; PubMed=10/J1131;
RA Adams M.D. Celniker S.E., Holt R.B., Evens C.A., Gocayne J.D.,
RA Adams M.D. Celniker S.E., Holt R.B., Hokkins R.A., Galle R.F.,
RA Adams M. Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Gutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Batton R.C., Rogers Y.H.C., Blazej R.G., Change M., Miklos G.L.G.,
RA Mank K.H., Doyle C., Baxter E.G., Helt G., Napambe M., Pfeiffer B.D.,
RA Bellew R.M. Bard M. Barden S.C., Helt G., Blandwin D.,
RA Bencos D., Borcham M.R., Bound J., Bayaklaroglu L., Beasley E.M.,
RA Berry J.M., Cawley S., Dahlke C., Davemport L.B., Bolehakov S.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu B., Center A., Chadra I.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu B., Center A., Chadra I.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu B., Center A., Chadra I.,
RA Burtis K.C., Gabrielian A.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Digan-Rocha S., Dunkov B.C.,
RA Dorbin K.J. Evangelista C.C., Ferraz C., Ferriar S., Davies P.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Gaun P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez T.R., Harrandez T.R., Redischman W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez T.R., Harnandez R.D.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Lasko P., Lei Y., McIntcoh T.C., McLeodo M.P., Moshrefi A.,
Nelson D.R., Milshima N.V. Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshima N.V. Mobarry C., Morris J., Moshrefi A.,
RA Renington K.A., Nixon K.A., Nixon K., Muny B., Sunk R., Shue B.C., Siden-Kiamos I. Simpson M., Strong K., Sunk H.,
RA Spier E., Spradling A.C., Stapleton M., Strong K., Sunk H.,
RA Shene K., Tector C., Turner R., Wang Z.-Y., Wassarman D.A., Welter E., Zhang X.H., Zhong F.N., Wolder T.,
66 IYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSNLVKEQRVY---QEATKEIP 119
                           Evans C.A., Gocayne J.D., Amanatides B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                       CG11098 protein.
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                                                                                                                             RESULT 15
Q9VMA7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 IYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSNLVKEQRVY---QEATKEIP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Gaps
                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Matchews B.B., Bayraktaroglu L., Campbell K., Hradecky, P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smuthiak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 90; DB 5; Length 1430;
; Pred. No. 1.9;
19; Mismatches 56; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AE003614; AAF52414.2; -.
Flybase; FBgn0031842; CG11098.
SEQUENCE 1430 AA; 159051 MW; FCF9988A95979349 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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25.6%;
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les 30; Conservative
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SEQUENCE FROM N.A.
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Rat MLP protein se

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(c) 1993 - 2003 Compugen Ltd.
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Mouse MLP protein
Rat MLP protein se
Human growth regul
Human anglogenesis
Human PRO9873 prot
Human PRO protein,
Novel human protein,
Mouse MLP protein

AAB69125 AAB69130 AAB82671 AAB69123 ABB95602 AAB84996 AAU99871 AAU09871

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| 215                     | 547                                                | 80.08<br>2.09.00       | 110                                                        | 2 2 2  | AAB69126<br>AAB82672                                            | uman M                                                        |
|-------------------------|----------------------------------------------------|------------------------|------------------------------------------------------------|--------|-----------------------------------------------------------------|---------------------------------------------------------------|
| 13                      | 449                                                | 99                     |                                                            |        | AAB69129                                                        | 13                                                            |
| 14                      | 277.5                                              | 41                     |                                                            |        | AAR69811                                                        | Ĕ;                                                            |
| 15                      | 277.5                                              | 4 4                    |                                                            |        | AAG65614<br>AAG65615                                            | Recombinant human                                             |
| 17                      | 247                                                | 36                     |                                                            |        | AAR69812                                                        | Melanoma inhibitin                                            |
| 18                      | 218                                                | 3 2                    |                                                            |        | ABB82119<br>AAI79304                                            | Human PRO polypept                                            |
| 70                      | 218                                                | 9 6                    |                                                            |        | AAB87608                                                        | Human PRO19670. H                                             |
| 21                      | 218                                                | 9 6                    |                                                            |        | ABG95933<br>ABB95600                                            | Human secreted/tra<br>Human angiogenesis                      |
| 23                      | 218                                                | 9 6                    |                                                            |        | ABB84994                                                        | Human PRO19670 pro                                            |
| 24                      | 218                                                | 32                     |                                                            |        | ABU71392                                                        | Human PRO19670 pro                                            |
| 25<br>26                | 218                                                | M W                    |                                                            |        | ABU/1588<br>ABU/2034                                            | Novel human secret                                            |
| 27                      | 218                                                | 35                     |                                                            |        | ABU72191                                                        | Human PRO polypept                                            |
| 78                      | 218                                                | W 0                    |                                                            |        | ABU65849<br>ARII66182                                           | Novel human secret                                            |
| 9 6                     | 218                                                | 9 6                    |                                                            |        | ABU67686                                                        | Human secreted/tra                                            |
| 31                      | 218                                                | m                      |                                                            |        | ABU65544                                                        | Human PRO polypept                                            |
| 32                      | 218                                                | W W                    |                                                            |        | ABU56880<br>ABU56216                                            | Human secreted/tra                                            |
| 0 K                     | 218                                                | 'n                     |                                                            |        | ABU57211                                                        | Human PRO polypept                                            |
| 35                      | 218                                                | Ä                      |                                                            |        | ABU10790                                                        | Human secreted/tra                                            |
| 36                      | 218                                                | e i                    |                                                            |        | AAY70209                                                        | Murine TANGO 130 p                                            |
| 37                      | 218                                                | m r                    |                                                            |        | ABB82117                                                        | Human protein segu                                            |
| χ σ<br>σ                | 208.0                                              | 7 ~                    |                                                            |        | ABB82120                                                        | TANGO 130                                                     |
| 04                      | 208.5                                              | กัพ                    |                                                            |        | AAY70210                                                        | TANGO 130                                                     |
| 41                      | 208.5                                              | ĕ                      |                                                            |        | ABB82118                                                        | Human TANGO 130 pa                                            |
| 42                      | 208.5                                              | ñč                     |                                                            |        | ABB8212/<br>AA179319                                            | PRO DO                                                        |
| 4 4<br>5 4              | 700                                                | Ñ                      |                                                            |        | ABU71407                                                        |                                                               |
| Ç.                      | )<br>N                                             | i                      |                                                            |        |                                                                 |                                                               |
|                         |                                                    |                        |                                                            |        | ALIGNMENTS                                                      |                                                               |
| RESULT                  | н                                                  |                        |                                                            |        |                                                                 |                                                               |
| ð                       | 5<br>B69125                                        | standard;              | d; Protein;                                                | ein;   | 128 AA.                                                         |                                                               |
|                         | AAB69125;                                          |                        |                                                            |        |                                                                 |                                                               |
| 23                      | -APR-2                                             | 001 (£i                | irst entry)                                                | ry)    |                                                                 |                                                               |
|                         | Mouse MLP                                          | protein                | in sequence                                                |        | SEQ ID NO:12.                                                   |                                                               |
| KW ML<br>KW jo<br>in in | MLP; MIA;<br>joint dise<br>cardiant;<br>inhibitor. | mel<br>aase<br>gen     | anoma inhibitory<br>; pathologic angi<br>e therapy; secret | .⊶ O @ | activity; cancer; k<br>ogenesis; diagnosis<br>ory cell function | oone disease;<br>;; antiinflammatory;<br>:egulator; promoter; |
| XX<br>OS Mus            | s musculu                                          | lus.                   |                                                            |        |                                                                 |                                                               |
|                         | WO2001025                                          | 64-A1.                 |                                                            |        |                                                                 |                                                               |
| ጀር!<br>11               | -JAN-200                                           | 01.                    |                                                            |        |                                                                 |                                                               |
| PF 29                   | -JUN-200                                           | 0; 20                  | 00WO-JP0427                                                | 4278   |                                                                 |                                                               |
| 30<br>30                | -JUN-199                                           |                        | 99JP-018671                                                | 6718   |                                                                 |                                                               |
|                         | (TAKE) T                                           | TAKEDA (               | CHEM IND                                                   | LTD (  |                                                                 |                                                               |
| HF                      | toh Y, l<br>anaka H;                               | Nishi 1                | K, Ogi                                                     | Х,     | Ohkubo S, Mogi S, Noguchi                                       | hi Y, Yoshimura K;                                            |
|                         | WPI; 2001-15<br>N-PSDB; AAF5                       | -159271/16<br>AF59068. | 1/16.                                                      |        |                                                                 |                                                               |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSNLVKEQRVYQEATKEIPT 120
                                                                                                                                                                                                                                             The present invention describes novel MLP proteins and their encoding DNAS. The MLP proteins and DNAS have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAS can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF5909 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                  Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MARILILLIGGLVVLCAGHGVFMDKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 676; DB 22;
100.0%; Pred. No. 1.8e-74;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat MLP protein sequence SEQ ID NO:47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nishi K, Ogi K, Ohkubo S,
                                                                                                                                                                                             Claim 4; Page 93-94; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB69130 standard; Protein; 128 AA.
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Best Local Similarity 100.0
Matches 128; Conservative
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                                                                                                                  DNAS. The MLD proteins and DNAS have antiinflammatory and cardiant cardivities, and can be used in gene therapy and as secretory cell function regulators. The MLD proteins and DNAS can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
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                                                                                 The present invention describes novel MLP proteins and their encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MARILILLIGGLVVLCAGHGVFMDKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.9%; Score 655; DB 22; Length 128; 96.1%; Pred. No. 6.7e-72; Live 3; Mismatches 2; Indels C
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/label= Mature_protein
/note= "separately claimed in Claim 10"
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/label= Signal_peptide
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                            Claim 6; Page 106; 111pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of a novel human growth regulatory-like polypeptide (GRLP). The amino acid sequence is predicted from a novel assembled CDRA (see AAH26431 of 14 kDa unglycosylated. CDC 1637227. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP elongs to the same protein family as growth regulatory protein. CD selongs to the same protein andly as growth regulatory protein. CD selongs to the same protein andly conver 111 amino acids) or melanoma inhibitory activity, cattle cartilage-derived creinoic acid sensitive protein (CD-RAP, 44) identity and 64% cattlnoic acid sensitive protein (CD-RAP, 44) identity and 64% can be used in the prophylaxis, treatment (including gene therapy) can diagnosis of disorders and oblymucleotides of the invention cartilage development and maintenance, inhibition of melanoma cell cartilage development and maintenance, inhibition of melanoma cell growth and tumours, including neuroectodermal tumours such as cartilage development and maintenance, inhibition of melanoma cell growth and tumours, including neuroectodermal tumours such as confiferentiation activity, tissue growth activity, chemocratic/chemokinein activity, tissue growth activity, inminion contivity, tissue growth activity, inmunosuppressive or immunostimulant activity, activity, including neuroprise and therapy, themocratic/chemokineit activity, and treatment of leukaemia, nervous system disorders, and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                           89.1%; Score 602; DB 22; Length 128; 86.7%; Pred. No. 2.1e-65;
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                          Claim 10; Page 116-117; 119pp; English.
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Best Local Similarity 86.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                      Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human angiogenesis related protein PRO9873 SEQ ID NO: 360.
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 91-92; 111pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB95602 standard; Protein; 128 AA
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2000WO-US20710.
2000US-222695P.
2000US-0643657.
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2000US-220624P.
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(TAKE ) TAKEDA CHEM IND LTD
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                                                                                                                                                                                        N-PSDB; AAF59065
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Length 128;

Query Match

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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardidovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoardal infarctions, thrombophibbitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma and wound healing. The present sequence is a PRO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerber H, Gerritsen ME, Goddard A;
,, Hillan KJ, Marsters SA, Pan J, Paoni NF;
K, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Fig 360; 567pp; English.
23-AUG-2000; 2000WO-US23522.
24-AUG-2000; 2000WO-US33328.
15-SEP-2000; 2000US-000000PP.
18-SEP-2000; 2000US-000000PP.
18-SEP-2000; 2000US-0664610.
18-SEP-2000; 2000US-0663350.
24-OCT-2000; 2000US-066322P.
08-NOV-2000; 2000US-0709238.
08-NOV-2000; 2000US-0709238.
10-NOV-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US3268.
21-ANA-2001; 2001US-0767669.
28-FEB-2001; 2001US-08066689.
28-FEB-2001; 2001US-0806689.
21-MAR-2001; 2001US-0808689.
22-MAR-2001; 2001US-0808689.
22-MAR-2001; 2001US-0808689.
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10-MAY-2001; 2001US-0854280.
25-MAY-2001; 2001US-0866028.
25-MAY-2001; 2001US-0866034.
25-WAY-2001; 2001WS-0866034.
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30-MAY-2001; 2001WO-US17443.
01-JUN-2001; 2001WO-US17800.
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20-JUN-2001; 2001WO-US19692.
28-JUN-2001; 2001WO-US00000.
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PJ, Gurney AL, I
JF, Watanabe CK,
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GODDARI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
PAN I P.
STEPHAN J F.
STEPHAN J F.
WILLIAMS P M.
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GERRITSEN M E.
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N-PSDB; ABL95740.
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FERRARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stephan JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baker KP,
Godowski P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HILL/) | (MARS/) | (PANJ/) | (PANJ/) | (STEP/) | (WATA/) | (WILL/) | (WILL/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/) | (WODD/
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(FERR/)
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Sequence

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                                                                                  61 KKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSNLVKEQRVYQEATKEIPT 120
                                                                                               Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; arge-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
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                                       1 MARILILLIGGLYVLCAGHGVFMDKLSSKKLCADEBCVYTISLARAQEDYNAPDCRFIDV
                                                    Gaps
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                     Indels
                      8
Score 602; DB 23;
Pred. No. 2.1e-65;
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                        9; Mismatches
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2000US-220664P.
2000WO-US20710.
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2000US-0643657.
2000WO-US23522.
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2001US-0854208.
2001US-0854280.
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2000US-230978P.
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2001WO-US06666
   89.1%;
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                                                                                                                                                                                                                                                         16-MAY-2002 (first entry)
            Local Similarity 86.7 es 111; Conservative
                                                                                                                                    TDIDFFCE 128
                                                                                                                                                       121 TDIDFFCE
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10-MAY-2001;
10-MAY-2001;
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08-NOV-2000;
10-NOV-2000;
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17-AUG-2000;
23-AUG-2000;
24-AUG-2000;
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18-SEP-2000;
18-SEP-2000;
24-OCT-2000;
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01-MAR-2001;
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20-DEC-2000;
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                Best Loca
Matches
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ABB84996
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WO200208288-A2

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The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides.

Sonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in periorte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AMU83592-AAMU83713 represent human PRO protein sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQBATKEVPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.1%; Score 602; DB 23; Length 128; 86.7%; Pred. No. 2.1e-65;
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                                                                                                                                                                                                                        2000US-220666P.
2000US-220893P.
2000WO-US20710.
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2000US-220607P.
2000US-220624P.
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2000US-220664P.
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2001WO-US17092
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Best Local Similarity 86.7'
Matches 111; Conservative
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                                31-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
activities, and can be used in gene therapy. The PRO polynucleotides,
proteins, agonists and antagonists are useful for treating or diagnosing
a cardiovascular, endothelial or angiogenic disorder in a mammal,
e.g. cardiac hypertrophy, trauma, cancer, age-related macular
degeneration, atherosclerosis, hypertension, arterial restenosis,
theumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
carcinoma and wound healing. The PRO polynucleotides have applications
in molecular biology, including use as hybridisation probes, and in
chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
probes used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                          Gerber H, Gerritsen ME, Goddard A;
L, Hillan KJ, Marsters SA, Pan J, Paoni NF;
CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                               One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.1%; Score 602; DB 23; Length 128; 86.7%; Pred. No. 2.1e-65; ive 9; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU83627 standard; Protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                        Claim 11; Fig 360; 565pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO protein, Seq ID No 72.
                    25-WAY-2001; 200109-0866034.
25-WAY-2001; 200109-0817092.
30-WAY-2001; 200109-08770933-WAY-2001; 200109-0871443.
01-JUN-2001; 2001WO-US17443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                          Baker KP, Ferrara N, Ger,
Godowski PJ, Gurney AL, I
Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111; Conservative
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TDIDFFCE 128
                                                                                                                               (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                   WPI; 2002-090516/12.
N-PSDB; ABL88251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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Wood WI;

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KKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSNLVKEQRVYQEATKBIPT 120 

TDIDFFCE 128 TDIDFFCE 128

MARILLLFLPGLVAVCAVHGI FMDRLASKKLCADDECVYTI SLASAQEDYNAPDCRFINV

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MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
                                                                                                                                                                                                                                       Mouse MLP protein sequence SEQ ID NO:26.
                                                                                                                                                     AAB69127 standard; Protein; 110
                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUN-2000; 2000WO-JP04278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAKE ) TAKEDA CHEM IND LTD.
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N-PSDB; AAF59080.
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                                                                                                                                                                                                                                                                                                                                             Mus musculus.
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                                                                                                                                                                                                                 23-APR-2001
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                                                                                                                                                                                                                                                                                                                 inhibitor
                                                                                                                                                                                     AAB69127;
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                                                                                                                              RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New secreted proteins or polypeptides, useful for treating e.g. cancer, autoimmune diseases, wound healing disorder, infections, haematopoietic disorders, inflammatory disorders, infertility, cancer
                                                                                                                                                                                                  Secreted protein; cytostatic; immunosuppressive; vulnerary; vaccine; antiinflammatory; neuroprotective; nephrotropic; cardiovascular; human; cancer; autoimmune disease; wound healing disorder; infection; haematopoietic disorder; inflammatory disorder; infertility; neurological disease; psychiatric disease; cardiovascular disease; respiratory disease; renal; gastrointestinal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.1%; Score 602; DB 23; Length 128; 86.7%; Pred. No. 2.1e-65; ive 9; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith RF, Xiang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 73-74; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders, inflammatory disorders,
                                                                                          AAU09871 standard; Protein; 128 AA
                                                                                                                                                                             Novel human secreted protein #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                  24-APR-2000; 2000US-199417P.
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                                                                                                                                                    (first entry)
                       TDIDFFCE 128
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121
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Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura

Nishi K,

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                                                                                                                                                                      The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing to retreating bone and joint diseases as well as pathologic angiogenesis. AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 HGVFMDKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEFWAGSVYGDHODEMGIVGYFPSNLVKEQRVYQEATKEIPTTDIDFFCE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 110;
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Pred. No. 3.7e-64;
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ive 0; Mismatches
                                                                                                                                Claim 3; Page 98-99; 111pp; Japanese.
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Matches 110; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       110 AA;
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MARILILLIGGLVVLCAGHGVFMDKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60

Query Match Best Local Similarity 86.7 Matches 111; Conservative

Yoshimura K;

AAB6913

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The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant extivities, and can be used in gene therappy and as secretory call function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing to retaining bone and joint diseases as well as pathologic angiogenesis. AAFS9063 to AAFS9099 and AABS9122 to AABS9132 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
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                                              MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
cardiant; gene therapy; secretory cell function regulator; promoter;
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ilarity 90.0%; Pred. No. 9e-59;
Conservative 7; Mismatches 4;
            Human MLP protein sequence SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 97-98; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                    Ogi K, Ohkubo S,
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                                                                                                                                                                                                                                                                    29-JUN-2000; 2000WO-JP04278.
                                                                                                                                                                                                                                                                                                         99JP-0186718.
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N-PSDB; AAF59079.
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Best Local Similarity
Matches 99; Conserv
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                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                11-JAN-2001
                                                                                                                   inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                        Tanaka H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mogi S, Noguchi Y, Yoshimura K;
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Pred. No. 4.5e-62;
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                                                                                                                                                                                                Rat MLP protein sequence SEQ ID NO:49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 107; 111pp; Japanese.
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                                                                                AAB69131 standard; Protein; 110
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78

Gaps

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Indels

in the

Matches

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RESULT 11
AAB69126
ID AAB69
XX
AC AAB69
XX
DT 23-AP

Length 110;

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84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probe; fusion protein.
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                                                                                                                                                                                                                                                                                                 Nishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 AA;
                                                                                                                               WO200102564-A1
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26-OCT-1995
                                                                                                                                                                                                                                 30-JUN-1999;
                                                                                                                                                                11-JAN-2001
                                                                                                 Rattus sp.
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                                                                Inhibitor
                                                                                                                                                                                                                                                                                                                   ranaka H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DRLASKKI.CADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKIVKENGAGEFWA 60
                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of a novel human growth regulatory-like polypeptide (GRLP) mature protein. The sequence is predicted from a novel assembled cDNA (see AAH56343) based on Hyseq clone number 16372272. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP belongs to the same protein family as growth regulatory proteins, growth factors, human melanoma derived growth regulatory proteins. Cormelanoma inhibitory activity, cattle cartilage-derived retinoic acid sensitive protein (CD-RAP, 44% identity and 64% retinoic acid sensitive protein (CD-RAP, 44% identity and 64% camilarity over 126 amino acids) and other retinoic acid-sensitive protein can be used in the prophylaxis, treatment (including gene therapy) and diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma cell
                                                                                                                                                                                                                                                                  Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 DKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth and tumours, including neuroectodermal tumours such as gliomas. The polypeptides, which include the GRLP mature protein, may also have nutritional uses, cytokine and cell proliferation or differentiation activity, stem cell growth factor activity, haematopoiesis regularing activity, tissue growth activity, immunosuppressive or immunostimulant activity, activin/inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity, chemotactic/chemotinetic activity, haemostatic and thrombolytic activity, use in cancer diagnosis and therapy, drug screening, receptor/ligand activity, antiinflammatory activity, and treatment of leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                   Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 GSVYGDHQDEMGIVGYFPSNLVKEQRVYQEATKEIPTTDIDFFCE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                   Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 76.8%; Score 519; DB 22; I Similarity 90.5%; Pred. No. 2.3e-55; 95; Conservative 6; Mismatches 4
                                                                                                                                                                     Arterburn MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat MLP protein sequence SEQ ID NO:39.
                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 117; 119pp; English
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                                                                                                                                                                       Ford JE,
                                                         25-JAN-2001; 2001WO-US02455.
                                                                                     25-JAN-2000; 2000US-0491404.02-MAY-2000; 2000US-0563786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity
                                                                                                                                                                                                                           WPI; 2001-483233/52.
                                                                                                                                                                         Boyle BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 AA;
                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                         N-PSDB; AAH26343.
                                                                                                                                                             Mize NK, Bu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-2001
                        02-AUG-2001
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                                                                                                                                                                                                                                                                                                                             disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB69129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKLSSKKLCADEECVYTISLARAQEDYNAPDCRFINVKKGQQIYVYSKLVTENGAGAFWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 DKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic anglogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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Pred. No. 6.5e-47;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSVYGDHQDEMGIVGYFPSNLVKEQRV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 9; Page 103; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Melanoma inhibiting protein (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR69811 standard; Protein; 131 AA.
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96.6%;
                                                                                                                                                                                                                                                                                                                                                     29-JUN-2000; 2000WO-JP04278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TAKE ) TAKEDA CHEM IND LTD.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 CRFLTIHRGQVVYVFSKL---KGRGRLFWGGSVQGDYXGDLAARLGYFPSSIVREDQTLK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This protein has melanoma-inhibiting activity and can be used to treat cancer (melanoma, glioblastoma, neuroblastoma, small cell lung cancer, neuroectodermal tumours) or as an immunosuppressant (it inhibits IL-2 or phytohaemagglutinin induced proliferation of peripheral blood lymphocytes). Antibodies raised against the protein can be used to detect cell producing the protein and also for protein purification. Probes derived from DNA encoding the protein (AAQ84050, AAQ84051) can be used to detect sequences encoding the protein (conjugated protein may be expressed as a fusion protein (conjugated with dihydrofolate reductase (DHFR)). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MARILILLIGGLVVLC---AGHGVF---MDKLSSKKLCADEECVYTISLARAQEDYNAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIA; melanoma inhibiting activity protein; antiinflammatory; human; antiarthritic; antirheumatic; antithyroid; osteopathic; nephrotropic; immunosuppressive; ophthalmological; dermatological; antidiabetic; neuroprotective; immune tolerance; T-cell tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                               New melanoma inhibiting protein and related nucleic acid -
vectors, transformed cells, antibodies etc., useful for treating
tumours and as immunosuppressant e.g. by gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                   41.1%; Score 277.5; DB 16; Length 131; 43.4%; Pred. No. 1.1e-25; Live 29; Mismatches 35; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG65614 standard; Protein; 131 AA
                                                                                                        ä
                                                                                   (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                Claim 1; Page 54; 85pp; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 PGKVDVKTDKWDFYCQ 131
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                                     94WO-EP02369.
                                                            93DE-4324247
                                                                                                                                          N-PSDB; AAQ84050, AAQ84051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MIA protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 43.4
                                                                                                          Buettner R,
                                                                                                                                  WPI; 1995-075191/10.
                                                                                                                                                                                                                                                                                                                                                                                  131 AA;
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                                      19-JUL-1994;
                                                            20-JUL-1993;
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                 02-FEB-1995
                                                                                                          Bogdahn U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG65614;
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The invention relates to the use of melanoma inhibiting activity (MIA) protein and/or its fragments that have anti-inflammatory effects and induce systemic immune tolerance or specific T-cell tolerance to MIA antigen, for manufacturing a preparation against inflammatory diseases and for induction of systemic immune tolerance or specific T-cell tolerance in patients suffering from or susceptible to inflammatory diseases. A fragment of MIA is useful as a therapeutic substance and is useful for manufacture of pharmaceutical preparations against inflammatory diseases such as an immune-cell mediated carrilage destruction disease, specifically rheumatoid arthritis, autoimmune diseases like Graves' disease, juvenile arthritis, syndrome, glomerulonephritis, polyarthritis, osteoarthritis, Syndrome, whysthenia gravis, Addison's disease, primary boiliary sclerosis, uveitis, systemic lupus erythematosis, inflammatory bowel disease, multiple aclerosis or diabetes. The MIA polypeptides have specific ceffect on the autoreactive T-cells thus leaving the other components of the immune system intact as compared to the non-specific suppressive effect of immunesuppressive drugs. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 CRFIDVKKGQQIYVYSKLVTENGAGE-FWAGSVYGDHQDEMGI-VGYFPSNLVKEQRVYQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MARILILLIGGLVVLC---AGHGVF---MDKLSSKKLCADEECVYTISLARAQEDYNAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                               Use of melanoma inhibiting activity protein or its derivatives as immune modulatory agents for the treatment of inflammatory diseases, specifically rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.1%; Score 277.5; DB 22; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 1.1e-25; 29; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           completed: December 29, 2003, 16:09:02
ne : 25.098 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 34; 41pp; English.
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                                                                                                                                                 Verheijden GFM
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116 PGKVDVKTDKWDFYCQ 131
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23-MAR-2000; 2000EP-0201063.
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Best Local Similarity 43.4
Matches 59; Conservative
                                                                        (ALKU ) AKZO NOBEL NV
                                                                                                                                                                                                                      WPI; 2001-611446/70.
N-PSDB; AAH47783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human MIA protein.
                                                                                                                                                 Nelissen RLH,
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us-10-019-455a-12.rapb

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US-10-216-163-72
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                                                                                                                                                                                                                                                                                                                              1 MARILILLIGGLVVLCAGHG......RVYQEATKEIPTTDIDFFCE 128
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| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_MBW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_MBW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_MBW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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US-10-219-066-72
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US-10-219-073-72
US-10-219-475-72
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## ALIGNMENTS

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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Wood, Milliam I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC3
CURRENT APPLICATION NUMBER: US/10/216,163
FRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-0-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-12-17
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PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
Sequence 72, Application US/10216163; Publication No. US20030149239A1 GENERAL INFORMATION:
                                                                                                        APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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PRIOR FILING DATE: 1998-06-06

PRIOR PELICATION NUMBER: 60/08523

PRIOR APPLICATION NUMBER: 60/08523

PRIOR APPLICATION NUMBER: 60/08532

PRIOR APPLICATION NUMBER: 60/08532

PRIOR APPLICATION NUMBER: 60/08532

PRIOR APPLICATION NUMBER: 60/08538

PRIOR APPLICATION NUMBER: 60/08538

PRIOR APPLICATION NUMBER: 60/08905

PRIOR APPLICATION NUMBER: 60/080631

PRIOR APPLICATION NUMBER: 60/08063

PRIOR PLING DATE: 1998-06-13

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APPLICANT: Goddard, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Woodw William I.
APPLICANT: Woodw William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
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89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels (
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CURRENT PEDLICATION NUMBER: US/10/218,765
CURRENT FILING DATE: 2002-08-12
PRIOR FULING DATE: 2002-08-12
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-28
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PRIOR PELICATION NUMBER: 60/064103
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PRIOR APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/081955
FILING DATE: 1998-04-15
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Publication No. US20030187201A1
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APPLICANT: Goddard, Mairy
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J. Christopher
APPLICANT: Gurmaldi, J. Christopher
APPLICANT: Gurmaldi, J. Christopher
APPLICANT: Sinth, Yatoria
APPLICANT: Sinth, Yatoria
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: 2002-04-09
FRIOR PLING DATE: 1997-00-113
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PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PLING DATE: 1997-10-128
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PRIOR PLING DATE: 1997-10-129
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PRIOR APPLICATION NUMBER: 60/06987
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89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels ( PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR PILING DATE: 1999-11-09
PRIOR PILING DATE: 1999-11-16
PRIOR PILING DATE: 1999-11-16
PRIOR PILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07 ; Sequence 72, Application US/10219063; Publication No. US20030187202A1; GENERAL INFORMATION: APPLICATION NUMBER: 60/151733 Baker, Kevin P. Desnoyers, Luc Gerritsen, Mary 121 TDIDFFCE 128 121 TDIDFFCE 128 US-10-219-063-72 APPLICANT: APPLICANT: APPLICANT: d 셤 g à Š 8

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APPLICANT: GGGGWSKi, Paul J.
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APPLICANT: GITMAIdi, J. Christopher
APPLICANT: Gurmaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
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                                                   1 MARILILLIGGLVVLCAGHGVFMDKLSSKKLCADBECVYTISLARAQEDYNAPDCRFIDV
                                                                                         Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
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86.7%; Pred. No. 2.7e-64;
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Matches 111; Conservative
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   111; Conservative
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US-10-219-067-72
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PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILLING DATE: 1002-04-09

PRIOR FILLING DATE: 1997-09-17

PRIOR PELING DATE: 1997-10-17

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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Suith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
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APPLICANT: WOW, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Pred. No. 2.7e-64;
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CURRENT APPLICATION NUMBER: US/10/219,066
CURRENT FILING DATE: 2002-08-13
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APPLICANT: Baker, Kevin P.
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Matches 111; Conservative
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Gerritsen, Mary
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; ORGANISM: Homo Sapien
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                                                          TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-063-72
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| Sequence 72. Application No. US20030187206A1
| General No. US20030187206A1
| General No. US20030187206A1
| APPLICANT: Baker, Kevin P. APPLICANT: General, Audrey
| APPLICANT: General, Audrey
| APPLICANT: General, Audrey
| APPLICANT: General, Audrey
| APPLICANT: Grimaldi, J. Christopher
| APPLICANT: Grimaldi, J. Christopher
| APPLICANT: Septeman, Jean-Philippe F. APPLICANT: Stephan, Jean-Philippe F. APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: ACIDS ENCODING THE SAME
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SENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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| Sequence 72. Application US/10219068
| Publication No. US2003018725A1
| Sublication No. US2003018725A1
| Sublication No. US2003018725A1
| APPLICANT: Baker: Kevin P. APPLICANT: Geritsen, Mary
| APPLICANT: Geritsen, Mary
| APPLICANT: Godowski, Paul J. APPLICANT: Godowski, Paul J. APPLICANT: Godowski, Paul J. APPLICANT: Godowski, Paul J. APPLICANT: Godowski, Paul J. APPLICANT: Suith, Viccoin I. APPLICANT: Stephan, Jean-Philippe F. APPLICANT: Suith, Viccoin I. APPLICANT: Stephan, Jean-Philippe F. APPLICANT: Wacanabe, Colin L. APPLICANT: Wacanabe, Colin L. APPLICANT: Wacanabe, Colin L. APPLICANT: Wacanabe, Colin L. TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS BOOLOGY THE SAME
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| FRIOR PLILING DATE: 1097-014
| FRIOR APPLICATION NUMBER: 60/063849
| FRIOR FILING DATE: 1997-12-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 89.1
Best Local Similarity 86.7
Matches 111; Conservative
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ORGANISM: Homo Sapien
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APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
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APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SERRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILER REFERENCE: P3530PL49
CURRENT APPLICATION NUMBER: US/10/219,475
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/06213
PRIOR APPLICATION NUMBER: 60/06287
PRIOR FILING DATE: 1997-00-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/06973
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/07956
PRIOR APPLICATION NUMBER: 60/07956
PRIOR APPLICATION NUMBER: 60/07965
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PRIOR APPLICATION NUMBER: 60/07965
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/07965
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APPLICANT: Goddard, Audrey,
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Srephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: WATANAWEWBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC38
CURRENT APPLICATION NUMBER: US/10/219, 480
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Best Local Similarity 86.7%
Matches 111; Conservative
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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ORGANISM: Homo Sapien
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APPLICAMT: Stephan, Jean-Philippe F.
APPLICAMT: Watanabe, Colin L.
APPLICAMT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSKEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TILLS OF INVENTION NUMBER: US/10/219,073
CURRENT APPLICATION NUMBER: US/119,480
PRIOR PILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR PELICATION NUMBER: 60/063249
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-12-17
PRIOR PELICATION NUMBER: 60/06973
PRIOR FILING DATE: 1997-12-17
PRIOR PELICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-26
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Publication No. US20030187208A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
                                                       Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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US-10-219-073-72
                               Gerritsen,
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APPLICANT:
APPLICANT:
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaidi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victorin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Mood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDE ENCODING THE SAME
FILE REPERENCE: P3330PLG3
CURRENT APPLICATION NUMBER: US/10/219,483
CURRENT APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-01-17
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Pred. No. 2.7e-64;
9; Mismatches 8; Indels (
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PRIOR PILING DATE: 2002-04-09
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PRIOR FILING DATE: 1997-10-17
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PRIOR PILING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-26
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Gerritsen, Mary
Goddard, Audrey
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Best Local Similarity 86.7
Matches 111; Conservative
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; ORGANISM: Homo Sapien
US-10-219-480-72
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| PRIOR FILING NATE: 1997-10-28
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APPLICANT: Geddard, Audrey
APPLICANT: Geddard, Audrey
APPLICANT: Geddard, Audrey
APPLICANT: Geddard, To Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: WATANAMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT FILING DATE: 2002-08-14
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SEQ ID NO 72
Remaining Prior Application data removed - See File Wrapper or PALM. WUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
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Pred. No. 2.7e-64;
9; Mismatches 8; Indels
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                                                                                                                                                                                                                                     Query Match 89.1%;
Best Local Similarity 86.7%;
Matches 111; Conservative 5
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TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-530-72
                                                                                                                               TYPE: PRT
ORGANISM: Homo Sapien
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APPLICANT: BAREI, Nevill F.
APPLICANT: Godwaki, Paul J.
APPLICANT: Godwaki, Paul J.
APPLICANT: Godwaki, Paul J.
APPLICANT: Godwaki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
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APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: MATANABA: Colin L.
APPLICANT: MATANABA: Colin L.
APPLICANT: MATANABA: L970-10-17
APPLICANT: MATANABA: L970-10-17
APPLICANTON NUMBER: L070-09-17
PRIOR PELING DATE: 1997-10-28
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PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
SEQ ID NOS: 246
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Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8;
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Publication No. US20030187212A1
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ORGANISM: Homo Sapien
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| GENERAL INFORMATION:
| APPLICANT: Baker, Kevin P. |
| APPLICANT: Baker, Kevin P. |
| APPLICANT: Geritsen, Mary |
| APPLICANT: Goddard, Audrey |
| APPLICANT: Goddard, Audrey |
| APPLICANT: Goddard, Audrey |
| APPLICANT: Goddard, Audrey |
| APPLICANT: Goddard, Audrey |
| APPLICANT: Goddard, Audrey |
| APPLICANT: Goddard, Audren |
| APPLICANT: Smith, Viccorabilippe F. |
| APPLICANT: Smith, Viccorabilippe F. |
| APPLICANT: Weach, Marin, Den-Philippe F. |
| APPLICANT: Weach, Millian |
| APPLICANT: Weach, Millian |
| APPLICANT: Weach, Millian |
| APPLICANT: Weach, Millian |
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| APPLICANT: Weach, Millian |
| APPLICANT: Weach, Millian |
| APPLICANT: Weach, Millian |
| TITLE OF INVENTION: ACIDS ENCODING THE SAME |
| FILE REFERENCE: P3530PLG6 |
| CURRENT PHILNG DATE: 2002-06-14 |
| PRIOR PILING DATE: 2002-06-14 |
| PRIOR APPLICATION NUMBER: 60/06287 |
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| PRIOR PILING DATE: 1998-03-26 |
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| PRIOR PILING DATE: 1998-03-26 |
| PRIOR APPLICATION NUMBER: 60/079294 |
| PRIOR PILING DATE: 1998-03-26 |
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89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels (
Query Match

89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels
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; ORGANISM: Homo Sapien
US-10-219-531-72
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194, App
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                                                     December 29, 2003, 16:03:18; Search time 9.32213 Seconds (without alignments) 580.961 Million cell updates/sec
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Sequence 4, A
Sequence 4, A
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(c) 1993 - 2003 Compugen Ltd
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US-08-491-861A-89
US-09-374-671A-89
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Match Length
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Sequence 118, Appl
Sequence 118, Appl
Sequence 118, Appl
Sequence 118, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35; Indels 13;
         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 131;
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
COUNTRY: USA
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: 1BM PS/2-
OPERATION SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
FILING DATE: 29-July-1994
CLASSIFICATION: 435
                     US-09-562-737-6
US-09-862-737-6
US-09-830-217-16
US-09-830-217-16
US-09-252-991A-18644
US-08-630-915A-125
US-08-630-915A-219
US-08-630-915A-217
US-08-630-915A-17
US-08-630-915A-17
US-08-630-915A-17
US-08-630-915A-198
US-08-996-639-15
US-08-996-139-15
US-09-915A-15
US-09-915A-15
US-09-915A-15
US-09-915A-15
US-09-915A-15
US-09-915A-15
US-09-915A-15
US-09-915A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATE:
APPLICATION NUMBER: DE P 43 24 247.2
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-Unly-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: BOER 1035-PFF/ALT
RELECOMMUNICATION INFORMATION:
TELEPAX: (212) 689-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRACATERISTICS:
LENGYTH: 131 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 43.4%; Pred. No. 2.5e-27;
Matches 59; Conservative 29; Mismatches 35
US-08-630-915A-136
US-08-630-915A-210
                                                                                                                                                                                                      US-09-577-800-15
US-09-466-496-15
                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/08578649
; Patent No. 5770366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
  linear
   TYPE: ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-578-649-2
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US-07-646-537B-2
; Sequence 2, Application US/07646537B
; Patent No. 5348864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 GQVVYVFSKL---KGRGRLFWGGSVQGGYYGDLAARLGYFPSSIVREDLNSKPGKIDMKT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 VLLGIVVLSVFSGPSRADRAMPKLADWKLCADEECSHPISMAVALQDYVAPDCRFLTIYR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 LLGGLVVLCAGHGV-----FMDKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKK 62
                                             55 CRFIDVKKGQQIYVYSKLVTENGAGE-FWAGSVYGDHQDEMGI-VGYFPSNLVKEQRVYQ 112
                                                                 1 MARSLVCL--GVIILLSAFSGPGVRGGPMPKLADRKLCADQECSHPISMAVALQDYMAPD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.5%; Score 247; DB 1; Length 130; ilarity 43.0%; Pred. No. 1.8e-23; Conservative 23; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-5/July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/ACENT INFORMATION:
NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31,575
REFENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELECHOME: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE (ATRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inch 1.44 Mb storage diskette
                                                                                                                                                                                                                                                       Sequence 5, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brightte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                             113 EATKEIPTTDIDFFCE 128
                                                                                                                                                       :: | ||:|:
116 PGKVDVKTDKWDFYCQ 131
                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Felfe & Lynch
805 Third Avenue
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PS/2
COMPUTER: PC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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|123 DQWDFYCQ 130
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Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-578-649-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                   RESULT 2
US-08-578-649-5
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RESULT 3

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44 ARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSN
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Factor No. 6381014
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Wang, Yinxiang
TITLE OF INVENTION: BR3-Containing Protein, DNA and Uses Thereof
FILE REFERENCE: D62210IP
GURRENT APPLICATION NUMBER: US/09/346,510B
CURRENT FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 08/871,732
FRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 21
LENGTH: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: Domain
; OTHER INFORMATION: amino acid sequence of Vav SH3 domain
US-09-346-510B-21
                                                                                                                                      CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/646,537B
GENERAL INFORMATION:
APPLICANT: Barbacid, Mariano
TITLE OF INVENTION: Vav Proto-Oncogene Protein
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches
                                                                                                      ADDRESSEE: Bristol-Myers Squibb Company STREET: P.O. Box 4000
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GRAU!, TIMOCHY J.
REGISTRATION NUMBER: 33,111
REFERENCE/POCKET NUMBER: DC10
TELECOMMUNICATION INFORMATION:
TELEFAM: (609) 921-5901
TELEFAM: (609) 921-5901
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 844 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 32.9
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 LVKEQRVYQF 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: unknown
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-583-799-4
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                                                                                                           46 AQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSNLV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 LSSKKLCADEECVYTISLARAQEDYNAP----DCRFIDVKKGQQIYVYSKLVTENGAGE 80
                                                                                                                                         RESULT 5
US-09-356-952-4
US-09-356-952-4
US-09-356-952-4

Sequence 4, Application US/09356952

Patent No. 6117663.
GENERAL INFORMATION:
APPLICANT: Bor-2691, Dafna
APPLICANT: Bor-2691, Dafna
APPLICANT: Bor-2691, Dafna
APPLICANT: Cole, Philip
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION OF USE US/09/356,952
CURRENT FILING DATE: 1999-07-19
EARLIER FILING DATE: 1999-07-19
EARLIER FILING DATE: 1999-07-21
SOUTHWARE: PATENTIN UNDER: 60/093,631
SOUTHWARE: PATENTIN UNDER: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 LSSSPSTSELTSIRPIGIVVAAYDFNYPIKKDSSSQLLSVQQGETIYILNK----NSSG-
                                                                   11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
11.6%; Score 78.5; DB 3; Length 1589;
Best Local Similarity 27.0%; Pred. No. 1.5;
Matches 24; Conservative 18; Mismatches 36; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: NAGASE, KAZUO
APPLICANT: NATSUI, HROSHI
ITILE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: PROM FISH
                         DB 3; Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: virginia
COUNTRY: u.S.A.
ZIP: 22202
                                                                   18; Indels
                       ;; Score 82.5; DB 3;
;; Pred. No. 0.0035;
13; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 FWAGSVYGDHQDEMGIVGYFPSNLVKEOR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 WWDGLVIDDSNGKVN-RGWFPQNFGRPLR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08164839
Patent No. 514573
GENERAL INPORMATION:
APPLICANT: YASUEDA, HISASHI
                           12.2%;
                       Query Match
Best Local Similarity 32.3%
Matches 20; Conservative
                                                                                                                                                                                                        106 KE 107
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50 EE 51
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LENGTH: 1589
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392 EVNADTIYWIVQKDGQR-----RKITEDHASVGKNISTKSVYGNHREDVTLHYKYPEGSQ 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 11.4%; Score 77; DB 1; Length 694; Best Local Similarity 27.5%; Pred. No. 0.69; Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: NAGASI, KAZUO
APPLICANT: NAGASI, KAZUO
APPLICANT: NAGASI, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSCLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
ATREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE:
CLASSIFICATION *435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
                                                                                                                                                                                                                                                                                                                                                                           10-599-0
                                                                                                                                                    PILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECHOMUNICATION INFORMATION:
TELECHONE: (703)412-3000
TELEFAX: (703)412-3000
TELEFAX: (703)413-2220
TELEFAX: (703)413-2220
TELEFAX: (703)413-2220
TELEFAX: (703)413-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 KEQRVYQEATKEI--PTTDI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447 KEREVYKKAGRRVTEPSNEI 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08583799; Patent No. 5607849; GENERAL INFORMATION:
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 694 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-164-839-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Arlington STATE: Virginia
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49 DYNAPDCRFIDVKKGQQIYVYSKLVTENGAG---EFWAGSVYGDHQDEMGIVGYFPSNLV 105
                                                                                                                                                                                                                                                                                     106 KEQRVYQEATKEI--PTTDI 123
                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION
TELEPHONE: (703)412-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 695 amino acids
TYPE: amino acid
TOPOLOGY: linear
: 695 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (703)413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248855 OPT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-08-583-799-6
                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-08-583-799-6
                                                                     ;
US-08-164-839-6
LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.4%; Score 77; DB 1; Length 694; 27.5%; Pred. No. 0.69; Live 20; Mismatches 28; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        us-uw-164-839-6

Sequence 6, Application US/08164839

Patent No. 5514573

GENERAL INFORMATION:

APPLICANT: YASUEDA, HISASHI
APPLICANT: NACANISHI, KAZUO
APPLICANT: NACASE, KAZUO
APPLICANT: NACASE, KAZUO
APPLICANT: NACASE, KAZUO
APPLICANT: NACASE, KAZUO
APPLICANT: NACASE, KAZUO
APPLICANT: NACASE, KAZUO
APPLICANT: NACASE, KAZUO
APPLICANT: NACHOUN
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: 1.22.02
2IP: 22.202
ZIP: 22.202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATA PC-TOOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
                                             NAME: Oblon, No. 5607849man F.
REGISTRATION NUMBER: 24,618
REGISTRANICHOCKET NUMBER: 10-599-0
TELEPHONE: (703)412-3000
TELEPHONE: (703)412-3000
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||: ||::| : : | : :| 447 KEREVYKKAGRRVTEPSNEI 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 KEQRVYQEATKEI--PTTDI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703)412-3000
TELEFAX: (703)413-222
TELEX: 248855 OPPT UR
INFORMATION FOR SEQ ID NO: 6:
            14-JAN-1993
               FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5607849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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Best Local Similarity 27.5
Matches 22; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-583-799-4
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US-08-164-839-6
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49 DYNAPDCRFIDVKKGQQIYVYSKLVTENGAG---EFWAGSVYGDHQDEMGIVGYFPSNLV 105
                                                                                                                                                          393 EVNADTIYWIVQXDGQR-----RKITEDHASVGKNISTXSVYGNHREDVTLHYKYPEGSQ 447
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Query Match 11.4%; Score 77; DB 1; Length 695; Best Local Similarity 27.5%; Pred. No. 0.69; Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-US-SSI-79-5
; Sequence 6, Application US/08583799
; Patent No. 5607849
; Patent No. 5607849
; GENERAL INFORMATION;
APPLICANT: YASUBDA, HISASHI
APPLICANT: NACOKI, MASAO
; APPLICANT: NAGASE, KAZUO
; APPLICANT: NAGASE, KAZUO
; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
; TITLE OF INVENTION: FROM FISH
; TITLE OF INVENTION: FROM FISH
; NUMBER OF SEQUENCES: 72
; CORRESPEDIDENCE ADDRESSE:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STEERT: 1155 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,799
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CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-ZAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5607849man F.
REGISTRATION NUMBER: 24,618
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JS-09-328-352-4886
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; Sequence 194, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: KAY, Brian K.
APPLICANT: RAY, Brian K.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
ADDRESSE: Pennie & Edmonds LLP
CITY: New York

CITY: New York

CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
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393 EVNADTIYWIVQKDGQR----RKITEDHASVGRNISTKSVYGNHREDVTLHYKYPEGSQ 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 NGAGEFWAGSVYGDHQDEMGIVGYFPSNLV--KEQRVYQEATK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 KD-GEWWTGSI-GDRS-----GIFPSNYVKPKDQESFGSASK 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 GHGVFMDKLSSKKLCA----DEECVYT----ISLARAQEDY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A FILING DATE: 03-APR-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.1%; Score 75; DB 4
22.1%; Pred. No. 0.8;
ive 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: FIR PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                 106 KEORVYQEATKEI--PTTDI 123
                                                                                      ||:||:||:|
448 KEREVYKKAGRRVTEPSNEI 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 509 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 22.1[†]
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
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                                                                                                                                                                         RESULT 10
US-08-630-915A-194
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RESULT 11

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Sequence 4886, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BADMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KK---GQQIYV---YSKLVTENGAGEFWAGSVYGD-----HQDEMGIVGY--FPSNLV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     791 GEPLANTÓLÝVLDEQORLÝPPGVMGELWIG---GDGLAVDÝWHRPELTDAOFRTLPS-LP 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 DYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPSNLV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: amino acid sequence of Vav SH3 domain at position 2 OTHER INFORMATION: through position 49 of SEQ ID No. 6281014 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SLARAQEDYNAPDCRFIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24, Application US/09346510B

Sequence 24, Application US/09346510B

Sequence No. 6231014

GENERAL INFORMATION:

SEQUENCE NO. 6231019

TITLE OF INVENTION:

SH3-Containing Protein, DNA and Uses Thereof

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/346,510B

CURRENT FILING DATE: 1999-07-01

PRIOR APPLICATION NUMBER: 08/871,732

PRIOR APPLICATION NUMBER: 08/871,732

PRIOR FILING DATE: 1997-06-09

NUMBER OF SEQ ID NOS: 32

SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                  11.0%; Score 74.5; DB 4; Length 1326; 26.3%; Pred. No. 3.7; ive 17; Mismatches 47; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.9%; Score 73.5; DB 3; Length 48; 31.6%; Pred. No. 0.041; ive 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 GLVVLCAGHGVFMDKLSSKKLCADEECVYTI----
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US-08-630-915A-40
Sequence 40, Application US/08630915A
Patent No. 6309820
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 KEORVYOEATKEIPTTD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                847 NAGRLYRTGDKVCLRTD 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Domain
LOCATION: 2...49
                                                                                                                                                                                                                                                                                                                                                                                          US-09-328-352-4886
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                                                                                                                                                                                                                                                                                                                    LENGTH: 1326
                                                                                                                                                                                                                                                                                            SEQ ID NO 4886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 48
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US-08-164-839-31
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                                                                                   APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: MCCONNELL Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 BGEEILVTQK-----DGEWWTGSI-GDRS-----GIFPSNYVKPKDQESFGSASK 103
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10.6%; Score 71.5; DB 4; Length 248;
Best Local Similarity 36.8%; Pred. No. 0.78;
Matches 21; Conservative 8; Mismatches 13; Indels 11
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARIN PC-DOS/MS-DOS
SOFTWARIN APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MS:TOCK, S. Leelie
REGISTRATION NUMBER: 1101-174
REBERBNCE/DOCKET NUMBER: 1101-174
TELEFHONE: (212) 790-9090
TELEFAX: (212) 869-8664/9741
TELEFAX: (512) 790-9090
TELEFAX: (512) 869-8644/9741
TELEFAX: (512) 869-8644/9741
TELEFAX: (512) 880-8664/9741
TELEX: 541 PERNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: ATRANBEDNESS:
STRANBEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
SPAKKS, Andrew B.
HOPFWAN, No. 6309820h
KAY, Brian K.
FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22202
COMPUTER READABLE FORM:
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
COUNTRY: USA
ZIP: 10036-2711
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356 ELSDGEYCCGPCPVTAIKEGNLSVKYDAP---FIFAEVNADIIYWWAGPGGERKKIDVDQ 412
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10.6%; Score 71.5; DB 1; Length 687;
Best Local Similarity 26.0%; Pred. No. 3.4;
Matches 27; Conservative 19; Mismatches 45; Indels 13
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APPLICANT: NAKANISHI, KAZUO
APPLICANT: NAGASE, MASAO
APPLICANT: NAGASE, MASAO
APPLICANT: NAGASE, MASAO
APPLICANT: NAGASE, MASAO
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
OWNBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
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STREET: 1755 Jefferson Davis Highway, Fourth Floor
STREET: Arlington
STATE: Virginia
COUNTRY: U.S.A.
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
COMPUTER: IBW PC Compatible
SOFTWARE Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE: CLASSIFICATION THE APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAM-1993
ATTONINY AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFRENCE/POCKET NUMBER: 24,618
REGISTRATION NUMBER: 22,00
TELEPHONE: (703)412-3200
TELEPAK: (703)412-3200
TELEPAK: (703)412-3200
TELEXA: (703)412-3200
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APPLICATION NUMBER: US/08/164,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/08164839; Patent No. 5514573; GENBRAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 687 amino acids
amino acid
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MEDIUM TYPE: Floppy
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US-08-164-839-33
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| ATTORNEY/AGENT INFORMATION:
| NAME: Oblon, No. 5514573man F. |
| REGISTRATION NUBBER: 24,618 |
| REGISTRATION NUBBER: 10-599-0 |
| TELECOMMUNICATION INFORMATION: |
| TELECOMMUNICATION INFORMATION: |
| TELECOMMUNICATION INFORMATION: |
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TYPE:	TOROLOGY:	TELECOMMUNICATION:		
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Search completed: December 29, 2003, 16:11:50 Job time : 10.3221 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                           BD010805
BD093106
BAF243504
BD010821
BD093122
MMU243939
APC33333
BD010835
BD093136
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BX510362
HS705D16
BT007044
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HSA242552
BD010817
BD093118
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BD010830
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AF233518
BD010829
BD093130
AF233519
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AX362311
AX454774
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AF233261
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BD010816
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BD093103
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-D6Ggn2_1/USPTO spool/US10019455/runat_29122003_160347_240/app_query.fasta_1.1770
-Q=(Ggn2_1/USPTO spool/US10019455/runat_29122003_160347_240/app_query.fasta_1.1770
-Q=(Ggn2_1/USPTO spool/US10019455/runat_2012003_160347_1_LOOPEL-0-LEOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40.cdi -LIST=45
-DOCALIGN=00 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=ptc -NORM=ext -HEAPSIZE=560 -MINLEN=0 -NAXLEN=200000000
-USER=US10019455 @CGN 1 1 6034 @runat_29122003 160347_240 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGARPOF=10 -XGAPEXT=0.5 -FGAPOP=6
                                                                     December 29, 2003, 16:11:59; Search time 2106.98 Seconds (without alignments) 2485,278 Million cell updates/sec
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1 MARILILLLIGGLVVLCAGHG.....RVYQEATKEIPTTDIDFFCE
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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length: 2000000000
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BT007044 Homo sapi BT00775 Synthetic A42942 Sequence 1 AX016785 Sequence AXX872508 Sequence AXX87209 Sequence X75450 H. sapiens m

Rattus no Mus muscu Human DNA

AC106161 BX510362 AL034428 BC005910 Homo sapi AX253435 Sequence U67884 Rattus norv

us-10-019-455a-12.rge

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 384)
1 (to,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
Novel polypeptide and its DNA
1 Patent: MO 0102564-A 6 11-UAN-2001;
TAKEDA CHEMICAL INDUSTRIES LID; YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDBYURI TANARA
OS Mus sp. (mouse)
PN WO 0102564-A/6
PD 11-JAN-2000
PP 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 UP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
CIZNIS/12,C12NS/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A61K39/395,A61K49/16,A61P19/02,A61P19/08,A61K31/7088//(C12P21/
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Eukaryota; Metazoa; Chordata; Sciurognathi; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.
1 (bases 1 to 384)
2 Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H. Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H. A. 21-MAR-2001;
Patent: JP 2010169994-A 6 21-MAR-2001;
Phy JP 2001069994-A/6
Phy JP 2001069994-A/6
Phy 29-JUN-2000 JP 2000195911
Phy 29-JUN-2000 JP 2000195911
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YUKO NOGICHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
CI2N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
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C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC
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PR YASUBAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI,

PI VIKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

PI VIKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

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1 to, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H. Novel polypeptide and DNA thereof Patent: JP 2001069994-A 22 21-MAR-2001;
ValPheMetAspiysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
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                                                                                                                                      ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 929)
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Cohen-Salmon,M., Frenz,D., Verpy,E., Voegeling,S. and Petit,C.
Direct Submission
Submitted (09-Maz.2000) Biotechnologies, Institut Pasteur, 25 rue
du Dr. Roux, Paris 75015, France
Location/Qualifiers
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Cohen-Salmon,M., Frenz,D., Liu,W., Verpy,E., Voegeling,S. and
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J. Biol. Chem. 275 (51), 40036-40041 (2000)
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Mus musculus fibrocyte-derived F
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/gene="Fdp"
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/gene="Fdp"
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MANU243939

Mus musculus mRNA for melanoma inhibitory activity-like protein
(Mial gene).
AJ243939
AJ243939
AJ243939.1 GI:12619174
melanoma inhibitory activity-like protein; Mial gene.
Mus musculus (house mouse)
Mus musculus
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tommerup, N.
Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation Genomics 71 (1), 40-52 (2001)
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                                                                                                                                                                                                LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu
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Direct Submitted (20-UUL-1999) Rendtorff N.D., Department of Medical Submitted (20-UUL-1999) Rendtorff N.D., Department of Medical Genetics, Institute of Medical Biochemistry and Genetics, Blegdamsvej 3, 2200 Copenhagen N, DENMARK
Related sequence: Al742552.
Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

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I to,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,

Yoshimura, X. and Tanaka,H.

Novel polypeptide and its DNA

L. Patenti and Tanaka,H.

Aptenti wO 0102564-A 22 11-JJAN-2001;

TAKEDA CHENICAL INDUSTRIES LID; YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,

OS Mus sp. (mouse)

PN WO 0102564-A/22

PD 11-JAN-2000

PP 29-JUN-2000 WO 2000JP004278

PR 30-JUN-1999 JP 99P 186718

PI XASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
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02,C12R1:19)
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C CI2N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00,
A61K38/17,
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Novel polypeptide and its DNA.
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BD093122.1 GI:22638710
WO 0102564-A/22.
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Denis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C.
A novel conserved cochlear gene, OTOR: identification, expression
analysis, and chromosomal mapping
AL Genomics 66 (3), 242-248 (2000)

BE 20334619
ED 10873378
ED 2 (bases I to 1054)
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/note="OTOR"
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                                                                                                                                                                                                                                                                                                                      /codon_start=1
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/facaslation="max1:LILLGGLVVTCAGHGFWAGSYYGDHQDEMGIVGYFPS
/RACDFYNAPDCRFIPTDIDFFCE"
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enmanalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1054)
Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S.,
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/gene="Mial"
23. .81
/gene="Mial"
24. .410
/gene="Mial"</pre>
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/gene="Mial"
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TLO,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
Novel polygeptide and its DNA
Novel polygeptide and its DNA
Patent: WO 0102564-A. 36 Il-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD,YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO
GGI, SHOICHI OKUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,
HIDEYUKI TANAKA
OS RATLUS SP. (rat)
PN WO 0102564-A/36
PN HIDEYUKI TANAKA
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29-JUN-2000 WO 2000JP004278
30-JUN-1999 JP 99P 186718
YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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YURO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
CI2N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00,
A61K38/17,
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/organism="Rattus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10118"
a 72 c 109 g 105
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                                                                             384 by Novel polypeptide and its DNA. BD093136
361 ACGGATATTGACTTCTTCTGTGAA 384
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WO 0102564-A/36.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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I (bases 1 to 384)
Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S. Yoshimura,K. and Tanaka,H.
Novel polypeptide and DNA thereof
Patent: JP 2001069994-A. 36 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Rattus sp. (rat)
PN JP 2001069994-A/36
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR
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Location/Qualifiers
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/mol_type="genomic DNA"
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PI YASUAKI ITO, KAZUNORI NISDAJJOS.

PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

PC CIZNIS, 09, A61K38/00, A61K48/00, A61P9/00, A61P39/00, PC
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I (bases 1 to 894)

Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.

Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 3 21-MAR-2001;

TAKEDA CHEMICAL INDUSTRIES LTD
OS Homo sapiens (human)
PN 2001069994-A/3

PD 201069994-A/3

PP 29-JUN-2000 JP 2000195911
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Novel polypeptide and DNA thereof.
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/mol_type="genomic DNA"
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Homo sapiens (human)
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29-JUN-2000 WO 2000JP004278
30-JUN-1999 JP 99P 186718
YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
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C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61X38/17,
A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088//(C12P21/02, C12R1:19)
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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| Qy         61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGlubsnGlyAlaGlyAlaGlyGlu         80           218 AAAAAGGGGAGATCTATGTATGTACTCAAAGCTGGAAAAAGAAAATGGACTGGAGAA         277           Qy         81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100           Db         278 TTTGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGAGTTGTTTTC 337           Cy         101 ProSerAsnLeuValLyGluGlATGGCCAGGACGAGACGGAGTGGGGTTATTTC 337           Db         338 CCCAGGAACTTGGTGATGGCCAGGACGAGACGAGATGCGAGGATTGCTATTTC CAGGAAGTTCCCACC 397           Cy         121 ThrAspIleAspPhePeCysGlu 128           Cy         121 ThrAspIleAspPhePeCysGlu 128           Cy         121 ThrAspIleAspPheCysGlu 128 | 13  AX362311  AX362311  AX362311  AX362311. G1:18694613  S Homo sapiens (human)  ISM Homo sapiens  Homo sapiens  Evkaryota; Metazoa; Chordata; Craniata; Vertebrata;  Rukaryota; Metazoa; Chordata; Craniata; Vertebrata;  Evkaryota; Metazoa; Coddard, A.  Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Watanabe, C.K. and Wood, W.I.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   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                                                                                                                                                                                                                                              | 10-019-455A-12 (1-128) x AX362311 (1-521)    MetalaarglleLeulleLeuLeuGlyGlyLeuValValLeuCysAladlyHisGly                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   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| 21   ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr   40                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 301<br>301<br>121<br>361<br>361<br>35818<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>80101<br>8010 | NOUNCE Homo sapiens (human)  ORGANISM Homo sapiens  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.  Nammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE Baker K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Matanabe, C.K. and Wood, W.I.  TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same JOURNAL Genetic Noulifiers  JOURNAL Genetic Noulifiers  Location/Qualifiers  JOURNAL HOMO Sapiens"  And Lype="Genomic DNA"  Mol_type="Genomic DNA"  Abbare COUNT 167 a 86 c 131 g 137 t  ORIGIN | Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Sect | Db 158 ATTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT 217 |

| Db 338 CCCAGGAACTGGTCAAGGAACAGGAAGCTGCCAAGGAAGCTACCAACGAAGTTCCCACC 397  Qy 121 ThrAspileAspPhePheCysGlu 128  Db 398 AcGATATTGACTTCTTCTGCGAG 421  RESULT 15  AX491252  LOCUS  DEFINATION Sequence 359 from Patent WO0200690.  ACGESSION AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491252  AX491 | Pred                                                                                       |
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| 101 ProSerA. 338 CCCAGGAA. 121 ThrASDI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | FEATURES  1.0.51    Corganism="Homo sapiens"     And and and and and and and and and and a |

Search completed: December 29, 2003, 19:57:16 Job time : 2108.98 secs

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Command line parameters:
-MODBL=frame+ pan.model -DEV=xlh
-Q=/Cgn2 1/USPTO_spool/US10019455/runat_29122003_160347_254/app_query.fasta_1.1770
-Q=/Cgn2 1/USPTO_spool/US10019455/runat_29122003_160347_254/app_query.fasta_1.1770
-Q=/Cgn2 1/USPTO_spool/US10019455/runat_29122003_160347_254/app_query.fasta_1.1770
-UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human-40.cdi -LIST=45
-UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human-40.cdi -LIST=45
-UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human-40.cdi -LIST=45
-UNITS=bits -STRAT=1 -END=-1 -MAX-LEN=200000000
-USER=US10019455_@CGN 1 1 6063_@runat_29122003_160347_254 -NCPU=6 -ICFU=3
-NO MAAP -LARGRQUERY -NEG_SCORES=0 -WAIT -DSPBIOCK=100 -LONGLOG
-EDV TINEOUT=120 -WARN TIMEOUT=30 -TRANS=LAND-10 -XGAPEXT=0.5 -FGAPOP=6
                                                                                                          December 29, 2003, 16:23:14; Search time 1324.28 Seconds (without alignments) 2349.180 Million cell updates/sec
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1 MARILILLLGGLVVLCAGHG......RVYQEATKEIPTTDIDFFCE 128
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version 5.1.6
- 2003 Compugen Ltd.
                                                                        OM protein - nucleic search, using frame_plus_p2n model
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Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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## 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description     | BQ570035 gil43 | BQ564607 gi19h02.y | BQ568498 gil09c02. | BQ564134 gilluut.y | RO564944 gi27g09.v | BOS68471 qi108q04. | BB611549 BB611549 | BQ565637 gi42g03.y | BQ563768 gi06c09.y | BQ566932 gi73g09.y | BQ565411 g137b12.y | BY232622 BX232622<br>BOSS2343 A100409 X | DEDOCATE GLOCOCO | BE235443 144545 MA<br>ROSER785 Gill4F04 | B0565179 0132907.v | RI748241 CH3#018 G | AK047965 Mus muscu | BOS63227 qi01a05.y | AL925854 AL925854 | BQS66776 gi69b07.y | BB647928 BB647928 | BU195892 AGENCOURT | BM715936 UI-E-EJO- | BM856478 K-EST0140 | 1250      | BQ892734 AGENCOURT | œ.        | BU157778 AGENCOURT | 961       | 67 K-ESI  | 328       | 65502 60273941 | 33401 UI-H- | df53d01. | 7297 nq68g01. | 509768 UI-R-FS | 665724 154861 | 647 zd   | D360404 AGENCOU | 275598 qm48a04 | 2569268 gil25al | 592759 AV592759 | 821 <b>4</b> 3 zt02b0 |
|-----------------|----------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-----------------------------------------|------------------|-----------------------------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-----------|--------------------|-----------|--------------------|-----------|-----------|-----------|----------------|-------------|----------|---------------|----------------|---------------|----------|-----------------|----------------|-----------------|-----------------|-----------------------|
| ΩI              | 3 BQ57003      | 3 BQ56460          | 3 BQ5684           | 3 BQ56413          | 3 BQ56974          | 2 BOSE847          | BB61154           | 3 BQ56563          | 3 BQ56376          | 3 BQ56693          | 3 BQ56541          | 3 BY23262                               | 3 BQ36/34        | 4ª L                                    | ביושטבעם נ         | 3 BTT74874         | 1 AK04796          | 3 BOS6322          | AL925854          | BQ56677            | 0 BB64792         | 3 BU19589          | 2 BM71             | BM85647            | 2 BM67425 | 3 BQ89273          | 3 BQ68197 | 3 BU15777          | 3 BU19456 | 2 BM79176 | 2 BG76632 | BG7655         | 4 CA43340   | AW02332  | AA627297      | 4 CAS097       | 0 BE6657      | 4 W74647 | 4 CD3604        | AI275598       | 3 BQ5           | 59275           | AA28214               |
| ry<br>ch Length | .0 398         | 0 488              | 0 514              | 534                | 000                | 000                | 969               | 3 474              | 0 684              | 6 409              | 4 490              | 365                                     | 9                | 2.3 527                                 | 4 c                | 70                 | 200                | , ,                | . 10              |                    | 2.                | 2.                 | .1                 | 1.                 | 1 5       | .1                 | .1        | .1                 | .1        | .1        | .1 8      | .1 11          | 6.          | .8       | .6            | 9.             | .5            | .4       | .4              | e.             | .9              | o.<br>4.        | ο.                    |
| core            | 76 10          | 76 10              | 76 10              | 76 10              | 107                | 97                 | 76 10             | 71 9               | 6 69               | 46 9               | 11 9               | 85                                      | 66               | 489 72                                  | ) O                | 441                | 0.11               | 0.47               | ıuı               | 366 5              | 59.5              | 78.5 4             | .5                 | 77.5 4             | 77.5 4    | 77.5 4             | 77.5 4    | 77.5 4             | 77.5 4    | 77.5 4    | 77.5 4    | 77.5 4         | 70          | 69       | 68            | 68             | 67            | 66.5     | rJ.             | 65.5           | ""              | 63              | 63                    |
| Result<br>No.   | -              | 7                  | м                  | 41                 | <b>л</b> ч         | 0 1                | ~ 00              | 0                  | 10                 | 11                 | 12                 | 13                                      | 14               | 15                                      | 9 [                | , r                | 0 0                |                    | 21                | 22                 | 23                | 24                 | 25                 | 26                 | c 27      | 28                 | 29        | 30                 | 31        | 32        | 33        | 34             | c 35        | 36       |               | c 38           | 39            | c 40     | 41              | c 42           | 43              | c 44            |                       |

## ALIGNMENTS

| RESULT 1<br>BQ570035 |                                                                     |
|----------------------|---------------------------------------------------------------------|
| LOCUS                | BQ570035 398 bp mRNA linear EST 19-JUN-2002                         |
| DEFINITION           | gi143b10.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA |
|                      | clone gi143b10 5', mRNA sequence.                                   |
| ACCESSION            | BQ570035                                                            |
| VERSION              | BQS70035.1 GI:21473352                                              |
| KEYWORDS             | BST.                                                                |
| SOURCE               | Mus musculus (house mouse)                                          |
| ORGANISM             | Mus musculus                                                        |
|                      | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |
|                      | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  |
| REFERENCE            | 1 (bases 1 to 398)                                                  |

AUTHORS TITLE JOURNAL

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BQ564607 488 bp mRNA linear EST 19-JUN-2002 gi19h02.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi19h02 5', mRNA sequence.
city, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PheTrpalaGlySerValTyrGlyAspHisGlnAspGluMetGly1leValGlyTyrPhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
                                                                                                                                                                                                                                                                                                                                            252
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
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                                                                                                                                                                                                                                                                                                  13 AIGGCAAGGAIATHGAITCTITIGCTIGGGGCCTIGIGGIICIAITHHHHHHHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                       41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal
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Matches:
Conservative:
Mismatches:
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Plate: 19 row: h column: 02
Seg primer: M13RP1 reverse primer (ABI).
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Fax: 301-402-1765
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Indels:

Best Local Similarity: 100.00% Query Match:

Query Match:

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//elone lib="Mouse Organ of Corti (cDNA pBluescript" The
//clone lib="Mouse Organ of Corti; Order of the cotal of 386
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                                                                                                                                                     db xref="taxon:10090"
clone="gi19h02"
Socation/Qualifiers
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488 128 0

Conservative:

2.02e-81 676.00 100.00%

Percent Similarity:

Scores:

ORIGIN

Pred. No.: Alignment

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organ of Corti (CC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
                                                                                                                       21 ValPheMetAspLysLeuSerSerLysLysLysLeuCysAlaAspGluGluCysValTyrThr
                                     1 MetalaargileLeulleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly
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Plate: 109 row: column: 02
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers

    .514
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1 MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 514 000 000 000 Length: Matches: Conservative: Mismatches: Indels: US-10-019-455A-12 (1-128) x BQ568498 (1-514) 2.18e-81 676.00 100.00% 100.00% Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB: . No. . BASE COUNT ORIGIN Best ò g

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/db xxef="texcon:10090"
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organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P3. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibbowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro fastrace x instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
digapack III Gold Cloning kit (catalog # 237512), both 534 bp mRNA linear EST 19-JUN-2002 gilld01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA BQ564134 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100 EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing 125 ATTICICIGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 184 244 245 TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGGAATTGTAGGTTATTTC 304 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 534) Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50,4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1765 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 185 AAGAAAGGCAGCAGCTCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal Email: kacharb@nidcd.nih.gov Plate: 11 row: d column: 01 Seq primer: M13RP1 reverse primer (ABI). Location/Qualifiers .534
 /organism="Mus musculus" 121 ThrAspileAspPhePheCysGlu 128 365 Accentatricacricitarica 388 Mus musculus (house mouse) /mol\_type="mRNA" /strain="BALB/c" BQ564134.1 GI:21467451 Unpublished Kachar, B. 61 source DEFINITION ACCESSION VERSION KEYWORDS ORGANISM AUTHORS JOURNAL REFERENCE BQ564134 FEATURES TITLE SOURCE g 셤 ద ð g ò

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from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia vitus reverse transcriptase (MMLV-RN) and S-methyl dCTP. The second strand was synthesized with DNA polymerase and Khase H. Complementary DNA was blunt ended with PFU DNA polymerase, ligated with BcoR I adapters in the presence of ligase and digested with Xho I. The CDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for CDNAs greater than 400bp and 1000 bp., respectively. The CDNA was then directionally ligated to the Uni-ZAP KR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on Xil Blue WRF cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exhasist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA krom the phages. Upon plating of the components of the cDNA clones were generated with the the form 200 ul of saturated culture with the the stength BigDye terminator sequencing reactions were performed on MJ Tetrad thermal cyclers (WJ Research, Waltham, MA), and analyzed on 3700 automated application as follows: 72% of genes have I copy; 14:3% 2:12% 3:10; 14% 11-50 and oil% 5:12% 3:10; 14% 11-50 and oil% 5:12% and 23% and 23% are unidentified.

Sa RP7 C 148 g 144 t C DNA clone were selection; 45% of genes are present in GenBank and have susigned function; 45% of genes are present in GenBank and analyse on 3700 auchariacians and present in GenBank and analyse on 3700 auchariacians and 271% of genes are pre
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534 128 0 0 Conservative: Mismatches: Indels: Matches: 2.3e-81 676.00 100.00% 100.00% 155 Percent Similarity: Best Local Similarit Alignment Scores: BASE COUNT ORIGIN No.:

Similarity:

| Query Match:<br>DB: | . H   |            | 100.00%                                      | Indels:<br>Gaps: | 0                                                               |     |
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| US-10-019-          | -455A | 12 (1-128  | US-10-019-455A-12 (1-128) x BQ564134 (1-534) | 1-534)           |                                                                 |     |
| ò                   | ٦     | MetAlaArgI | [leLeuIleLeuLeu]                             | LeuGlyGlyLeuVal  | MetAlaArglleLeuIleLeuLeuCeuClyGlyLeuValValLeuCysAlaGlyHisGly    | 20  |
| DP                  | e     | ATGGCAAGGA | ATATTGATTCTTTTG                              | cricadaccricia   |                                                                 | 62  |
| ò                   | 21    | ValPheMetA | AspLysLeuSerSer                              | LysLysLeuCysAla  | ValPheMetAspLysLeùSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr    | 40  |
| DP                  | 63    | GTATTTATGG | BATAAACTTTCTTCT                              | aagaagttgtgtgcg  |                                                                 | 122 |
| ٥¾                  | 41    |            | AlaArgAlaGlnGluA                             | AspTyrAsnAlaPro  | IleSerLeuAlaArgAlaGluGluAspTyrAsnAlaProAspCysArgPheIleAspVal    | 09  |
| qa                  | 123   | ATTTCTCTG  | SCAAGAGCACAGGAA                              | GATTACAATGCCCCA  |                                                                 | 182 |
| ζ                   | 61    | LysLysGlyG | 3lnGlnIleTyrVal                              | TyrSerLysLeuVal  | 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu | 80  |
| QQ                  | 183   | AAGAAAGGG  | PAGCAGATCTATGTT                              | TACTCCAAGCTGGTA  |                                                                 | 242 |
| ò                   | 81    |            | 31ySerValTyrGly                              | AspHisGlnAspGlu  | PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe    | 100 |
| gg                  | 243   | TTTTGGGCTG | SGCAGTGTTTATGGT                              | GACCACCAGGATGAG  | TTTTGGGCTGCCTGTTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGTATTTC 302   | 302 |

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/Glone="gq135101"
// Gave="gq135101"
// Gave="gq135101"
// Gave="gq135101"
// Gave="gq135101"
// Glone="lb="mouse organ of Corti CDNA pBluescript; The Corti CDN was fine dissected from a total of 386 oc as follows: 102 samples from post-natal (p) day S; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P1; 14 from P1 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K193-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Unizap XR vector kit (catalog # 23721), strategene) and Unizap XR vector kit (catalog # 23721), strategene) and Unizap XR digapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(d7) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine lunker brimer everse transcribed using whom we was a prime of the second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second strand was carefully dCTP. The second was car
                                                                                                                                                                                                                                                                                                                                                                                              BQ569741 560 bp mRNA linear EST 19-JUN-2002 gil35f01.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gil35f01 5', mRNA sequence.
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EST analysis of gene expression in the mouse Organ of Corti at the
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 560)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kachar, B.
Structural Cell Biology
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Bmail: kacharb@nidcd.nih.gov
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and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
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Seg primer: M13RP1 reverse primer (ABI).
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                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="gil35f01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kachar, B.
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COMMENT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                          RESULT 5
BQ569741
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

AUTHORS TITLE

REFERENCE

JOURNAL

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columns to enrich for cDNAs greater than 400bp and 1000 bp
, respectively. The cDNA was then directionally ligated to
the Dni-ZAP XR vector, which had been predigested with
ECOR I and Xho I. The phagemid was packaged with Gigapak
III Gold and, upon titration on XLI Blue MRF' cells, the
yield of the phage library was estimated to be 11,100,000
recombinants. Stratagene's ExAssist Interference
resistance helper phage (catalogue # 211203) was adopted
to rescued library, individual cDNA clones were selected and
grown in 96-well, and growth plate. Plasmid DNA was
purified from 200 ul of saturated culture with the
concerts (TM) plasmid purification kit (Invirogen,
Carlebad, CA) as instructed by the manufacturer. ESTs from
the 5' end of the cDNA clones were generated with the
universal MRI zeverse primer (CAGGAAACAGCTRAGAC) and 25$
strength BigDye terminator sequencing chemistry (Applied
Biosystems, Foster City, CA). Sequencing reactions were
performed on MJ Tetrad thermal cyclers (MJ Research,
Waltham, MA), and analyzed on 3700 automated capillary
sequencers using POPS polymer (Applied Biosystems, Poster
City, CA). The frequency distribution of the library is
as follows: 72% of genes have I copy: 14.3% 2; 12% 3-10;
1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of
genes are present in GenBank and have know function;
12% are uncharacterized ESTS and 20% are unidentified."
12 to there
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 ATTICICIGGCAGAGGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly
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à 셤 ò 임  $\delta$ 셤 à 셤 ò g à d BQ564944 608 bp mRNA linear BST 19-JUN-2002 gi27g09.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi27g09 5', mRNA sequence.

RESULT 6 BQ564944 LOCUS DEFINITION

source

FEATURES

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                                                                                                                                                                                                                                                                                                     EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing Unpublished
                                                                                                                                                          Chordata, Craniata, Vertebrata, Euteleostomi, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Dive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1559
Fax: 301-402-1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: kacharb@nidcd.nih.gov
Plate: 27 row g colum: 09
Seq primer: MI3RP1 reverse primer (ABI).
Location/Qualifiers
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/organism="Mus musculus"
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GI:21468261
                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 608)
                                                                                                                     Mus musculus
    30564944.1
                                                                                                                                                                                                                                                                                Kachar, B.
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National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Structural Cell Biology

Tel: 301-402-1599
Fax: 301-402-1765
Baail: Kacharb@nidcd.nih.gov
Plate: 108 row: g column: 04
Seg primer: M13RP1 reverse primer (ABI).

/organism="Mus musculus"

/mol\_type="mRNA" /strain="BALB/c"

Location/Qualifiers

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source

FEATURES

us-10-019-455a-12.rst

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Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (GAGGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capilary sequencers using POS5 polymer (Applied Biosystems, POSter City, CA). The frequency distribution of the library is as follows: 72% of genes have I copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have bits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaglyGlu
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corgan of Corti; Ocol: was tine dissected from a total of 136
organ of Corti; Ocol: was tine dissected from a total of 136
organ of Corti; Ocol: was tine dissected from a total of 136
organ of Corti; Ocol: was tine post-attal (p) day 5; 72
from PD; 50 from PD; 46 from PD; 18 from PD; 20 from PD;
if from PD; 50 from PD; 46 from PD; 18 from PD; 20 from PD;
ocopsile of the ocollea was chipped away; rira vascularis
and Spiral ligament were removed and the sensory
expise of the cocllea was chipped away; rira vascularis
expitalitum was carefully dissected out of the modious.
Foral ARA was extracted vising the micro Pastrack Kit
(catalog # K159:02) instructions. Reverse transcription and
library construction were carried out with the Unit Zap XR
vector kit (catalog # 23721), Stratagene) and Unit Zap XR
vector kit (catalog # 23721), Stratagene and Unit Zap XR
vector kit (catalog # 23721), Stratagene and Unit Zap XR
vector kit (catalog # 23721), Stratagene and Unit Zap XR
vector kit (catalog # 23721), Stratagene and Gligested with
figapack III Gold Cloning Xit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manutacturer's instructions. Briefly: 1: 5 ug mRNA was
printed with the linker- primer and transcribed with
Solome with the linker- primer strand synthesis was
printed with the linker presence of ligase and digested
with Xho I. The cDNA was sequentially; size fractionated
over Pharmacia size Sep400 (Pharmacia, Uppsala, Swedny
columns to enrich for cDNAs greater than 400bp and 1000 by
the United Chroma Spiral Ocolones were selected on the resecue plasmid DNA clones were selected on the page of the phage (latalogue # 211203) was adopted
to rescue plasmid DNA from the phages. Upon plasmid puritied from 200 ul of saturated culture with the
second library, individual companies (Malalogue # 211203) was adopted
to selected library and analyzed on 3700 automated with the
selecti
/db_xref="taxon:10090"
                                    /clone="gi108g04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     630 bp mRNA linear EST 19-JUN-2002
gil08g04.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
Elone gil08g04.5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 630)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 ACGGATATTGACTTCTTCTGTGAA 396
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EST.
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Contact: Kachar, B.

hearing

onset of hea Unpublished

JOURNAL

Kachar, B.

AUTHORS TITLE

REFERENCE

Mus musculus

ORGANISM

DEFINITION

BQ568471

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ACCESSION VERSION KEYWORDS

ORIGIN

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Percent Similarity:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 696)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Ckazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takabashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Riken Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB611549 mRNA linear EST 31-AUG-2001 BB611549 RIKEN full-length enriched, 13 days embryo head Mus musculus cDNA clone 3110083012 5', mRNA sequence.
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Laboratory for Genome Exploration Research Toup, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
Fre Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGG 252
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12% are uncharacterized ESTs and 20% are unidentified." 111 c 167 g 174 t
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Matches:
Conservative:
Mismatches:
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                      Gaps:
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Mus musculus
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                                                                                                            2.92e-81
676.00
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Best Local Similarity:
Query Match:
                                                                                                Alignment Scores:
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                                                                                                                       No.:
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JOURNAL
                                  BASE COUNT
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KEYWORDS
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encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,K., Fukuda,S., Hara,A., Itch,M., Kawai,J., Shibata,K., Arakawa,T., Ishi, Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-186 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                       RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (Cono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer based methods for the mouse full-length CDNA
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new aggist. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura Hayashizaki, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'clone_lib="RIKEN full-length enriched, 13 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="head"
/dev_stage="13 days_embryo"
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="3110083012"
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/Grown and female" // Grown and female of Corti CDNA pBluescript" // Grown and Grown of Corti; Vector: pBluescript; The organ of Corti; Occ was fine dissected from a total of 386 OC as followed was fine dissected from a total of 386 OC as followed by Grown PD; Drown PD; Grown PD; 46 from PD; 18 from PD; 19 from PD; 19 from PD; 19 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 from PD; 10 f
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gl42g03.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gi42g03 5', mRNA sequence.
BQ565637
                                                                                                                                                                                                                                                                                                                                                                                                                                      101 ProserAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
                                                                                                                                                                  EST analysis of gene expression in the mouse Organ of Corti at the
81 PherrpalaglySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 CCCAGCAACTIGGTGAAGGAGCAGCGTGTATACCAGGAGGCCCACCAAGGAGATCCCAACC 383
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                       LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
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National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
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Plate: 42 row: g column: 03
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sonrce
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEATURES
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reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcripted using Moloney murine leukemia virus reverse transcripted using Moloney murine leukemia virus reverse transcripted using Moloney murine leukemia virus reverse transcripted using Moloney murine leukemia virus reverse transcripted using by moloney murine leukemia virus reverse transcripted using synthesized with DNA polymerase, and digested with DNA was blunt ended with Ptu DNA Molymerase, ligated with EcoR I adapters in the presence of ligase and digested virus to enrich for cDNAs greater than 400pp and 100 bp. respectively. The cDNA was stend directionally ligated to the UnizAbx Kn vector, which had been predigested with Gigapak III Gold and, upon titration on XII Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exhasist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the result of trom 200 ul of satulogue # 211203) was adopted to rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of satulogue # 211203 was adopted to rescue plasmid purification kit (Invitrogen, Carlabad, CA) as instructed by the manufacturer. ESTS from the 5' end of the cDNA clones were generated with the universal MI3 reverse primer (CAGGAAACAGCTATCACC) and 25\* strength BigDye terminator sequencing reactions were performed on MI Tetrad thermal cyclers (MJ Research, Wallham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA).

The frequency distribution of the library is as follows: 72\* of genes have Icopy, 14.3\* 2; 12\* 3-10; 1.4\* 11-50 and 0.1\* 51-150. As to gene function, 45\* of genes are present in GenBank and have know this individual double are uncharacterized & STS and cold the cold of the cold of the cold o

BASE COUNT

|                   | 474        | 127      | 0                   | Н                      | 0            | 0     |
|-------------------|------------|----------|---------------------|------------------------|--------------|-------|
|                   | Length:    | Matches: | Conservative:       | Mismatches:            | Indels:      | Gaps: |
|                   | 9.27e-81   | 671.00   | 99.22%              | 99.22%                 | 99.26%       | 13    |
| Alignment Scores: | Pred. No.: | Score:   | Percent Similarity: | Best Local Similarity: | Query Match: | DB:   |

US-10-019-455A-12 (1-128) x BQ565637 (1-474)

| λŏ | н   | 1 MetAlaArglleLeulleLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20      |
|----|-----|---------------------------------------------------------------------|
| qq | 14  | AFGCCAAGGATATTGATTCTTTTGCTTGGGGGCCTTGTGGTTCTATGTGCCGGGCATGGT 73     |
| ò  | 21  | ValPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysValTyrThr 40        |
| Dp | 74  | 74 GTATTTATGGATAAACTTTCTTCTAATAAGTTGTGTGGGGATGAGGAGTGTGTCTATACT 133 |
| ò  | 41  | lleSerLeualaArgalaGluGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60     |
| Db | 134 | ATTICTCTGGCAAGAGCACAGGAAGATTACAATGCCCCCAGACTGTAGGTTCATCGATGTC 193   |
| ò  | 61  | LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80     |
| Db | 194 | 194 AAGAAAGGCAGACACATATTTTTTTTTTTTTTTTTTTTT                         |
| È  | 81  | PheTrpalaGlySerValTyrGlyaspHisGlnAspGluMetGlylleValGlyTyrPhe 100    |
| qq | 254 | TITIGGGCAGGCAGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTC 313       |

101 ProSerAsnLeuValLygGluGlnArgValTyrGlnGluAlaThrLygGluIleProThr 120

RESULT 10

BQ563768

ACCESSION

KEYWORDS

VERSION

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Total RNA was extracted using the micro Fastrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap KR vector kit (catalog # 237211, Stratagene) and Uni-Zap KR Gigapack III Gold Cloning kit (catalog # 23721), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcribed using virus reverse transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex=mare must remard day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/clone_lib="Mouse Organ of Corti; vector: pBluescript; The
/note="Organ of Corti; vector: pBluescript; The
organ of Corti (CC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament ware removed and the sensory
epithelium was carefully dissected out of the modiolus.
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                                                                                                                                                                                                                                                                                         EST 19-JUN-2002
                                                                                                                                                                                                                                          684 bp mRNA linear EST 19-JUN-2003
2106:09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gi06:09 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
Unpublished
314 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 684)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Kachar, B. Structural Cell Biology National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA Tel: 301-402-1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: kacharb@midcd.nih.gov
Plate: 06 row: c column: 09
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="taxon:10090"
/clone="gi06c09"
/sex="male and female"
                                                                      121 ThraspileaspPhePheCysGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ563768.1 GI:21466749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .684
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                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
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FEATURES

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

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the Uni-ZAP XR vector, which had been predigested with ECOR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exhasist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlabad, CA) as instructed by the manufacturer. ESTS from the 5' end of the CDNA clones were generated with the universal MI3 reverse primer (CAGGAAACAGCTAATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA).

The frequency distribution of the library is as follows: 72% of genes have I copy; 14.3% 2; 12% 110, 1.4% 11-50 and 0.1% 51-160. As to gene function, 45% of genes are present in Genbank and have know function; 13% have winch aracterized ESTs and 20% are unidentified."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409 bp mRNA linear EST 19-JUN-2002 gi73909.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA EQ56932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 GTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGCGGGAAGAGGAGGAGTGTCTATACT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGAG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetalaArgIleLeuIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 IleSerLeuAlaArgAlaGluGluAspTyrAsnAlaProAspCysArgPheIleAspVal
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127
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Mismatches:
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99.22%
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Query Match:
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REFERENCE AUTHORS JOURNAL

TITLE

KEYWORDS

FEATURES

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/dev stage="Post natal" day 5 to 13"
//dev stage="Post natal" day 5 to 13"
//clone_lib="Mouse Organ of Corti cDNA pBluescript"
//clone_lib="Mouse Organ of Corti, Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P0; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After Killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bouy
capsule of the cochlea was chipped away, stria vasularis
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epithelium was carefully dissected out of the modiolus.
Total RNA was actracted using the mairor Fastrack Kit
(catalog # K1591-02; Invitrogen, Carlsbad, CA), according
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vector Kit (catalog # 237211, Stratagene) and Uni-Zap XR
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vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
vector kit (catalog # 137211, Stratagene) and Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
vector with the linker- primer and transcripted using
Noloney murina an Xb I site. First strand synthesis was
primed with the linker- primer and transcripted
Noloney murina leukemia virus reverse transcriptes
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested
vith Xho I. The CDNA was then directionally ligated the
Cook I adapter Contaction on XLI Blue MRF' cells, the
Vield of the phage library was estimated to be 11,100, or
respectively. The CDNA was then direction be 11,100, or
respectively. Strat
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                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Unridae; Murinae; Mus.
1 (bases 1 to 409)
                                                                                                                                                                                                                                              EST analysis of gene expression in the mouse Organ of Corti at the
                                                                                                                                                                                                                                                                                                                                                                               Confect: Kachar,B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: kacharbenidcd.nih.gov
Plate: 73 row: g column: 09
Seg primer: M13RP1 reverse primer (ABI).
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/clone="gi73g09"
/sex="male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .409
                                                                                                                                                                                                                                                                                                          onset of hearing
                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                  ORGANISM
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universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3.10; 1.4% 11.50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                490 bp mRNA linear EST 19-JUN-2002 gi37b12.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA EQ565411.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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National Institute of Deafness and other Communication Disorders
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FEATURES

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BASE COUNT

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Mus musching Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Muscati, I. (Dases I to 365)

I. (Dases I to 365)

Sokazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Golobori, T., Baldarelli, R., Hill, D., P., Bult, C., Hume, D., A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisell, K.M., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Grimmond, S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Guogh, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarkson, J. J., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P. A., Magloctt, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pettea, G., Percosky, M., Shimada, M., Sandelin, B., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wanner, L., Walner, Boris, A., Yang, L., Yang, L., Yang, L., Yang, L., Yang, L., Yang, L., Yang, L., Yang, C., Yanlan, R., Zanwer, R., Zimmer, A., Yang, L., Yang, L., Yang, L., Yang, L., Yang, L., Yang, R., Yang, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, R., Zimmer, 
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BY232622 RIKEN full-length enriched, adult inner ear Mus musculus
CDNA clone F930026J20 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 AGAGCACAGGAAAATTACAATGCCCCAAACTGTAGGTTCATCGATGTCAAAAAGGGGAG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 SerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsnLeu 104
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Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Exploration Research GENOME Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Lesues. Univision of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Kirk W. Beisel ( Boys Town National Research Hospital 555 North 30th Street Omana, NE 68131 USA ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakan.go.jp/
A.T. imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibaki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizuwe, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyaza, A., Sakai, K., Sasaki, B., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
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Tel: 81-45-503-9222
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/clone lib="RIXEN full-length enrites adult inner ear"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="inner ear"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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/clone="F930026J20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.07e-69
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99.12%
99.12%
86.54%
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                                                                                                                                                                                                                                                                        22354683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                       JOURNAL
MEDIINE
PUBMED
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24 ATGGCAAGGATATTGATTCTTTTGCTTGGGGGCCTTGTGGTTCTATGTGCCGGGCATGGT 83

g

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/sex="male and female"
/dev stage="Post natal day 5 to 13"
/dev stage="Post natal day 5 to 13"
/close lib="Mouse Organ of Corti CDNA pBluescript"
/close lib="Mouse Organ of Corti; Vector: pBluescript; The
/note="Organ of Corti: Vector: pBluescript; The
/note="Organ of Corti: Vector: PBluescript; The
/note="Organ of Corti: Vector: PBluescript; The
/note="Organ of Corti: Vector: PBluescript; The
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gi88d08.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gi88d08 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (catalog # X1593-02, Invitrogen, Carlabad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
                                                    84 GTATTTATGGATAACTTTCTTCTAAGAAGTTGTGCGCGATGAGGAGTGTGTCTATACT 143
                                                                                                                                                                                                                                                                                                             144 ATTICICIOGCAAGAGCACAGGAAGATACAATGCCCCAGACTGTAGGTTCATCGATGT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGGG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 ringgagengacadnardirinardicaccaddargadangagaangaganantre 323
21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
                                                                                                                                                                                                                      61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Bmail: Acatarbenided.nih.gov
Blate: 88 row: d column: 08
Seq primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total RNA was extracted using the micro Fasttrack kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 ProSerAsnLeuvalLysGluGlnArgValTyrGlnGluAla 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 CCCAGCAACTIGGGGAAGGAGCAGCGTGTATACCAGGAGGCC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="gi88d08"
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/strain="BALB/c"
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3E236443

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manufacturer's instructions. Briefly: 1.5 ug mENA was reverse transcribed using a hybrid oligo(d7) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker primer and transcribed using primed with the linker primer and transcribed using primed with the linker. Primer and transcribed using moloney murine leukemid virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA was blund made with PIU DNA was blund made with PIU adapters in the presence of ligase and digested with Xho I. The CDNA was sequentially size fractionated over pharmacia Size Sept00 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for CDNA greater than 400bp and 1000 bp. respectively. The CDNA was then directionally ligated to the Dni-ZAP XR vector, which had been predigested with BcoR I and Xho I. The phagemid was packaged with Gigapax III Gold and, upon titration on Xil Blue MRF cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference resistence helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the resistance helper phage (catalogue # 211203) was adopted rescued library, individual cDNA clones were selected and grown in 66-well. 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated outlure with the concerts of TM) plasmid purification kit (Invitrogen, Carlebad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the bestormed on MJ retrad thermal cyclers (WA Research, Waltham, MA), and analyzed on 3700 automated capillary sequences using POP5 polymer (Applied Biosystems, Foeter City, CA).

Sequencers using POP5 polymer (Applied Biosystems, Foeter City, CA).

Sequencers using POP5 polymer (Applied Biosystems, Foeter City, CA).

Sequencers using POP5 polymer (Applied Biosystems, Foeter City, CA).

Sequencers using POP5 polymer (Applied Biosystem
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89 AspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsnLeuValLysGluGln 108 61 GATTACAATGCCCCAGACTGTAGGTTCATCGATGTCAAGAAAGGGCAGCAGCAGTCTATGTT 120 181 GACCACCAGGATGAGATGGGAATTGTAGGTTATTTCCCCAGCAACTTGGTGAAGGAGCAG 240 88 29 LysLysLeuCysAlaAspGluGluCysValTyrThrIleSerLeuAlaArgAlaGlnGlu 48 1 AAGAAGTTGTGTGCGGATGAGGAGTGTGTCTATACTATTTCTCTGGCAAGAGCACAGGAA 60 49 AspTyrAsnAlaProAspCysArgPheIleAspValLysLysGlyGlnGlnIleTyrVal 69 TyrSerLysLeuValThrGluAsnGlyAlaGlyGluPheTrpAlaGlySerValTyrGly Length: Matches: Conservative: Mismatches: Indels: US-10-019-455A-12 (1-128) x BQ567343 (1-604) 1.13e-62 539.00 100.00% 100.00% 79.73% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: No.: g ò g à g ⋧ g ò

RESULT 15

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[ (Dasses 1 to 527) Smith, T.P. L., Grosse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T., Grosse, W. Wary, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
EST 25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 ATTICICIGGCCAGAGCTCAAGAAGATTACAATGCTCCGGACTGTAGATTCATTAACGTT 214
                                                                                                                                                                                     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 ATATITIATGGACAGACTIGGTICCAAGAAGCTGTGTGCAGATGAATGAATGTGTCTATACT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/mol_type="mRNA"
/db xref="teaxon:9913"
/tisare type="pooled"
/lab_host="pH10B"
/clone lib="MARC 4BoV"
/note="weeter: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
/note="weeter: pCMV SPORT6; Site 1: Not1)
                                                                                                                                                                                                                                                                                                                                                                     Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetAlaArglleLeuIleLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly
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BE236443 527 bp mRNA linear 144645 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
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44
44
44
7
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4360
Fax: 402 762 4390
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Matches:
Conservative:
Mismatches:
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/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 54 row: C column: 18
Seg primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORWARD: AGGAAACAGCTATGACCAT
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                                                                         BE236443.1 GI:9021161
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489.00
82.17%
72.87%
72.34%
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                                                                                                                      Bos taurus (cow)
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Best Local Similarity:
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       LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE
PUBMED
                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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BASE COUNT

| DÞ                    | 215 AAAAAGGACAGTGGATCTATGTTTACTCAAAGCTG-                                 | GTTTACTCAAAGCTG250                                                   |  |
|-----------------------|--------------------------------------------------------------------------|----------------------------------------------------------------------|--|
| δλ                    | 81 PheTrpAlaGlySerValTyr                                                 | 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyr 99      |  |
| QQ                    | 251GTCTAI                                                                | GTCTATGGCAATCAGTCTGAGGATGAAATGGGAACCGTGGGTTAT 295                    |  |
| ò                     | 100 PheProSerAsnLeuValLys                                                | 100 PheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIlePro 119 |  |
| qq                    | 296 TTCCCAGCAACTIGGTCCAG                                                 | 296 TTTCCCAGCAACTTGGTCCAGGAACAACATGTGTACCAAGAAGCCACCAAGGAGGTTCCT 355 |  |
| ò                     | 120 ThrThrAspileAspPhePheCysGlu 128                                      | CysGlu 128                                                           |  |
| qa                    | 356 ACCACGGATATTGACTTTTTC                                                |                                                                      |  |
| Search co<br>Job time | Search completed: December 29, 2003, 22:00:46<br>Job time : 1326.28 secs | ), 22:00:46                                                          |  |

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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December 29, 2003, 16:10:49 ; Search time 154.353 Seconds (without alignments) 2238.558 Million cell updates/sec
                                                                                                                                                                             1 MARILILLEGELVVLCAGHG.....RVYQEATW FTTDIDFFCE 128
OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                            2552756 seqs, 1349719017 residues
                                                                                                                                                                                                                                                  Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                               BLOSUM62
                                                                                                                                                                 score:
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                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                 Perfect
                                                    Run on:
                                                                                                                                           Title:
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Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q-Con2 1/USFTO spool/US10019455/runat 29122003 160347 230/app\_query.fasta\_1.1770
-Q-Cop2 1/USFTO spool/US10019455/runat 29122003 160347 230/app\_query.fasta\_1.1770
-Q-CopEXT=0 -UNITS=bits -STRXT=1 -MXFIXEX=blosum62 -TRANS-human40.cdi
-LOOPEXT=0 -UNITS=bits -STRXT=1 -END=-1 -MXFIXEX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=PEAPSIZE=500 -THR MAX=100 -THR MIN=0 -ALIGN=10
-WODE=LOCAL -OUTFNT=pto -NONH=sext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10019455 @CGN 1 1 0 @runat 2912203 160347 230 -NCFU=6 -ICFU=3
-NO WMADP -LAGGEQUERY -NEGS SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=3 0 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

(SIDS.) gogdata/geneseqn=embl./NA198.DAT:
(SIDS.) gogdata/geneseqn=embl./NA198.DAT:
(SIDS.) gogdata/geneseqn=embl./NA199.DAT:
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(SIDS.) gogdata/geneseqn/emeseqn-embl./NA199.DAT:
(SIDS.) gogdata/geneseqn/emeseqn-embl./NA2000.DAT:
(SIDS.) gogdata/geneseqn/embl./NA2000.DAT:
(SIDS.) gogdata/geneseqn/embl./NA2001.DAT:
N Geneseq 19Jun03:\*

| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\*
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\*
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:\*
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:\*
| SIDS1/gcgdata/geneseqf/geneseqn-embl/NA1983.DAT:\*
| SIDS1/gcgdata/geneseqf/geneseqn-embl/NA1983.DAT:\*
| SIDS1/gcgdata/geneseqf/geneseqn-embl/NA1985.DAT:\*
| SIDS1/gcgdata/geneseqf/geneseqn-embl/NA1985.DAT:\* /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

## ALIGNMENTS

RESULT 1

| AAF59068  ID AAF59068 standard; DNA; 384 BP.  AC AAF59068;  XX  XX  XX  XX  XX  XX  XX  XX  XX |
|------------------------------------------------------------------------------------------------|
| KW MLP; MIA; melanoma innibicory accivity; cancer; bone di                                     |
| XX<br>KW MLP: MIA: melanoma inhibitory activity; cancer; bone di                               |
| DE Mouse MLP nucleotide sequence SEQ ID NO:10.                                                 |
| DT 23-APR-2001 (first entry)                                                                   |
| AC AAF59068;                                                                                   |
| XX                                                                                             |
| ID AAF59068 standard; DNA; 384 BP.                                                             |
| AAF59068                                                                                       |

nflammatory; Julia Laborae, pariologic anglogicals, cassions, antimitamiscol, cardiant; gene therapy; secretory cell function regulator; promoter; inhibitor; ds. ease;

Mus musculus. X S X Z Z

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ProSerAsnLeuvalLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ATTICTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATCGATGTC 180
                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAPS9063 to AAPS9089 and AABS9122 to AABS9122 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGGCAAGGATAITGATTCTTTTGCTTGGGGCCCTTGTGGTTCTATGTGCCGGGCCATGGT 60
                                                                                                                                                                Noguchi Y, Yoshimura K;
                                                                                                                                                                                                                                                                                                     joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetalaargileLeulleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGCGGATGAGGAGTGTGTATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 ValPheMetAspLysLeuSerSerLysLysLysLeuCysAlaAspGluGluCysValTyrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal
                                                                                                                                                                                                                                                               Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                  Nishi K, Ogi K, Ohkubo S, Mogi S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.98e-84
676.00
100.00%
100.00%
                                                               29-JUN-2000; 2000WO-JP04278.
                                                                                                  99JP-0186718.
                                                                                                                               (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                     WPI; 2001-159271/16.
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                       P-PSDB; AAB69125.
WO200102564-A1
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                                                                                                  30-JUN-1999;
                                  11-JAN-2001
                                                                                                                                                                                    Tanaka H;
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RESULT 2

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71 GTATTTATGGATAAACTTTCTTAAGAAGTTGTGTGCGGATGAGGAGTGTGTCTATACT 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promocrers and inhibitors for preventing or treating bone and joint diseases as well as pathologic anglogenesis.

AMF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                                                                                                                                                                                                                                                                                                                                                                                        Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 ATGGCAAGGATATTGATTCTTTTGCTTGGGGGCCCTTGTGGTTCTATGTGCCGGGCATGGT
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                                                                                                                                        MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter; inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in the exemplification of the present invention.
                                                                                                              Mouse MLP nucleotide sequence SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 100-101; 111pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                             99JP-0186718.
               AAF59084 standard; DNA; 947
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                                                                                                                                                                                                                                Mus musculus.
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                                                                                                                                                                                                                                                                                               11-JAN-2001.
                                                                                23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                            Tanaka H;
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                                                 AAF59084;
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AAF59084
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US-10-019-455A-12 (1-128) x AAF59098 (1-384)

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ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
                                                                                                                                                                                                                              191 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCTGGAGA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antinfinametory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of prometers and inhibitors for preventing or treating bone and joint diseases as well as pathologic anglogenesis.

ARFS9063 to AARS9099 and AABS9122 to AABS9132 represent sequences used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MLP, MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter; inhibitor; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat MLP nucleotide sequence SEQ ID NO:46.
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                                                                                                                                                                                                                                                                                                                           ThraspileaspPhePheCysGlu 128
                                                                                                                                                                                                                                                                                                                                                             371 ACGGATATTGACTTCTTCTGTGAA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF59098 standard; DNA; 384 BP.
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Conservative: Mismatches: Matches:

Similarity:

Query Match: Best Local

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Alignment Scores:

Length:

1.64e-81 655.00 98.44% 96.09% 96.89%

Indels: Gaps:

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181 AAGAAAGGCAGCAGATCTATGTTTATTCCAAGCTGGTAACAGAAAATGGAGCTGGGGCA 240
                                                                                                                                                                                                                                                                              241 Tringegeregeagrerriaregreaceaccaccacardagardegaarreregerrarric 300
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                                                                                                                        41 IleSerLeuAlaArgAlaGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
1 MetalaargileLeuileLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly
                            1 Areschaghararearrerrirecrisseseccrisisesererereresesesearese
                                                            21 ValpheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human MLP nucleotide sequence SEQ ID NO:4.
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function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69112 represent sequences used
                                                                                                                                                                                                                                                                                                               1 MetAlaArgileLeulleLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly
                                                                                                                                                                                                                                                                                                                                    21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein, cytostatic; immunosuppressive; vulnerary; vaccine; antiinflammatory; neuroprotective; nephrotropic; cardiovascular; human; cancer; autoimmune disease; wound healing disorder; infection; haematopoietic disorder; inflammatory disease; inflammatory disease; infertility; neurological disease; psychiatric disease; cardiovascular disease; respiratory disease; renal; gastrointestinal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal
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                                                                                                     Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;
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/*tag= a
/product= "Human secreted protein"
                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                       in the exemplification of the present invention.
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                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                               US-10-019-455A-12 (1-128) x AAF59065 (1-384)
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93.75%
86.72%
89.05%
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Best Local Similarity:
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The invention relates to an isolated novel secreted polypeptide (I) and polynucleotide (II). (I) and (II) are useful for treating cancer, autoimmune diseases, wound healing disorder, infections, haematopoietic disorders, inflammatory disorders, infertility, neurological and send polyneating disorders. Infertility neurological and disorders, and diseases, cardiovascular diseases, respiratory diseases, cardiovascular diseases, respiratory diseases, cardiovascular diseases, respiratory diseases, cardiovascular diseases, respiratory diseases, cardiovascular diseases, respiratory diseases, cardiovascular diseases, respiratory diseases, cardiovascular diseases, respiratory diseases, cardiovascular diseases, and cardiocase for induction and/or metabolism of the genes, as vaccines for inducing immunological response in a mammal, and in cardior many and polypeptide in cells. The polypeptides can be used as immunogens to produce antibodies immunospecific for the polypeptides, and be used as diagnostic reagents, in chromosome localisation studies, and in tissue expression studies. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AAAAAAGGGCAGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAATGGAGCTGGAGAA 240
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                                                                                                                                                                                                                                                                                                  New secreted proteins or polypeptides, useful for treating e.g. cancer, autoimmune diseases, wound healing disorder, infections, haematopoietic disorders, inflammatory disorders, infertility, cancer
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                                                                                                                                                                                            Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
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                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 44; 92pp; English.
                                                                                       24-APR-2000; 2000US-199417P.
                                                             13-APR-2000; 2000US-196603P.
                11-APR-2001; 2001WO-US11797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of Hyseq clone identification number 16372272, which was obtained from a human thymus CDNA library using standard PCR with primers specific for vector sequences clanking the inserts, sequencing by hybridisation sequences signature analysis, and Sanger sequencing techniques. This expressed sequence tag was used in the assembly of a full-length cDNA sequence (see AAH2643) encoding a novel human growth contactor-like polypeptide (GRLP, see AAB82671). The GRLP belongs to the same protein family as growth regulatory proteins growth factors, human melanoma derived growth regulatory protein prouts of 64% similarity and 45% identity over 111 amino acids) comelanoma inhibitory activity, cattle cartilage-derived criminarity over 126 amino acids) and other retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid sensitive proteins. GRLP polypeptides and polynucleotides of the invention and diagnosis of disorders and diseases caused by, or involving, and diagnosis of disorders and diseases caused by, or involving, cartified the acid the acid the analysis and maintenance, inhibition of mile meaning and polynucleotides and diagnosis of disorders and diseases caused by, or involving, cartified the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid the acid t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide-nucleic acid molecules, and to produce transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth regulatory-like polypeptide; human; cartilage; melanoma; neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth and tumours, including neuroectodermal tumours such as gliomas. The polynucleotides can also be used to design probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human growth regulatory-like polypeptide clone 16372272.
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121 ThraspileAspPhePheCysGlu 128
                                                  361 ACGGATATTGACTTCTTCTGCGAG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 114; 119pp; English.
                                                                                                                                                                                                                                                                                                                  AAH26341 standard; cDNA; 426 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-2001; 2001WO-US02455.
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAH26341;
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Matches: Conservative; Length:

4.39e-74 602.00 93.75%

Percent Similarity:

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Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
antiarteriosclerotic; gene; ss.
                                                                                                                                                                                 81 PheTrpalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 378
                                                                                                                                                                                                                                                                139 ATTICTCTGGCTAGTGCTCAAGAAGATATAATGCCCCGGACTGTAGATTCATTAACGTT 198
                                                                                                                                                                                                                                                                                                                               199 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAA 258
                                                                                                                                                                                                                                                                                                                                                                                                 259 TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGGATGGGAGTCGTGGGTTATTTC 318
                                                                                                                  19 ATGGCAAGAATATTGTTACTTTCCTCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA 78
                                                                                                                                                               41 IleSexLeualaargalaGlnGluaspTyrasnalaaProAspCysArgPheIleAspVal 60
                                                                                                                                                                                                                                                                                                61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
                                                                                                1 MetAlaArglleLeulleLeuLeuClyGlyLeuValValLeuCysAlaGlyHisGly
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 800
Mismatches:
Indels:
                                 Gaps:
                                                                 US-10-019-455A-12 (1-128) x AAH26341 (1-426)
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07-SEP-2000; 2000US-230978P.
15-SEP-2000; 2000US-000000P.
18-SEP-2000; 2000US-0666410.
18-SEP-2000; 2000US-0665350.
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2000US-0643657.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
 86.72%
 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200208284-A2.
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17-AUG-2000;
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28-JUL-2000;
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                 Query Match:
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, theumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ferrara N, Gerber H, Gerritsen ME, Goddard A; PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF; PF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              healing. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 359; 567pp; English.
                                                                                                                                                          2001US-0866028.
2001US-0866034.
2001US-0817092.
2001US-0870574.
2001WO-US17443.
                                                        2001WO-US06520.
2001WO-US06666.
2001US-0802706.
                                                                                            2001US-0808689.
2001US-0816744.
2001US-0828366.
                                                                                                                                  2001US-0854208
2001US-0854280
                                                                                                                                                                                                                        01-JUN-2001; 2001WO-US17800
20-JUN-2001; 2001WO-US19692
28-JUN-2001; 2001WO-US00000
                     2000WO-US34956
                                                                                                                                                                                                                                                                                                                                     GODDARD A.
GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
PAN J.
                                                                                                                                                                                                                                                                                                                          GERRITSEN M E.
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WATANABE C K.
WILLIAMS P M.
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                                                                                                                                                                                                                                                                                      BAKER K P.
FERRARA N.
                                                                                                                                                                                                                                                                                                                                                                                                                PAONI N F.
                                                                                                                                                                                                                                                                         GENENTECH
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                                                                    01-MAR-2001; 2

09-MAR-2001; 2

22-MAR-2001; 2

22-MAR-2001; 2

05-APR-2001; 2

10-MAY-2001; 2

10-MAY-2001; 2

25-MAY-2001; 2
                                 22-JAN-2001;
28-FEB-2001;
28-FEB-2001;
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521 111 9 8 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

5.85e-74 602.00 93.75% 86.72%

Similarity:

Query Match:

Best Local

Percent Similarity:

Alignment Scores:

. No. .

JS-10-019-455A-12 (1-128) x ABL95740 (1-521)

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157
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                                                                                                                                  101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
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                                                                                                                                                                                                                            PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
                                                                                                                                                                                                                                                                                                           CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerctic; PRO agonist; PRO antagonist; trauma; yene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; theumatoid arthritis; mycoardial infarction; thromopophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
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                                                                                                                                                                   LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
                                                                        MetAlaArgl1eLeulleLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly
                       38 Ardecaadaararrerracritrecreeedgrerrergecrerrergeargea
                                                        21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr
                                                                                                               41 IleSerLeuAlaArgAlaGluGluAspTyrAsnAlaProAspCysArgPheIleAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO9873 cDNA sequence SEQ ID NO:359.
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18-SEP-2000; 2000US-0664610.
18-SEP-2000; 2000US-0665350.
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20-JUL-2000; 2000US-219556P.
25-JUL-2000; 2000US-220624P.
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28-JUL-2000; 2000WO-US20710.
02-AUG-2000; 2000US-222695P.
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2000WO-US23328.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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23-AUG-2000; 2
24-AUG-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                              TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTAGTTTC
                                             PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe
                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breat cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha; gene; ss.
                                                                                                                                                                                                                                                                                                                                           cDNA encoding human PRO protein, Seg ID No 71.
                                                                                                                                                             ThrAsp1leAspPhePheCysGlu 128
                                                                                                                                                                                                                                                      BP.
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2000US-220863P
2000US-220893P
2000WO-US20710
2000WO-US23522
2000WO-US23328
                                                                                                                                                                                                                                                      ABK33571 standard; cDNA; 521
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2000US-220605P.
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2000US-253646P.
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2000US-220624P.
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P-PSDB; AAU83627.
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10-NOV-2000;
28-NOV-2000;
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23-AUG-2000;
24-AUG-2000;
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20-DEC-2000;
20-DEC-2000;
28-FEB-2001;
10-MAY-2001;
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Grimaldi JC,
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25-JUL-2000;
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ABB85003. The PRO proteins and polymucleotides have cardiant, cytostatic,
antiangiogenic, bypotensive, vulnerary and antiarteriosclerctic
activities, and can be used in gane therapy. The PRO polymucleotides,
proteins, agonists and antagonists are useful for treating or diagnosing
a cardiovascular, endothelial or angiogenic disorder in a mammal,
e.g. cardiac hypertrophy, trauma, cancer, age-related macular
degeneration, atherosclerosis, hypertension, arterial restenosis,
cheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
lymphangitis, tunnour angiogenesis (such as breast carcinoma and liver
carcinoma) and wound healing. The PRO polynucleotides have applications
in molecular biology, including use as hybridisation probes, and in
chromosome and gene mapping. Abl88259 to ABL88267 represent primers and
probes used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                             Paoni NF;
                                                                                                                                                                                                                                                                                                                                                                                               One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                          Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
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20-DEC-2000, 2000WO-US34956.
22-JAN-2001; 2001US-076'609.
28-FEB-2001; 2001US-076'6498.
28-FEB-2001; 2001WO-US06520.
01-MAR-2001; 2001WO-US06666.
04-MAR-2001; 2001US-0802706.
14-MAR-2001; 2001US-0802706.
10-MAY-2001; 2001US-0816744.
10-MAY-2001; 2001US-084280.
10-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001US-0866034.
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                      The invention relates to one hundred and twenty two nucleic acids cocding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of or gene expression, in paricyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating continuating the release of tumour necrosis factor-alpha from human blood, stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABK33556-ABK33657 represent human processes the invention.
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Indels:
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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forematics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA biodiversity and for nutritional purposes.
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                                                                                                                                                                                                                                                            Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use
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25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                    Tang YT, Liu .,
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Best Local Similarity:
                                                                                                      (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of a novel nucleic acid that was assembled from human thymus CDNA library-derived Hyseq clone casembled from human thymus CDNA library-derived Hyseq clone identification number 16372272 (see AAH26341). A recursive algorithm was used to extend the clone by pulling additional sequences from different databases. A full-length sequence (see AAH26343) encoding novel human growth regulatory-like polypeptide (GRLP, see AABB2671) was subsequently obtained. Human GRLP belongs to the same protein family as growth regulatory proteins, growth factors, human melanoma derived growth regulatory proteins, growth factors, human melanoma derived growth regulatory proteins, growth factors, human melanoma derived growth regulatory proteins, or melanoma inhibitory activity, cattle cartilage-derived cretinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid-sensitive similarity over 126 amino acids) and polynucleotides of the invention can be used in the prophylaxis, treatment (including gene therapy) and diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenenance, inhibition of melanoma cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cotein, in the generation of antisense, ribozyme and acid molecules, and to produce transgenic animals.
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                                                                                                                                                                                                             Growth regulatory-like polypeptide; human; cartilage; melanoma;
neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis
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ACGGATATTGACTTCTTCTGCGAG 402
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                                                                                  AAH26342 standard; cDNA; 891
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02-MAY-2000; 2000US-0563786
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                      379
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891 111 9 8

Matches: Conservative: Mismatches: Indels:

1.25e-73 602.00 93.75% 86.72% 89.05%

Percent Similarity: Best Local Similarity: Query Match:

Length:

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                                                                                                                                          139 ATTICTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATTAACGTT 198
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                PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe
                                                        21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr
                                                                                                                41 IleSerLeuAlaArgAlaGluAspTyrAsnAlaProAspCysArgPheIleAspVal
                                                                                                                                                                          61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
1 MetAlaArglleLeulleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human MLP nucleotide sequence SEQ ID NO:29.
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                                                                                                                                                                                                                                                                                                                                                        ThraspileAspPhePheCysGlu 128
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Tanaka H;
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activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                         21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth regulatory-like polypeptide; human; cartilage; melanoma; neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
                                                          Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;
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Matches:
Conservative:
Mismatches:
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The present sequence is that of a novel nucleic acid encoding human prowth regulatory-like polypeptide (GRLP, see AAB82671).

The sequence was assembled using human thywus CDNA library derived Hyseq clone identification number 16372272 (see AAB6544) as seed, using software programs to pull additional sequences from Hyseq's proprietary database containing expressed sequence tag sequences, and by gel sequencing using primers to extend both 5' and 3' ends. The predicted protein has a mol. wt. of 14 kDa unglycosylated. GRLP belongs to the same protein family as growth regulatory proteins, growth factors, human melanoma derived growth regulatory proteins, crown and a seme protein (GD-RAP), 44% identity or ention acid sensitive protein (GD-RAP), 44% identity and 64% imminatity over 126 amino acids) and other retinoic acid-sensitive similarity over 126 amino acids) and other retinoic acid-sensitive similarity over 126 amino acids) and other retinoic acid-sensitive similarity over 126 amino acids) and other retinoic acid-sensitive carbinacy acid isorders and diseases caused by, or involving, and diagnosis of disorders and diseases caused by, or involving, and diagnosis of disorders and diseases caused by, or involving, and primers, for chromosome and gene mapping, in the recombinant complement, in the generation of antisense, riboxyme and peptide-nucleic acid molecules, and to produce transgenic animals. They may also have cytokine and cell proliferation of protein, in the generation of antisense, riboxyme and peptide-nucleic acid molecules, and to produce transgenic animals. They may also have cytokine and cell proliferation of protein, in the generation of antisense, riboxyme and peptide-nucleic acid molecules, and to produce transgenic animals. They may also have cytokine and cell growth factor activity, chementopolesis regulating activity, itssue growth activity, activity, thementopolesis regulating activity, itssue growth activity, activity, and and attended and activity of an activity of an activity of an activit
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system disorders -
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                                                                                                                                                                                                                                                  Liu C;
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                                                                                                                                                                                                                                              Tang YT,
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                                                                 25-JAN-2000; 2000US-0491404.
02-MAY-2000; 2000US-0563786.
25-JAN-2001; 2001WO-US02455
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Best Local Similarity:
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                                                                                                                                                                                                                                                                      GlyGluPheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly
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P-PSDB; AAB69127.
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The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
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Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;

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| Length: Matches: Conservative: Mismatches: Indels:                                         | 199 (1-330)          | HisGlyValPheMetAspLysLeuSerSerLysLeuC | ACTITCTICIAAGAAGITG                                        | TyrThrileSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheI | BAGCACAGGAAGACTACAATG                                         | leTyrValT                     | AGATCTATGTTTATTCCAAGG                                         | rValTyrGlyAspHisGln2                        | retrratecteaccaccae                                        | LysGluGlnArgValTy      | TAGAGGAACGAGTGTACC                                          | nePheCysGlu 128                | CTTCTGTGAA 330                 |
| :: 2.37e-70<br>574.00<br>.ty: 99.09<br>.arity: 96.36\$                                     | 2 (1-128) × AAF59099 | SGlyValPheMetAspLy                    | TGGCATGTTTATGGATAA                                         | rThrlleSerLeuAlaAr                                         | TACCATTCTCTGGCAAG                                             | AspvallysLysGlyGlnGlnI        | TGTCAAGAAAGGGCAGCA                                            | GlyGluPheTrpAlaGlySe                        | secatrictedecreecae                                        | PyrPheProSerAsnLeuVa   | rtrccccagcaacriggr                                          | ProThrThrAspIleAspPhePheCysGlu | CCAACCACGGATATTGACTTCTTCTGTGAA |
| nt Scores: ).: Similarity sal Similar tch:                                                 | 55A-1                | 19 H                                  | -6<br>-7                                                   | 39 17                                                      | 61 T7                                                         | 59 A                          | 121 A                                                         | 79 67                                       | 181 G                                                      | 99<br>F.               | 241 T/                                                      | 119 P                          | 301 C                          |
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APPLICANT: Boyle, Bryan J
APPLICANT: Ford, John E
APPLICANT: Ford, John E
APPLICANT: Atterburn, Matthew C
APPLICANT: Tang, Y Tom
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Song, Yong
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APPLICANT: Sjasstad, Michael
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FILE REFERENCE: HYS-7CIP
FILE REFERENCE: Word
CURRENT FILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-01-25
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NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mize, Nancy K
APPLICANT: Boyle, Bryan J
APPLICANT: Ford, John B
APPLICANT: Arterburn, Matthew
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US-10-216-163-71
US-10-216-163-71
Sequence 71, Application US/10216163
Sequence 71, Application No. US20030149239A1
Sequence 71, Application No. US20030149239A1
SERNEXAL INPORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Goddard, Audrey.
APPLICANT: Goddard, Audrey.
APPLICANT: Goddard, Audrey.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smeth, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe Colin L.
APPLICANT: Watanabe Colin L.
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APPLICANT: Watanabe Colin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
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Conservative:
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CURRENT APPLICATION NUMBER: US/10/216,163
CURRENT FILING DATE: 2002-08-09
PRICH APPLICATION NUMBER: 10/119,480
PRICH FILING DATE: 2002-04-09
PRICH APPLICATION NUMBER: 60/059113
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SOFTWARE: PatentIn version 3.1
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LENGTH: 426
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; LOCATION: (426)..(426)
; OTHER INFORMATION: n = A, T,
US-10-216-038-1
                                                                    ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity:
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                                                          TYPE: DNA
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338 CCCAGGAACTTGGTCAAGGAACAGGGTGTACCAGGAAGCTACCAAGGAAGTTCCCACC 397
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PRIOR FILING DATE: 1997-09-17
PRIOR PELICATION NUMBER: 60/062287
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PRIOR APPLICATION NUMBER: 60/06349
PRIOR APPLICATION NUMBER: 60/064103
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PRIOR PELING DATE: 1997-10-31
PRIOR PELING DATE: 1997-12-31
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR PELING DATE: 1988-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR PELING DATE: 1988-03-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.11e-83
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey,
APPLICANT: Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo Sapien
US-10-216-163-71
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Best Local Similarity:
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LENGTH: 521
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TT: Grimaldi, J. Christopher
NT: Stephan, Visional Manatinia, Canalandi, J. Christopher
NT: Stephan, Visional Manatinia, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, Canalandi, 
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FILING DATE: 1998-08-26
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R FILING DATE: 1998-09-24

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R APPLICATION NUMBER: 60/101786

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R FILING DATE: 1998-09-24

R FILING DATE: 1998-09-24

R FILING DATE: 1998-09-24

R FILING DATE: 1998-09-24

R APPLICATION NUMBER: 60/106178

R FILING DATE: 1998-10-28

R FILING DATE: 1998-10-28

R APPLICATION NUMBER: 60/106464

R APPLICATION NUMBER: 60/106464

R APPLICATION NUMBER: 60/106464

R APPLICATION NUMBER: 60/106965

R FILING DATE: 1998-10-30

R APPLICATION NUMBER: 60/106965

R FILING DATE: 1998-11-3

R APPLICATION NUMBER: 60/106965

R FILING DATE: 1998-11-17

R APPLICATION NUMBER: 60/106965

R FILING DATE: 1998-11-17
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R FILING DATE: 1998-09-23
R FILING DATE: 1998-09-24
R FILING DATE: 1998-09-24
R APPLICATION NUMBER: 60/101741
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DR APPLICATION NUMBER: 60/108849

DR FILING DATE: 1998-11-18

DR APPLICATION NUMBER: 60/112422

DR FILING DATE: 1998-12-15

DR APPLICATION NUMBER: 60/113296

DR FILING DATE: 1998-12-22

DR APPLICATION NUMBER: 60/113651

DR FILING DATE: 1998-12-23

DR FILING DATE: 1998-12-23

DR APPLICATION NUMBER: 60/113651
APPLICATION NUMBER: 60/099544
FILLING DATE: 1998-08-31
APPLICATION NUMBER: 60/09559
FILLING DATE: 1998-09-09
APPLICATION NUMBER: 60/099598
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FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099812
FILING DATE: 1998-09-10
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FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/100038
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APPLICATION NUMBER: 60/100385
FILING DATE: 1998-09-15
APPLICATION NUMBER: 60/100390
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APPLICATION NUMBER: 60/100848
FILING DATE: 1998-09-18
APPLICATION NUMBER: 60/100919
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FILING DATE: 1999-01-12
APPLICATION NUMBER: 60/115565
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FILING DATE: 1999-01-12
APPLICATION NUMBER: 60/119549
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APPLICATION NUMBER: 60/123618
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APPLICANT Goddard, Audrey
APPLICANT Goddard, Audrey
APPLICANT Goddard, Audrey
APPLICANT Goddard, Audrey
APPLICANT Goddorski, Paul J.
APPLICANT Gurney, Austin L.
APPLICANT Gurney, Austin L.
APPLICANT Stephan, Jean-Philippe F.
APPLICANT STEPHAN, Jean-Philippe F.
APPLICANT STEPHAN, Jean-Philippe F.
APPLICANT Watanabe, Colin L.
APPLICANT Watanabe, Colin L.
APPLICANT WATANION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE OF INVENTION: 2002-08-13
TITLE OF INVENTION: 2002-08-13
FRICH PLING DATE: 2002-08-13
PRIOR PLING DATE: 1002-04-09
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06334
PRIOR PLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06349
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/06354
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Publication No. US20030187202A1
GENERAL INFORMATION:
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Gerritsen, Mary
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                              DR FILING DATE: 1999-03-23

DR APPLICATION NUMBER: 60/126773

DR FILING DATE: 1999-03-29

DR FILING DATE: 1999-04-05

DR FILING DATE: 1999-04-05

DR FILING DATE: 1999-04-21

DR APPLICATION NUMBER: 60/131022

DR FILING DATE: 1999-04-26

DR APPLICATION NUMBER: 60/131020

DR FILING DATE: 1999-04-27

DR APPLICATION NUMBER: 60/131270

DR FILING DATE: 1999-04-27

DR APPLICATION NUMBER: 60/131445

OR FILING DATE: 1999-04-28

OR APPLICATION NUMBER: 60/134287

OR APPLICATION NUMBER: 60/14050

OR PILING DATE: 1999-06-22

OR APPLICATION NUMBER: 60/14050

OR PILING DATE: 1999-06-22

OR APPLICATION NUMBER: 60/14050

OR PILING DATE: 1999-06-22

OR APPLICATION NUMBER: 60/14050

OR PILING DATE: 1999-06-22

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OR APPLICATION NUMBER: 60/14050

OR PILING DATE: 1999-06-22

OR APPLICATION NUMBER: 60/14663

OR APPLICATION NUMBER: 60/14663

OR APPLICATION NUMBER: 60/14663

OR APPLICATION NUMBER: 60/14663

OR APPLICATION NUMBER: 60/149638

OR PILING DATE: 1999-08-03

OR PILING DATE: 1999-08-03

OR PILING DATE: 1999-08-17

OR PILING DATE: 1999-08-17

OR APPLICATION NUMBER: 60/149638

OR PILING DATE: 1999-08-17

OR PILING DATE: 1999-08-17

OR PILING DATE: 1999-08-17

OR PILING DATE: 1999-08-17

OR PILING DATE: 1999-08-17

OR APPLICATION NUMBER: 60/16418

OR PILING DATE: 1999-08-17

OR PILING DATE: 1999-08-17

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FILING DATE: 1999-12-07
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WS-10-219-067.71

WS-10-219-067.71

Sequence 71, Application US/10219067

Publication No. US20030187204A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc.

APPLICANT: Geritsen, Mary

APPLICANT: Geritsen, Mary

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

PRIOR INVENTION: ACIDS ENCODING THE SAME

FILE REFRENCE: PS304PCG.

CURRENT APPLICATION NUMBER: 60/062287

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/06313

PRIOR APPLICATION NUMBER: 60/06349

PRIOR APPLICATION NUMBER: 60/063849

PRIOR APPLICATION NUMBER: 60/063813

PRIOR APPLICATION NUMBER: 60/063813

PRIOR PILING DATE: 1997-10-12

PRIOR APPLICATION NUMBER: 60/063813

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-17

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US-10-219-067-71
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GENERAL INFORMATION:
APPLICANT: Baker, Kewin P.
APPLICANT: Gerritsen, Mary
APPLICANT: Geodewski, buc
APPLICANT: Geodewski, Paul J.
APPLICANT: Gerritsen, Mary
APPLICANT: Gerriadid, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Steehan, Jean-Philippe P.
APPLICANT: Wandanabe, Colin L.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
FILE REFERENCE: P3530PL67
CURRENT APPLICATION NUMBER: US/10/219,066
CURRENT PILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR FILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1998-03-20
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NUMBER OF SEQ ID NOS: 246
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ORGANISM: Homo Sapien
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US-10-219-066-71
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GENERAL INFORMATION:
APPLICANT: Beaker, Kevin P.
APPLICANT: Deenoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Sephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Watanabe, Colin L.
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APPLICANT: Sephan, Jean-Philippe F.
APPLICANT: Sephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079556
PRIOR PILING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
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Mismatches:
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86.72%
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ORGANISM: Homo Sapien
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CURRENT APPLICATION NUMBER: US/10/219,068
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-08-13
PRIOR FILING DATE: 1997-09-13
PRIOR FILING DATE: 1997-09-13
PRIOR PILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-28
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ORGANISM: Homo Sapien
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APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Gecriteen, Mary
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Grinald, J. Christopher
APPLICANT: Grinald, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin L
APPLICANT: Wood, Milliam I:
APPLICANT: Mood, Milliam I:
APPLICANT: Wood, : 10/119,480
PRIOR APPLICATION NUMBER: 60/06287
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06313
PRIOR APPLICATION NUMBER: 60/06314
PRIOR PLING DATE: 1997-10-13
PRIOR APPLICATION NUMBER: 60/06349
PRIOR APPLICATION NUMBER: 60/06349
PRIOR PLING DATE: 1997-03-12
PRIOR APPLICATION NUMBER: 60/063919
PRIOR APPLICATION NUMBER: 60/063919
PRIOR PLING DATE: 1998-03-20
PRIOR PLING DATE: 1998-03-26
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ProSerAsnieuVallysGluGlnArgVallYrGlnGluAlaThriysGlulleProThr 120
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                                                                                                               ThraspileaspPhePheCysGlu 128
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ORGANISM: Homo Sapien
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Query Match:
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APPLICANT: Goddard, Audrey
APPLICANT: Goddweki, Paul J.
APPLICANT: Godweki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Autein L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Western D.
APPLICANT: Worder D.
APPLICANT: Word, William I.
APPLICANT: Word, William I.
APPLICANT: Word, William I.
APPLICANT: Word DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-10-13
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PRIOR APPLICATION NUMBER: 60/07956
PRIOR APPLICATION NUMBER: 60/07956
PRIOR PILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/07956
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                                      Desnoyers, Luc
Gerritsen, Mary
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SEQ ID NO 71
LENGTH: 521
             Baker, Kevin P.
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US-10-219-069-71
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APPLICANT: Besnoy-Kevin F.
APPLICANT: Geartiesn, Mary
APPLICANT: Geddard, Audrey,
APPLICANT: Goddard, Audrey,
APPLICANT: Goddard, Audrey,
APPLICANT: Goddard, Audrey,
APPLICANT: Goddard, Austin L.
APPLICANT: Grimald, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, Milliam I.
APPLICANT: Wood, Milliam I.
APPLICANT: Wood, Milliam I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SOCKETED SAME
FILE REPERBACE: P5530p1C49
CURRENT FILING DATE: 2002-04-09
FRIOR APPLICATION NUMBER: 60/062287
FRIOR PILING DATE: 1997-10-13
FRIOR APPLICATION NUMBER: 60/06287
FRIOR APPLICATION NUMBER: 60/06287
FRIOR PILING DATE: 1997-10-31
FRIOR PILING DATE: 1997-10-31
FRIOR PILING DATE: 1997-10-31
FRIOR PILING DATE: 1997-10-31
FRIOR APPLICATION NUMBER: 60/06287
FRIOR APPLICATION NUMBER: 60/06287
FRIOR PILING DATE: 1999-10-31
FRIOR PILING DATE: 1999-10-31
FRIOR APPLICATION NUMBER: 60/06349
FRIOR PILING DATE: 1998-03-20
FRIOR APPLICATION NUMBER: 60/079294
FRIOR PILING DATE: 1998-03-20
FRIOR PILING DATE: 1998-03-20
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Publication No. US20030187208A1
APPLICANT: Baker, Kevin P.
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LENGTH: 521
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Alignment Scores:

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GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc
APPLICANT: Gerritean, Mary
APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

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APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

FRICK APPLICATION NUMBER: 60/06387

PRIOR APPLICATION NUMBER: 60/06387

PRIOR FILING DATE: 1997-10-18

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/06387

PRIOR FILING DATE: 1997-12-17

PRIOR FILING DATE: 1997-12-17

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1997-12-17

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-20

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Matches:
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; Sequence 71, Application US/10219480
; Publication No. US20030187209A1
; GENERAL INFORMATION:
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US-10-219-483-71

Sequence 71, Application US/10219483

Publication No. US20030187210A1

Publication No. US20030187210A1

APPLICANT: Baker, Kevin P.

APPLICANT: Gerritsen, Mary

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Austin L.

APPLICANT: Smith, Victorial

APPLICANT: Smith, Victorial

APPLICANT: Smith, Victorial

APPLICANT: Smith, Victorial

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APPLICANT: Smith, Victorial

APPLICANT: Smith, Victorial

APPLICANT: Smith, Victorial

APPLICANT: Smith, Victorial

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P333091C43

CURRENT APPLICATION NUMBER: US/10/219,483

FRIOR APPLICATION NUMBER: 10/119,480
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Conservative:
Mismatches:
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Gaps:
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PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 60/079728

PRIOR FILING DATE: 1998-03-27

Remaining Prior Application data removed - S

NUMBER OF SEQ ID NOS: 246

LENGTH: 521
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ORGANISM: Homo Sapien
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Best Local Similarity:
Query Match:
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Pred. No.:
                                                                                                                                                      US-10-219-480-71
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PRIOR FILING DATE: 2002-04-09
PRIOR PELIAGON NUMBER: 60/059113
PRIOR PELIATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-17
PRIOR PELIAGON NUMBER: 60/063549
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
PRIOR PELIAGON NUMBER: 60/069873
PRIOR PILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/069873
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1998-03-20
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APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc; APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.11e-83
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) ORGANISM: Homo Sapien
US-10-219-483-71
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Best Local Similarity:
Query Match:
DB:
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Mismatches:
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                                           ThraspileAspPhePheCysGlu 128
                                                               Sequence 71, Application US/10219526; Publication No. US20030187212A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Desnoyers, Luc; APPLICANT: Gerritsen, Mary
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86.72%
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; ORGANISM: Homo Sapien
US-10-219-526-71
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Best Local Similarity:
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                                 APPLICANT: Goddward, Audrey
APPLICANT: Goddward, Audrey
APPLICANT: Goddward, Austin L.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Santh, Victoria
APPLICANT: Stath, Victoria
APPLICANT: Stath, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Mood, Milliam I.
APPLICANT: MOOd, Milliam I.
APPLICANT: MOOD AND TRANSMEMBRANE POLYBEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 1933.020-08-13
CURRENT FILING DATE: 2002-04-09
FRIOR APPLICATION NUMBER: 60/062913
FRIOR APPLICATION NUMBER: 60/06287
FRIOR APPLICATION NUMBER: 60/06349
FRIOR APPLICATION NUMBER: 60/06349
FRIOR APPLICATION NUMBER: 60/06391
FRIOR APPLICATION NUMBER: 60/06391
FRIOR APPLICATION NUMBER: 60/06993
FRIOR FILING DATE: 1997-10-17
FRIOR APPLICATION NUMBER: 60/07924
FRIOR PELING DATE: 1998-03-20
FRIOR PELING DATE: 1998-03-26
FRIOR FILING DATE: 1998-03-27
FRIOR FILING DATE: 1998-03-26
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; ORGANISM: Homo Sapien
US-10-219-525-71
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Pred. No.:
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LENGTH: 521
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APPLICANT: Geritlean: Mary
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APPLICANT: Geritlean: Mary
APPLICANT: Geddard, Audfrey
APPLICANT: Geddard, Audfrey
APPLICANT: Geddard, Audfrey
APPLICANT: Geddard, Audfrey
APPLICANT: Germaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe P.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
CURRENT APPLICATION NUMBER: US/10/19, 480
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR APLICATION NUMBER: 60/06349
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/06393
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
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APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Madrey
APPLICANT: Goddard, Martin L.
APPLICANT: Grimadi, J. Christopher
APPLICANT: Grimadi, J. Christopher
APPLICANT: Grimadi, J. Calin L.
APPLICANT: Smith, Victoria
APPLICANT: Sephan, Jean-Philippe F.
APPLICANT: Sephan, Jean-Philippe F.
APPLICANT: Marcanbe, Colin L.
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APPLICANT: Marcanbe, Milliam I.
APPLICANT: Marcanbe, Milliam I.
APPLICANT: MARCAND: ACIDS ENCODING THE SAME
FILE REPERENCE: P3530PIC54
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Matches:
Conservative:
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; Sequence 71, Application US/10219530
; Publication No. US20030187213A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.11e-83
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Gerritsen, Mary
Goddard, Audrey
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                                                                   21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
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                                               US-10-019-455A-12 (1-128) x US-10-219-530-71 (1-521)
 Mismatches:
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Job time: 289.193 secs
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Sequence 1, Appli Sequence 193, App Sequence 61, Appl

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Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli

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Sequence Sequence Sequence

Scoring table:

Searched:

Perfect score:

Title:

Run on:

Sequence:

Sequence Sequence 1, Appli 197, App 3, Appli 14, Appl

Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Appl

Sequence

Sequence

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ADDRESESE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
RICH BATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31.575
REGISTRATION NUMBER: 31.575
REGISTRATION NUMBER: 31.575
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REGISTRATION NUMBER: 31.575
REGISTRATION NUMBER: 31.575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brighte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
UNDER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                     US-00-164-839-32
US-08-583-799-30
US-08-583-799-32
US-08-164-839-71
US-08-583-799-71
PCT-US95-08493-12
US-09-330-217-3
US-09-252-991A-2073
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US-08-630-915A-29
US-09-076-259-1
US-08-630-915A-197
US-09-444-053-3
                                             US-08-916-421B-1
US-08-630-915A-193
US-08-961-527-61
US-09-32B-352-760
US-08-630-915A-39
US-08-164-839-30
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US-08-995-659-14
US-09-215-649A-14
US-09-577-780-14
US-09-577-800-14
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REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                           US-09-871-856-14
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                                  US-08-583-799-5
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Sequence 18, Appl
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Sequence 24, Appli
Sequence 1, Appli
Sequence 48, Appli
Sequence 48, Appli
Sequence 79, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Appli
                                                                                    December 29, 2003, 16:24:24; Search time 40.6947 Seconds (without alignments) 1388.315 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                               1 MARILILLEGGLVVLCAGHG......RVYQEATKEIPTTDIDFFCE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_NA:*
11. /GGTQ_6/ptodatc/lina/5A_COMB.seq:*
12. /GGTQ_6/ptodatc/lina/5B_COMB.seq:*
3: /GGTQ_6/ptodatc/lina/6A_COMB.seq:*
41. /GGTQ_6/ptodatc/lina/6B_COMB.seq:*
51. /GGTQ_6/ptodatc/lina/6B_COMB.seq:*
62. /GGTQ_6/ptodatc/lina/PCTUG_COMB.seq:*
63. /GGTQ_6/ptodatca/lina/backfiles1.seq:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                             OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-578-649-1
US-08-578-649-4
US-08-578-649-4
US-08-578-649-8
US-08-578-649-24
US-08-578-649-3
US-07-646-5378-1
US-07-646-6918-48
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US-09-300-958A-30
US-09-300-958A-28
US-09-356-952-11
                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                  569978 seqs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                     BLOSUM62
Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                       US-10-019-455A-12
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   581
305
305
3565
3565
2793
2757
2757
4762
467
5398
                                                                                                                                                                                                                                                                                                                                                                                                          Command line parameters:
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Database :

277.5 261.5 247.5 219.5 210.5 177.5 89.5 89.5 82.5 87.5 87.5 88.5

26456786011

Result

COMPUTER READABLE FORM:

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75 GluàsnGlyàlaGlyGlu---PheTrpàlaGlySerValTyrGlyàspHísGlnàspGlu 93 [1] [1] [1] [1] [1] [1] [1] [1] [1] 268 ---AagGGCCGTGGGCGCTTTCTGGGGAGCAGCGTTCAGGGAGATTACTATGGAGAT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 TGCCGATTCCTGACCATTCACGGGCCAAGTGGTGTGTGTCTTCTCCAAGCTG---- 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 MetGly11e---ValGlyTyrPheProSerAsnLeuValLysGluGlnArgValTyrGln 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 CTGGCTGCTCGCCTGGGCTATTTCCCCAGTAGCATTGTCCGAGAGGACCAGAACCTGAAA 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CysArgPhelleAspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThr 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValValLeuCys-----Ala 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 ATGGCCCGGTCCTGGTGTGCCTT-----GGTGTCATCATCTTGCTGTCTTCTCC 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 GlyHisGlyValPhe-----MetAspLysLysLeuSerLysLysLysLeuCysAlaAsp 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 GluGluCysValTyrThrileSerLeuAlaArgAlaGluAspTyrAsnAlaProAsp 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 GlualaThrLysGluIleProThrThrAspIleAspPhePheCysGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 CCTGGCAAAGTCGATGTGAAAGACAAATGGGATTTCTACTGCCAG 432
                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/08578649
; Patent No. 577036
; GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
COTATION New York
                                                                                                                                                                                                                                                                                                                                            Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-019-455A-12 (1-128) x US-08-578-649-1 (1-459)
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                            5.94e-31
277.50
64.71%
43.38%
41.05%
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                           mat_peptide
                                                                                                                                                                                           NAME/KEY: sig_peptide LOCATION: 40..111
                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                            40..432
                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                        NAME/KEY: CDS
LOCATION: 40..
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US-08-578-649-18
                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                             LOCATION:
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3 3 ATGGCTGTGGCCCTTCAGGACTACATGGCCCCCGACTGCCGATTCCTGACCATTCACGG 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 rascassicadocaricassicarinacranssasarcrescrescrescressicative 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu---Phe 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 MetAspLysLeuSerSerLysLysLysLeuCysAlaAspGluGluCysValTyrThrlleSer 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 LeualaargalaGlnGluAspTyrAsnAlaProAspCysArgPhelleAspValLysLys 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REALBABLE FORM:

MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: Wedgerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION WHERE: DF 43 24 247.2
PRIOR APPLICATION NUMBER: DF 94 3 24 247.2
FILING DATE: 20-July-1993
ATONRAY/AGBAT INPORMATION
NAME: Andrew L. Tialoloff
REGISTRATION NUMBER: 31,575
RESPERNCE/POCKET UNMBER: 31,575
RESPERNCE/POCKET UNMBER: 31,575
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9300
TELEPRATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 4..6
OTHER INFORMATION: /function= "Startcodon Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-019-455A-12 (1-128) x US-08-578-649-18 (1-330)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 GACAAATGGGATTTCTACTGCCAG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 4, Application US/08578649
; Patent No. 5770366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261.50
67.59%
45.37%
38.68%
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 330 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: mat peptide LOCATION: 7..327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ropology:
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305 GGCCAAGTGTGTGTCTTCTCCAAGTTG-----AAGGCCGTGGGCGTTTTC 355
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                                                                                        101 ProserAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
                                                                                                                                                             |||||||:::::|||::::|||
416 CCCAGTAGCATTGTCCGGGAGGACCTGAACTCGAAACCTGGCAAAATTGATGAAGAACC 475
                                                          82 TrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIle---ValGlyTyrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER KEADABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOCTAMES: Wordeperfor
SOCTAMES: Wordeperfor
SOCTAMES: Wordeperfor
SOCTAMES: Wordeperfor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-7uly-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-7uly-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoloff
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brigite Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pelfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: join[1..29, 277..305)
OTHER INFORMATION: /function= "Primer"
                                                                                                                                                                                                                                             |||||||:::|||:::
476 GATCAATGGGATTTCTACTGCCAG 499
                                                                                                                                                                                                                         121 ThraspileaspPhePheCysGlu 128
                                                                                                                                                                                                                                                                                                                                    ; Sequence 8, Application US/08578649
; Patent No. 5770366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.64e-23
219.50
64.65%
44.44%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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Pred. No.:
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US-08-578-649-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 LeuAlaArgAlaGluGluAspTyrAsnAlaProAspCysArgPhelleAspValLysLys 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 GlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu---Phe 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 MethsplysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThrileSer
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23
23
40
10
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: 1BM PS/2
OPPRATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
FILLING DATE: 29-July-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIPECATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
APPLICATION NUMBER: DE P 93 24 247.2
FILING DATE: 20-3011/9-1993
ATTONEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: BOER 1035-PFF/ALT
REPERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELEPOMNICATION INFORMATION:
TELEPOMNICATION INFORMATION:
TELEPOMNICATION INFORMATION:
TELEPOMNICATION SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 base pairs
TENGTH: 581 base pairs
TENGTH: 581 base pairs
TENGTH: S81 base pairs
TENGTH: S81 base pairs
TENGTH: S81 base pairs
TENGTH: S81 base pairs
TENGTH: S81 base pairs
                                      APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brighte Kaluza
TITLE OF INVENTION: MELANOWA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-..0-019-455A-12 (1-128) x US-08-578-649-4 (1-581)
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247.00
60.94%
42.97%
36.54%
                                                                                                                                                             ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sig_peptide
110..178
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110..499
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                                                                                                                                                                                                                         New York
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Best Local Similarity:
Query Match:
                                GENERAL INFORMATION:
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LOCATION:
FEATURE:
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FEATURE:
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LOCATION:
US-08-578-649-4
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LOCATION:
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                                                                                  89 AspHisGln---AspGluMetGlyIleValGlyTyrPheProSerAsnLeuValLysGlu 107
                                                                                                                                                                                                                                            7 AAGITITCGGCGGATCAGGAGTGCASCCACCTATCTCCATGGCTGTGGCCTTTCAGGAC 66
                                                                                                                                                      70 SerLysLeuValThrGluAsnGlyAlaGlyGlu---PheTrpAlaGlySerValTyrGly 88
                 30 LysLeuCysAlaAspGluGluCysValTyrThrIleSerLeuAlaArgAlaGluGluAsp 49
                                                                                                                                                                                                                                                                                       108 GlnArgValTyrGlnGluAlaThrLysGluIleProThrThrAspIleAspPhePhe 126
                                                                                                                                                                                                                                                                                                           238 GACCAGACCTGAAACCTGGCAAAGTCGATGTGAAGACAGATAAATGGGATTTCTAC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(40..111, 40..166, 214..347, 393..503, 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALT: X-02.
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/08578649
Patent No. 577036
GENERAL INPORMATION
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brightre Kaluza
TITLE OF INVENTION: MELANOWA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOER 1035-PFF/ALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: DE P 43 24 247.2 FILING DATE: 20-July-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordberfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-Duly-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIOKNELL AGENT LITERATION.

NAME: ALGEW L. TTAJOIOFF
REGISTRATION NUMBER: 31,575
REFRENCE/DOCKET NUMBER: BOER
TELECOMMUNICATION INFORMATION:
TELEPAK: (212) 638-3200
TELEPAK: (212) 838-384
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sig_peptide
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LOCATION:
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86 -----ValTyrGlyAspHisGlnAspGluMetGlyIle---ValGlyTyrPhePro 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 GACCCTATCTCCATGGCTGTGGGCCTTCAGGACTACATGGCCCCCGACTGCCGATTCCTG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------AspPhe 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 GACGIGGAGIGICAIGGGGGCIGGCANTITCCCCTITICITTTTCAGAAAIGGGAITITC 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 GGGCGCTCTTCTGGGGAGGCAGCGTGGGTCTTGGGAGAGTGAAANAGCTTTTAACTCCT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThrThr 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetAlaArglleLeulleLeuLeuGlyGlyLeuValValLeuCys-----Ala 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 GluGluCysValTyr---- 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 ---ThrileSerLeuAlaArgAlaGinGluAspTyrAsnAlaProAspCysArgPheile 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 ATGGCCCGGTCCCTGGTGTCTT-----GGTGTCATCATCTTGCTGTCTTCTCC 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 GlyHisGlyValPhe------MetAspLysLeuSerSerLysLysLeuCysAlaAsp 34
                                                                                                                                                                                              LOCATION: one-of(194, 369, 527)
OTHER INFORMATION: /note= "N in positions 194, 369
OTHER INFORMATION: and 527 denotes an indefinite number and sequence
OTHER INFORMATION: of nucleotides "
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29
33
62
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Matches:
Conservative:
Mismatches:
Indels:
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48.63%
32.79%
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                                                                                               393..503
                                                                                                                                                     549..569
                                                214..347
40..166
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                  exon
                                                                                    exon
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                                                                                                                                   NAME/KEY:
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                                NAME/KEY:
                                                LOCATION:
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                                                                                  NAME/KEY:
                                                                FEATURE
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---AGAGTGAAA 1740
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1492 CAGGAGTGCAGCCGTAAGAATGGGGAGGGGTAGAATTGGGCTTGGGTGTTAGCCTGTGTG 1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 TyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsnLeuValLys 106
                                          18 GlyHisGlyValPhe-----MetAspLysLeuSerSerLysLysLeuCysAlaAsp 34
                                                                                                                                                                                                                                                                                                                                                                                                            68 ValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu---PheTrpAlaGlySerVal 86
                                                                                                                                                                                                                               .-----ValTyrThrileSerLeuAlaArgAlaGln 47
                                                                                                                                                                                                                                                                                                                    48 GlukspTyrAsnAlaProAspCysArgPheIleAspValLysLysGlyGlnIleTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1741 GAGGAAGGGTACAGAGCTGGGGTAGACTCATTATCCCC 1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 GluglnArgValTyrGlnGluAlaThrLysGluilePro 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/646,537B FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Barbacid, Mariano
TITLE OF INVENTION: Vav Proto-Oncogene Protein
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Bristol-Myers Squibb Company STREET: P.O. Box 4000 CITY: Princeton STREET: New Jersey COUNTRY: U.S.A. ZIP: 08543-4000 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPATIBLE FORM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --cgrcrrddg----
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Patent No. 5348864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GAU1, Timochy J.
REGISTRATION NUMBER: 33,111
REFERENCE/DOCKET NUMBER: DC10
TELECOMMUNICATION INFORMATION:
TELEFRAX: (609) 921-5901
TELEFRAX: (609) 921-5901
TELEFRAX: (609) 921-6501
TELEFRAX: (609) 921-6501
TELEFRAX: (799) 921-6501
TELEFRAX: (799) 921-6501
TELEFRAX: (799) 921-6501
TELEFRAX: (799) 921-6501
TELEFRAX: (799) 921-6501
SEQUENCE CHARACTERISTICS: LENGTH: 2793 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                         38 -----
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LOCATION: 2804..2914

NAME/KEY: exon

LOCATION: 3232..3252

LOCATION: 0ne-of(2216)

LOCATION: one-of(2216)

OTHER INFORMATION: /note= "N in position 2216

OTHER INFORMATION: nucleotides"
                                 APPLICANT: ULTICA DAYBOARD
APPLICANT: Brighte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 13.5 inch 1.44 Mb storage diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER READABLE FORM:
ADDIOMY TATA:
APPLICATION NUMBER: 105-001/4-1994
APPLICATION NUMBER: 31,575
REGISTRATION NUMBER: 31,575
RELEFAX: (212) 888-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3565 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
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177.50
46.41%
35.29%
26.26%
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LOCATION: 1378..1449
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1586..1719
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Best Local Similari
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Pred. No.:
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NAME/KEY:
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14..2545

, NAME/KEY: , LOCATION: US-07-646-537B-1

MetAlaArgileLeuileLeuLeuGlyGlyLeuValValLeuCys------Ala 17

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2429 GATATCATC------AAGATCCTCAATAAGAAGGACAGCAAGGCTGGTGGCT 2476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-306-691B-48

| Sequence 48, Application US/08306691B
| Sequence 48, Application US/08306691B
| Patent No. 5734039
| Patent No. 5734039
| GENERAL INFORMATION:
| APPLICANT: Calabretta, Bruno
| APPLICANT: Skorski, Tomasz
| TITLE OF INVENTION: OLIGONUCLECTIDES TARGETING COOPERATING ONCOGENES
| TITLE OF INVENTION: OLIGONUCLECTIDES TARGETING COOPERATING ONCOGENES
| TITLE OF INVENTION: OLIGONUCLECTIDES TARGETING COOPERATING ONCOGENES
| TITLE OF INVENTION: OLIGONUCLECTIDES TARGETING COOPERATING ONCOGENES
| TITLE OF INVENTION: OLIGONUCLECTIONS & Monaco, P.C.
| ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
| STREET: Two Penn Center, Suite 1800
| CITY: Philadelphia
| STATE: Pennsylvania
| COUNTRY: OLIGONUCLECTIONS & MONACO, P.C.
| COUNTRY: OLIGONUCLECTIONS & MONACO, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                          84 GlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsn 103
                                                                                                                                                                                                                                      44 AlaArgAlaGluAspTyrAsnAlaProAspCysArgPheIleAspValLysLysGly 63
                                                                                                                                                                                                                                                                                                                                           64 GlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGluPheTrpAla 83
                                                                                                                                                                                            US-10-019-455A-12 (1-128) x US-07-646-537B-1 (1-2793)
                                                                  Conservative:
Mismatches:
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COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 LeuvalLysGluGlnArgvalTyrGlnGlu 113
                                             Matches:
                                                                                                                 Indels:
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SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                               Gaps:
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TELEPHONIC (215) 568-833
TELEPHONE: (215) 568-5549
TELEPHONE: (215) 568-5549
INFORMATION: 9734039
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2757 base pairs
TENE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Monaco, Daniel A. REGISTRATION NUMBER: 30,480
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                                             91.50
52.86%
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13.54%
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US-08-306-691B-48
                                                                                            Best Local Similarity:
                                                                          Percent Similarity:
Alignment Scores:
Pred. No.:
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Alignment Scores:

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Sequence 79, Application PC/TUS9306251
; Sequence 79, Application PC/TUS9306251
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
                                                                                                                                            2433 GGGAGAGATCTATGGCCGG-------GTTGGCTGGTTGCTGCCTGCCAAC 2471
                                                                                                                                                                                                                                                                               84 GlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsn 103
                                                                                                                                                                                                           64 GlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGluPheTrpAla 83
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23
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APPLICATION NUMBER: PCT/US93/06251
                                                                                                                US-10-019-455A-12 (1-128) x US-08-306-691B-48 (1-2757)
                               Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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 Length:
Matches:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELERPHONE: 516-742-4343
TELEFAK: 516-742-4366
TELEFAK: 530 901 SANS UR
INFORMATION FOR SEQ ID NO: 79:
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
0.0104
89.50
52.86%
32.86%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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Best Local Similarity:
Query Match:
DB:
                               Percent Similarity:
Best Local Similarity:
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CLASSIFICATION:
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; Sequence 28, Application US/09300958A; Patent No. 6495319
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30.77%
12.13%
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Best Local Similarity:
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LOCATION: (462)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (428)
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US-09-300-958A-28
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Sequence 30, Application US/09300958A

Sequence 30, Application US/09300958A

Setent No. 6495119

GENERAL INFORMATION:

APPLICANT: McClelland, Michael

APPLICANT: Trenkle, Thomas

TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of

TITLE OF INVENTION: Using Same

FILE REFERENCE: P-PH 3457

CURRENT PAPLICATION NUMBER: US/09/300,958A

CURRENT PILING DATE: 1999-04-27

PRIOR APPLICATION NUMBER: 60/093,331

PRIOR APPLICATION NUMBER: 60/093,331

PRIOR PILING DATE: 1998-04-27

PRIOR PILING DATE: 1999-02-04

PRIOR FILING DATE: 1999-02-04

NUMBER OF SEQ ID NOS: 85

SOFTWARE: PATENTING DATE: 1998-08-27

NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2405 CTGGGCATTGCCATCGCTCGGTATGACTTCTGTGCCAAGAGATATGAGAGATTGTCCTTG 2464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2465 TTGAAAGGAGGTGTGGGGAAGATTTACACAAAGATG-----AGTGCAAATGGC 2512
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                                                                                                                                                                                                       81 PherrphlaglyServalryrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 IleSerLeuAjaArgAjaGlnGluAspTyrAsnAjaProAspCysArgPhelleAspVal 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LyslysglyglnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
                                                                                                                             64 GlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGluPheTrpAla 83
                                                   44 AlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspValiysLysGly 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-019-455A-12 (1-128) x US-09-300-958A-30 (1-4762)
                 US-10-019-455A-12 (1-128) x PCT-US93-06251-79 (1-2757)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
                                                                                                                                                                                                                             2433 GGGGAGATCTATGGCCGG------
                                                                                                                                                                                                                                                                                                                   2472 TACGTGGAGGÁGAT-----TATTCTGAA 2495
                                                                                                                                                                                                                                                                                 104 LeuValLysGluGlnArgValTyrGlnGlu 113
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Matches:
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2513 TGGTGGAGAGGAGAAGTAAATGGCAGG---
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Best Local Similarity:
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| GENERAL INFORMATION:
| APPLICANT: McClelland, Michael |
| APPLICANT: McClelland, Michael |
| APPLICANT: McClelland, Michael |
| APPLICANT: Welsh, John |
| APPLICANT: Welsh, John |
| APPLICANT: Trenkle, Thomas |
| TITLE OF INVENTION: Using Same |
| TITLE OF INVENTION: Using Same |
| FILE REFERENCE: P-PH 3457 |
| CURRENT APPLICATION NUMBER: US/09/300,958A |
| CURRENT PILING DATE: 1999-04-27 |
| PRIOR APPLICATION NUMBER: 60/098,070 |
| PRIOR PILING DATE: 1998-04-27 |
| PRIOR FILING DATE: 1998-02-04 |
| PRIOR FILING DATE: 1998-02-04 |
| NUMBER OF SEQ ID NOS: 85 |
| SOFFWARE: PRECEIT VERSEL OF SEQ ID NOS: 85 |
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APPLICANT: Margarit, S. M.
APPLICANT: Bor-Sogi, Dafna
APPLICANT: Cole, Philip
APPLICANT: Kuriyan, John
APPLICANT: Kuriyan, John
TITLE OF INVENTION: THEREOF
FILE REPERENCE: 600-1-228N
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Matches:
Conservative:
Mismatches:
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CURRENT FILING DATE: 1999-07-19
EARLIER APPLICATION NUMBER: 60/093,631
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us-10-019-455a-12.rni

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610 TGGTGGGATTGGTTATTGACGACAGTAATGGGAAAGTTAAC---AGAGGCTGGTTT 666
                                                                                                                                                                                                                                                                                                                                                                                                                                        81 PhejrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     505 GCTGCTTATGACTTTAATTATCCCATTAAAAAGACAGTTCTTCGCAACTTTTGTCTGTA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 AlaGlnGluAspTyrAsnAlaPro------AspCysArgPhelleAspVal 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
                                                                                                                                                                                                                                                                                                                                                                                                          26 LeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThrileSerLeuAlaArg 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: NACOKI, MASAO
APPLICANT: NACASE, KAZUO
APPLICANT: NACASE, KAZUO
APPLICANT: NATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSER: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                  US-10-019-455A-12 (1-128) x US-09-356-952-11 (1-5398)
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                                                                                                                                                                                                                   Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                               ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 3, Application US/08164839; Patent No. 5514573; GENERAL INFORMATION:
EARLIER FILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 5398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                      US-09-356-952-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-164-839-3
                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                       No.
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1174 GAGGTGAACGCTGACACCATCTACTGGATCGTCCAAAAAGATGGCCAACGA----- 1224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 LysGluGlnArgValTyrGlnGluAlaThrLysGluIle-----ProThrThrAspIle 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 valtyrglyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsnLeuVal 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 AspTyrAsnAlaProAspCysArgPheileAspValLysLysGlyGlnGlnIleTyrVal 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-583-799-3
Sequence 3, Application US/08583799
Sequence 3, Application US/08583799
Patent No. P607849
Sequence 3, Application US/08583799
Sequence 3, Application
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANUSHI, KAZUO
APPLICANT: NAKANUSHI, KAZUO
APPLICANT: MAGASH
APPLICANT: MAGASH
APPLICANT: MAGASH
APPLICANT: MACAUGH
APPLICANT: MATUH
ITILE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-019-455A-12 (1-128) x US-08-164-839-3 (1-2085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                   REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Oblon, No. 5514573man F.
                                                                                     TELEPHONE: (703)412-3000
TELEFAX: (703)413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Pagrus major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.44
77.00
52.50%
27.50%
11.39%
                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..2082
                                                                                                                                                                                                                                                                           linear
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STATE: Virginia
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
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STREET: 1755 Jefferson Davis Highway, Fourth Floor
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                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELEFAX: (703)412-3000
TELEFAX: (703)412-3000
TELEFAX: (703)412-3000
TELEFAX: (703)412-3000
TELEFAX: (703)412-3000
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2520 base pairs
                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pagrus major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.579
77.00
52.50%
27.50%
11.39%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 34..2121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                  CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                          22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                      COUNTRY:
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DB:
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Patent No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MAGASE, KAZUO
APPLICANT: MAGASE, KAZUO
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,799
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/004,729
FILING DATE: 14-1933
ATYORNEY AGENT INFORMATION:
NAME: Oblon, No. 5607849man F.
REFERNCE/DOCKET NUMBER: 24,618
REFERNCE/DOCKET NUMBER: 10-599-0
TELECHANISICATION INFORMATION:
TELECHANIS (703)412-3000
TELEFAX: 240855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE: ORGANISM: Pagrus major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.00
52.50%
27.50%
11.39%
                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..2082
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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1210 GAGGTGAACGCTGACACCATCTACTGGATCGTCCAAAAAGATGGCCAACGA----- 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 ASDTyrASnAlaProASpCySArgPheIleASpValLySLySGlyGlnGlnIleTyrVal 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252
22
20
20
28
10
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-019-455A-12 (1-128) x US-08-164-839-5 (1-2520)
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Matches:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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| c - nucleic search, using sw model | December 29, 2003, 22:08:26 ; Search time 1045 Seconds (without alignments) 12918.830 Million cell updates/sec | US-10-019-455A-23 COFE: 330 1 catggaatattatggaccgatattgacttcttctgcgag 330 | : 1DEN1111<br>Gapop 10<br>2888711 | of hits satisfying chosen par | B seq length: 0<br>B seq length: 200000000 | essing: Minimum Match 0%<br>Maximum Match 100%<br>Listing first 45 summaries | GenEmbl:*  1: qbbba:*  2: qbbba:*  4: qbba:*  5: qbbng:*  6: qbpat:*  7: qbbpt:*  8: qbbpt:*  9: qbbp:*  10: qbbp:*  11: qbbr:*  11: qbbr:*  12: qbbp:*  13: qbbn:*  14: qbv:*  15: qbbn:*  16: qmbp:*  17: qmbr:*  18: qbbn:*  18: qbbn:*  19: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  11: qbbn:*  12: qbbn:*  13: qbbn:*  14: qbv:*  15: qmbn:*  16: qmbr:*  16: qmbr:*  17: qmpr:*  18: qmbn:*  18: qmbn:*  18: qmbn:*  19: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:*  10: qmbr:* |  |
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|                                    |                                                                                                                | score:                                                                    |                                   | mber of                       | Minimum DB seq le<br>Maximum DB seq le     | Post-processing:                                                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |  |

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description        | 0.0      | lovel    | lovel    | AX358818 Sequence<br>AX362311 Sequence | equenc   | eque<br>Tomo | Omol           | love]    | omo<br>Jomo | love]    | BD093118 Novel pol<br>BD010805 Novel pol | Vove     | AF243504 Mus muscu<br>RD010821 Novel pol | Nove     | Mus          |          | Nove     | Nove           | Nove       | Nove     | Nove<br>Gall | Ношо      | Huma       | Mus              | AC106161 Rattus no | attus          | BT007044 Homo sapi<br>BT007775 Synthetic | Sequence       | 2 Seg  | AX016785 Sequence | 200           |            | A Tan-2002           | THEAT FOR T                   |                   |                                  | 9 . 0                                           |                                                       |
|-----------|--------------------|----------|----------|----------|----------------------------------------|----------|--------------|----------------|----------|-------------|----------|------------------------------------------|----------|------------------------------------------|----------|--------------|----------|----------|----------------|------------|----------|--------------|-----------|------------|------------------|--------------------|----------------|------------------------------------------|----------------|--------|-------------------|---------------|------------|----------------------|-------------------------------|-------------------|----------------------------------|-------------------------------------------------|-------------------------------------------------------|
| SUMMARIES | GI.                | BD010816 | BD093117 | BD093103 | AX358818                               | AX454774 | AX491252     | AF243505       | BD010820 | BD093121    | BD010817 | BD093118                                 | BD093106 | .0 AF243504                              | BD093122 | .0 MMU243939 | BD010836 | BD093137 | BD093136       | 5 BD010830 | BD010829 | S BD093130   | HSA252325 | 9 HS705D16 | 2 BX510362       | AC106161           | 9 RNU67884     | BT007044                                 | ~ ~            | A42942 |                   | AX28720       | ALIGNMENTS |                      | 330 DP<br>and DNA thereof.    | 39189             | · (u                             | rdata; Crania<br>nates; Catari                  | H.<br>WA thereof                                      |
|           | ry<br>ch Length DB | 330      | 330      | 384      | 521                                    | 521      | 521          | 865            | 923      | 923         | 330      | 330                                      | 384      | 929                                      | 947      | 958          | 330      | 330      | 384            | 307        | 261      | 7 261        | 232       | 0 121151   | 8 144765         | 1 215581           | 0 259<br>4 545 | 2 396                                    | 2 396<br>2 433 | 2 459  | 2 459             | 2 459<br>459  |            | ·                    | BD010816<br>Novel polypeptide | 16<br>16.1 GI:186 | 01069994-A/17.<br>sapiens (human | ota; Metazoa;<br>ia; Eutheria;<br>ses 1 to 330) | Yoshimura, K. and Tanaka,<br>Novel polypeptide and Di |
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|           | Result<br>No.      | 1        | 00 (     | ሳ ቀ      | ın v                                   | ۰,       | ω (          | φ <del>-</del> | 11       | 12          | 14       | 15                                       | 17       | 18                                       | 20       | 21           | 23       | 24.      | 52<br>52<br>72 | 27         | 7 R      | 30           | 32        | 33         | 3 7<br>5 5       | c 36               | 33             | 36                                       | 4<br>41<br>41  | 42     |                   | Ω<br>4 4<br>5 |            | RESULT 1<br>BD010816 | DEFINITI                      | ACCESSION         | SOURCE                           | REFERENCE                                       | TITLE                                                 |

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29-JUN-2000 WO 2000JP004278
30-JUN-1999 JP 99P 186718
YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
                                                                                                                                                                                                                    C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
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02,C12R1:19)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 384)

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OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
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Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 3 21-MAR-2001,
TAKEND CHEMICAL INDUSTRIES LTD
OS Homo sapiens (Numan)
PN JP 2001069994-A/3
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100.0%; Pred. No. 6.7e-90;
tive 0; Mismatches 0;
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/organism="Homo sapiens"
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Patent: WO 0102564-A 17 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
                                                                                                                                                                                      YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
CIZNI5/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 330)
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Yoshimura,K. and Tanaka,H.
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    Patent: JP 2001069994-A 17 21-MAR-2001;
TAKEDA CHMICAL INDUSTRIES LTD
OS HOMO SAPIENS (human)
PN JP 2001069994-A/17
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/db_xref="taxon:9606"
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29-JUN-2000 JP 2000195911
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Homo sapiens (human)
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Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
11-JAN-2001
29-JUN-2000 WO 2000JP004278
30-JUN-1999 JP 99P 186718
YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                               I YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
C C12N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00,
A61K38/17,
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100.0%; Score 330; DB 6;
Best Local Similarity 100.0%; Pred. No. 6.9e-90;
Matches 330; Conservative 0; Mismatches 0;
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Genentech Inc. (US)
Location/Qualifiers
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Sequence 71 from Patent WO0193983.
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/mol_type="genomic DNA"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
70 c 106 g 109
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WO 0102564-A/3.

Homo sapiens (human)
Homo sapiens (human)

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,

Yoshimura; K. and Tanaka,H.

Novel polypeptide and its DNA

Novel polypeptide and its DNA

AL TAKEDA CHEMICAL INDUSTRIES ITD,YABURXI ITO,KAZUNORI NISHI, KAZUHIRO

OGI, SHOICHI OKUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,

HIDBYURI TANAKA

OS Homo sapiens (human)

PN WO 0102564-A/3
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                                                                       YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
CIZNIS/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A6
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                                              YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO,
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Location/Qualifiers
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Novel polypeptide and its DNA.
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29-JUN-2000 JP 2000195911
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PI YUKO NOGU
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241 TATTTCCCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTT 300
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Matanabe,C.K., Milliams,P.M., Nood,W.I.
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Sequence 359 from Patent WO0208284.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_tref="texton:9606"
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                                                                                                        Length 521;
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llarity 100.0%; Pred. No. 7.1e-90;
Conservative 0; Mismatches 0;
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Genentech, Inc. (US)
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/organism≈"Homo sapiens"
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/db_xref="taxon:9606"
                /db_xref="taxon:9606"
86 c 131 g
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Robertson,N.G., Heller,S., Lin,J.S., Resendes,B.L., Weremowicz,S.,
Denis,C.S., Bell,A.M., Hudspeth,A.J. and Morton,C.C.
Direct Submission
Submitted (09-FEB-2000) Pathology, Brigham and Women's Hospital, 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="otoraplin"
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/db_xref="G1:8927428"
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NLVKRQRVYQBATKEVPTTDIDFFCE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 TATACTATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATT 218
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                     1 (bases 1 to 846)
Robertson, N. G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Bebris, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C.
A novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping Genomics 66 (3), 242-248 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
mol_type="makk"
db_xref="taxon:966"
/chromosome="20"
/map="20pf11.23-cpl2.1"
/tissue_type="cochlea"
/dev_stage="fetus"
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Matches 330; Conservative 0
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                       Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 330; DB 6;
Best Local Similarity 100.0%; Pred. No. 7.1e-90;
Matches 330; Conservative 0; Mismatches 0;
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Patent: WO 0200690-A 359 03-JAN-2002;
Genentech, Inc. (US)
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                              CCCACCACGGATATTGACTTCTTCTGCGAG 330
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Sequence 359 from Patent W00200690.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
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                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 92.)

Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H.
Yoshimura,K. and Tanaka,H.
Paten: JP 201069994-A 21 21-YAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                         YUKO NOGUCHI,KOJI YOSHIMURA,HIDBYUKI TANAKA
CI2N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02,
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Novel polypeptide and DNA thereof.
BD010820
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/db_xref="taxon:9606"
_147 c 213 g 26
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JP 2001069994-A/21
21-MAR-2001
                                          BD010820.1 GI:18639193
JP 2001069994-A/21.
                                                                                 Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                               Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear
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                                                                                   Eukaryora, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 865)
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Cohen-Salmon,M., Frenz,D., Verpy,B., Voegeling,S. and Petit,C.
Direct Submission
Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue
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                                                                                                                                          Cohen-Salmon,M., Frenz,D., Liu,W., Verpy,E., Voegeling,S. and Petit,C.
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J. Biol. Chem. 275 (51), 40036-40041 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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Location/Qualifiers
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            AF243505.1 GI:11991843
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/gene="FDP"
                                                   Homo sapiens (human)
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/produčt="melanoma inhibitory activity like protein"
/protein_id="CAC27443.1"
/db_xref="G1:12619173"
/translation="MARILLELPGLVAVCAVHGIFWDRLASKKLCADDECVYTISLA
/translation="MARILLELPGLVAVCAVHGIFWDRLASKKLCADDECVYTISLA
SAGEDYNAPDGRPINVTKGQQIYYYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPR
NLVKEQRVYQEATKEVPTTDIDFFCE"
                                                                                                                                                                             Idencification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation Genomics 71 (1), 40-52 (2001)
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                             Thirty (bases 1 to 1422)

Rendtorff, N.D.

Rendtorff, N.D.

Birect Submission

Submitted (21-MAY-1999) Rendtorff N.D., Department of Medical Genetics, Institute of Medical Biochemistry and Genetics,

Blegdamsvej 3, 2200 Copenhagen N, DENMARK

Revised by author 03-A051399 (Mus musculus mRNA)

Related sequence: AJ253324 to AJ252327 (genomic sequence).

Related sequences: AJ25324 to AJ252327 (genomic sequence).
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                                                                                                                                         Rendtorff,N.D., Frodin,M., Attie-Bitach,T., Vekemans,M. and
melanoma inhibitory activity like protein; Mial gene
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/db_xref="mcNA"
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/fissue_type="brain and cochlea"
i. .1422
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364..387
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AA242552.1 GI:12619172
                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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CI2N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC
A61K38/17,
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29-JUN-2000 WO 2000JP004278
30-JUN-1999 JP 99P 186718
YASUJAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
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a _147 c 213 g 260
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
WO 0102564-A/21
                       GI:22638709
                       BD093121.1 GI:22638'
WO 0102564-A/21.
Homo sapiens (human)
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
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S 1to, Y., Nasiali, R., Ogi, R., Okubo, S., Mogl, S., Noguchi, Y.,
Yoshimura, R. and Tanaka, H.
Novel Polypeptide and DNA thereof
L Patent: JP 2001069994-A 18
EN JP 2001069994-A 18
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PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
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iive 0; Mismatches 0;
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/mol_type="genomic DNA"
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 /gene="MIAL"
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YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
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                                                                                                                                                            61 PATACTATTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATT 120
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Score 252.2; DB 6; Length 330;
Pred. No. 4.5e-66;
0; Mismatches 48; Indels 0
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Query Match 76.4%; Score 252.2; DB 6; Length 330; Best Local Similarity 85.4%; Pred. No. 4.5e-66; Matches 281; Conservative 0; Mismatches 48; Indels 0;
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Search completed: December 30, 2003, 04:07:58 Job time : 1046 secs

gil35f01. gi27g09.y gi108g04. gi06c09.y BB611549

nucleic

ä Run Sequence:

Searched:

Minimum D Maximum D

Database

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Landysis of gene expression in the mouse Organ of Corti at the onset of hearing
Unpublished
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kacharbenided.nih.gov
Plate: 143 row: b column: 10
Plate: 143 row: b column: 10
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Location/Qualifiers
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BC569268 gi125a12.r
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gil43bl0.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gil43bl0 5', mRNA sequence.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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        BQ570035 gi143b10.
BQ564607 gi19h02.y
BQ568498 gi109c02.
BQ564134 gi11d01.y
                                                                                                                                               December 30, 2003, 01:02:37 ; Search time 1098.31 Seconds (without alignments) 7302.593 Million cell updates/sec
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                                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                    22781392 seqs, 12152238056 residues
                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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DB seq length: 200000000
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as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have know function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
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                                                                                                                                                 /clone="gi143b10"
/sex="male and female"
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BQ564607

VERSION

RESULT 2

76.4%; Score 252.2; DB 13; Length 398; 85.4%; Pred. No. 9.5e-64; trive 0; Mismatches 48; Indels 0; Query Match Best Local Similarity 85.49 Matches 281; Conservative

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/sex="male and female"
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/dev stage="Post natal day 5 to 13"
/dev stage="Post natal day 5 to 13"
/clone lib="Mouse Organ of Corti; Vector: pBluescript: The note="Organ: Organ of Corti; Vector: pBluescript: The organ of Corti (OC) was fine dissected from a total of 386 oc as follows: 102 samples from pst-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epitehlum was carefully dissected out of the modiolus. 240 488 bp mRNA linear EST 19-JUN-2003. Alibh02.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA BQ564607 Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and 67 CATGGTGTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGGGGGATGAGGAGTGTGT 126 EST analysis of gene expression in the mouse Organ of Corti at the 61 TATACTATTTCTCTGGCTAGTGCTCAAGAATTATAATGCCCCGGACTGTAGATTCATT 120 180 187 GATGTCAAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCT 246 241 TATTICCCCAGGAACTIGGICAAGGAACAGCGIGIGIACCAGGAAGCIACCAAGGAAGIT 300 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 488) 127 TATACTATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATC 186 Contact: Kachar, B. Structural Cell Biology National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA Tel: 301-402-1599 181 GGAGAATTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGT 121 AACGITAAAAAAGGGCAGCAGAATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCT Fax: 301-402-1765
Baal: kachbarbanided.nih.gov
Plate: 19 row: h column: 02
Seg primer: Ml3RP1 reverse primer (ABI). 301 CCCACCACGGATATTGACTTCTTCTGCGA 329 367 ccaaccaccararreactrererera 395 'organism="Mus musculus" db\_xref="taxon:10090" Location/Qualifiers Mus musculus (house mouse) Mus musculus /mol\_type="mRNA" /strain="BALB/c" BQ564607.1 GI:21467924 onset of hearing .488 Unpublished Kachar, B. DEFINITION SOURCE ORGANISM ACCESSION JOURNAL REFERENCE AUTHORS KEYWORDS

TITLE

FEATURES

BASE COUNT ORIGIN

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(MMLYRT) and 5-metnyy durit. The Second Siliand was synthesized with Day Dolymerase and Rhase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with BCOR adapters in the presence of ligate and digeted with ECOR adapters in the presence of ligate fractionated with Xho I. The CDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for CDNAs greater than 400pp and 1000 bp, respectively. The CDNA was then directionally ligated to the UnizAPR XR vector, which had been predigested with Gigapak III Gold and, upon titration on XLI Blue MRF cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exhasist Interference resistence helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescue plasmid DNA from the phages. Upon plating of the rescue plasmid DNA from the phages. Upon plating of the rescue plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the CDNA clones were generated with the universal MN3 reverse primer (CAGAAAACGTNIGAC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MY Tetrad thermal cyclers (MY Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on My Tetrad thermal cyclers (MY Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA). Sequencing reactions were green in Genbank and have know function; 23% have bits in Genbank and have know function; 12% are uncharacterized ESTS and 20% are unidentified.
library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR digapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA) according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney mutine leukemia virus reverse transcribtase (MMLV-RT) and 5-methyl dCTP. The second strand was
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ORGANISM

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

DEFINITION

RESULT 3 BQ568498 LOCUS

ACCESSION

VERSION KEYWORDS

ö 0; Gaps DB 13; Length 488; 48; Indels tch 76.4%; Score 252.2; DB al Similarity 85.4%; Pred. No. 1e-63; 281; Conservative 0; Mismatches 4 Query Match Best Local S: Matches 281 BASE COUNT ORIGIN

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                                                                       TATACTATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATT 120
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//sex="maile and female"
//dev\_stage="grivour"
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//clone lib="Mouse Organ of Corti; Vector: pBluescript; The
//clone lib="Mouse Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensor
ppiral ligament were removed and the modiclus.
Total RNA was extracted using the micro Fasttrack kilt
(catalog # \$13211, Stratagene) and Uni\_Zap XR
vector kit (catalog # \$23211, Stratagene) and Uni\_Zap XR
vector kit (catalog # \$23211, Stratagene) and Uni\_Zap XR
digapack III Gold Cloning kit (catalog # \$23721), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker primer
that contains an Xho I site. First strand synthesis was
primed with the linker- primer and transcribed using
poined with the linker- primer and transcribed using
primed with DNA polymerase and RNAse H. Complementary
NNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
and Clontech Chroma Spin-1000 (Clontech, Palo Ablo, CD)
columns to enrich for CDNAs greater than 400bp and 1000 b
/ respectively. The cDNA was then directionally ligated to
the Uni-ZAP XR vector, which had been predigested with
EcoR I and Xho I. The phagemid was packaged with digapak
III Gold and who ritration on Xil Blue MRR' cells, the BQ568498 514 bp mRNA linear BST 19-JUN-2002 gil09c02.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gil09c02 5', mRNA sequence. EST analysis of gene expression in the mouse Organ of Corti at the Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 514) Contract: Kachar,B. Structural Cell Biology
National Institute of Deafness and other Communication Disorders
National Institute of Marchar, MD 20892-8027, USA
Tel: 301-402-1765
Fax: 301-402-1765 Email: Kacharb@nidcd.nih.gov Plate: 109 row: c column: 02 Seq primer: M13RPL reverse primer (ABI). Location/Qualifiers /organism="Mus musculus" /mol\_type="mRNA" /strain="BALB/c" /db\_xref="taxon:10090" /clone="gi109c02" Mus musculus (house mouse) BQ568498.1 GI:21471815 onset of hearing Unpublished Kachar, B.

Bource

FEATURES

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strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MT Terrad thermal cyclers (MA Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification ktc (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTS from the 5' end of the CDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25%
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BASE COUNT ORIGIN

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FEATURES

59 carccrarrrargearaacirrcricraacarrererererecearcacacierere 118 61 TATACTATITCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATT 120 119 TATACTATTICTCTGGCAAGAGACACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATC 178 181 GGAGAATITITGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGT 240 241 TATTTCCCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTT 300 1 CATGGAATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTC 60 179 GATGTCAAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCT 239 geagagririgescrescaererrraresreaceaceaceagareagaresaarreinerager 121 AACGTTAAAAAGGGCAGCAGCAGCTCTATGTGTACTCAAAGGTAAAAGAAAATGGAGAGCT 0; Gaps Score 252.2; DB 13; Length 514; Pred. No. 1.1e-63; 0; Mismatches 48; Indels 0; 301 CCCACCACGGATATTGACTTCTTCTGCGA 329 Query Match
Best Local Similarity 85.4%;
Matches 281; Conservative d g В à 8 g ò g ઠ ò ò

BQ564134 inhear EST 19-JUN-2002 gilddl.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gilddl 5', mRNA sequence.
BQ564134  ${\tt EST}$  analysis of gene expression in the mouse Organ of Corti at the onset of hearing Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 534) Contact: Kachar,B. Structural Cell Biology National Institute of Deafness and other Communication Disorders Mus musculus (house mouse) Mus musculus BQ564134.1 GI:21467451 Unpublished Kachar, B. DEFINITION ORGANISM REFERENCE AUTHORS ACCESSION RESULT 4 BQ564134 VERSION KEYWORDS JOURNAL TITLE SOURCE

359 CCAACCACGGATATTGACTTCTTCTGTGA 387

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BASE COUNT

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/dev stage="Post neated" | // dev stage of conti (OC) was fine dissected from a total of 386 oC as follows: 102 samples from post-natal (P) day 5; 72 from P12 and 24 from P13. After killing animals by term p12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The boul capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithehium was carefully dissecred out of the modiolus. Total RNA was extracted using the micro Fastrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library constructions were carried out with the Uni-Zap XR oliganed [In Gold Cloning kit (catalog # 237211, Stratagene) and Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR oligane (In John Cloning kit (catalog # 237211, Stratagene) and Sintenscribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with be linker- primer and transcribted using Nollmerse and Rnase H. Complementary DNA was blunt ended with Pfu DNA polymerase and digasted with EcoR I adapters in the presence of ligase and digasted vith Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontecch Chroma Spin-1000 (Clontech, Palo Alto, CA) and clontecch Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 by recombinants Stratagenes as Stratagenes and Statagenes and Sastagenes and Algases and Algases and Algases and Algases and Algases and Algases and A
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50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
                                                                                                                                                 Email: kacharb@nidcd.nih.gov
Plate: 11 row: d column: 01
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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/db_xref="taxon:10090"
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/sex="male and female"
/dev stage="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti; Vector: pBluescript:"
/note="Organ: Organ of Corti; Vector: pBluescript: The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ569741 560 bp mRNA linear BST 19-JUN-2002 gil35f01.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gil35f01 5', mRNA sequence.
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EST analysis of gene expression in the mouse Organ of Corti at the
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 560)
                                                                                                                                            TATACTATTICICIGGCTAGIGCTCAAGAGATTATAAIGCCCCGGACTGTAGATTCATT 120
                                                                                                                                                                            117 TATACTATTTCTCTGGCAAGAGCACAGAAGATTACAATGCCCCAGACTGTAGGTTCATC 176
                                                                                                      57 CAIGGIGIAITITAIGGATAAACITICITCTAAGAAGIIGIGIGIGGGAIGAGGAGIGIGIC 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  onset of hearing
Unpublished
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1559
                                                                                                                                                                                                                   121 AACGTTAAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCT
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                                                                 1 CATGGAATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTC
                                   Gaps
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Length 534;
                                   48; Indels
DB 13;
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Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
 Score 252.2; DB 1
Pred. No. 1.1e-63;
                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357 ccaaccaceeararreacricricrerea 385
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/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus (house mouse)
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 tch 76.4%;
al Similarity 85.4%;
281; Conservative (
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         Query Match
                             Best Local
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was removed and opened in Leibowitz meature, ine boily capaballe of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiculus. Fortal RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Caribad, CAN, according to manufacturer's instructions. Reverse transcribtion and the manufacturer's instructions. Reverse transcribed and uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR vector in Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to primed with the linker primer any synthesis was primed with the linker primer any synthesis was primed with the linker primer any synthesis was that contains an Xho I site. First strand was synthesized with NA polymerase and RNAse H. Complementary Synthesized with NA polymerase and RNAse H. Complementary Synthesized with NA polymerase and RNAse H. Complementary Synthesized with NA polymerase and digested with XDO I. The cDNA was sequentially size fractionated voter pharmacia size septod (Pharmacia, Uppsal, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) and the Uni-Zap XR vector, which had been predigested with Bcom titration on XLI Blue RRF calls, the Vield of the phage library was estimated to be 11,100,000 recombinants. Stratagener's Exhasist Interference resistance helper phage (Stratagener's Upon plating of the resound library, individual cDNA the Ships stranscribed with the Competited from 200 ul of saturated culture with the Competited from 200 ul of saturated culture with the Secul Albrary, Poly as instructed by the manufacturer. ESTs erronger Derformed on My Tetrad themaly purification on My Tetrad the 119 179 180 TATACTATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATT 120 239 240 9 CATGGAATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTC 60 cardengrarrandearaacirrcircraadaagricreidededaadaadarene AACGTTAAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCT 180 GATGTCAAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGCT GGAGAATTTTGGGCTGGCGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGT Gaps was removed and opened in Leibowitz medium. The bony ö DB 13; Length 560; 48; Indels 76.4%; Score 252.2; DB 1 85.4%; Pred. No. 1.1e-63; iive 0; Mismatches 48 U Matches 281; Conservative Similarity

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DEFINITION

BQ564944

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/ Gave="male and female"
/ Geve="male and female"
/ Geve="male and female"
/ Glone lib="mouse Organ of Corti cDNA pBluescript; The
/ Clone lib="mouse Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as followed from pot-matal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiculus.
Total RNA was extracted using the micro Fasttrack kit
(catalog # K1593-02; Invitrogen, Carlabad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
digapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Johla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(d7) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker- primer and transcribed using
Moloney mutina eleukemia virus reverse transcriptes
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
RCOR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ564944 608 bp mRNA linear BST 19-JUN-2002 gi27g09.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi27g09 5', mRNA sequence.
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TATTICCCCAGGAACTIGGICAAGGAACAGCGIGIGIAACCAGGAAGCIACCAAGGAAGTT 300
                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 608)
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Contact: Kachar, B.

Structural Cell Biology

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/mol_type="mRNA"
/strain="BALB/c"
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/clone="gi27g09"
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FEATURES

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and clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for CDNAs greater than 400bp and 1000 bp respectively. The CDNA was then directionally ligated to the inizAp XR vector, which had been predigested with ECOR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the concerts6 (TM) plasmid purification kit (Invitrogen, Carlabad, A) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal MN1 sleverse primer (CAGGAAACAGCTAAGAC) and 25* strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MN Terrad thermal cyclers (MN Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Poster City, CA). The frequency distribution of the library is a follows: 72% of genes have I copy; 14.3% 2; 12% 3-10; 14 11-50 and 0.1% 51-150. As to gene function, 43% of genes are present in GenBank and have know function; 23* have bits in GenBank, but do not have assigned function; 12% are uncharacterized ESTS and 20% are unidentified."
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gil08g04.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gil08g04 5', mRNA sequence.
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Mus musculus
Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 630)
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AUTHORS TITLE JOURNAL COMMENT source

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Sequenty, as of gene expression in the mouse Organ of Corti at the Describilishments of gene expression in the mouse Organ of Corti at the Describe and Content. Marchard. Biology
National Institute of Deafness and other Communication Disorders
50/449 South Drive. NIH, Bethesda, MD 20092-8027, USA
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684 bp mRNA linear EST 19-JUN-2002 gi06c09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi06c09 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 684)
city, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
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Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1765
Pax: 301-402-1765
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/dev_stage="Post natal day 5 to 13"
                                                                                                                                                                                                    Query Match 76.4%; Score 252.2; DB 13; Best Local Similarity 85.4%; Pred. No. 1.2e-63; Matches 281; Conservative 0; Mismatches 48;
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Seq primer: M13RP1 reverse primer (ABI)
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/clone="gi06c09"
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Plate: 06 row: c column: 09
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/strain="BALB/c"
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KEYWORDS
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187 GATGTCAAGAAAGGGCAGCAGATCTATGTTTACTCCAAGGTGGTAACAGAAACGGAGCT 246

GGAGAATTTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGT 

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epithelium was carrentuly dissected out of rem Modicius. Total RNA was extracted using the micro Fasttrack kit catalog # K159-02; Invitrogen, Carlbadd, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237512). Stratagene) and Uni-Zap XR vector kit (catalog # 237612), both Gigapack III Gold Cloning kit (catalog # 237612), both Gigapack III Gold Cloning kit (catalog # 237612), both Gigapack III Gold Cloning kit (catalog # 237612), both Gigapack III Gold Cloning kit (catalog # 237612), both Gigapack III Gold Cloning kit (catalog # 237612), both Gigapack III Gold Cloning kit (catalog # 237612), both Gigapack III Gold Cloning kit (catalog # 237612), both Gigapack III Gold Cloning kit (catalog # 237612), both Gigapack III Catalog Manual Clonital Record Size Septon Gigapace II Complementary DNA was blunt ended with Ptu DNA polymerase, ilgated with EcoR I adapters in the presence of ligase and digested with EcoR I adapters in the presence of ligase and digested with EcoR I adapters in the presence of ligase and digested with EcoR I adapters in the Dresence of ligase and digested vith EcoR I adapters in the Dresence of Ligase and digested vith EcoR I adapter for CDNA was sequentially size fractionated over pharmacia Size Septon (Pharmacia, Uppsala, Sweden) and Clontech Chrome Spiricho (Contech, Pana) All Columns to enrich for CDNA greater than 400bp and 1000 by recombinants. Strategene ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the abase submarted to be 11,100,000 vecombinants. Strategene ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the Phages. Upon plating of the phage library, individual CDNA clones were generated with the universal M13 reverse primer (CDG Concerts) (M1) plasmid purification kit (Invitrogen, Carlbad, CA) as instructed by the manufacturer. EcoR perference of the CDNA clones were
/clone lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti, Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 10.2 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P13. After Willing animals by
14 from P12 and 24 from P13. After Willing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modicular.
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DB 13; Length 684;
                                          48; Indels
76.4%; Score 252.2; DB 1
85.4%; Pred. No. 1.2e-63;
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                       Best Local Similarity 85.4
Matches 281; Conservative
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BASE COUNT

Location/Qualifiers

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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
KONDO,4., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-L86 (2001
Func. Genomics 2 pre, L72-L86 (2001
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Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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URL:http://genome-gsc.riken.go.jp,
URL:http://genome-reseggsc.riken.go.jp,
Oarninch, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
N., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi, K., Fullwake, S., Inoue, W., Togawa, Y., Izawa, M., Ohara, E.,
Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
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BB611549 RIKEN full-length enriched, 13 days embryo head Mus musculus cDNA clone 3110083012 5', mRNA sequence.
241 TATTICCCCAGGAACTIGGICAAGGAACAGCGIGIGIACCAGGAAGCTACCAAGGAAGIT 300
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Contact: Yoshihide Hayashizaki
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further details.
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Unpublished
JOURNAL
                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                       474 bp mRNA linear BST 19-JUN-2002 gi42g03.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA BQ565637
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Kachar, B.
EST analysis of gene expression in the mouse Organ of Corti at the
onset of hearing
                                                                                                                                                                                                /note="Site 1: XhoI; Site 2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TATTTCCCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 TATTTCCCCAGCAACTTGGTGAAGGAGCAGCGTGTATAACCAGGAGGCCACCAAGGAGATC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 474)
                                                                                                                                                        'clone_lib="RIKEN full-length enriched, 13 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 GATGTCAAGAAAGGGCAGCAGATCTATGTTTACTCCCAAGCTGGTAACAGAAAACGGAGCT
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cch
al Similarity 85.4%; Pred. No. 1.2e-63;
281; Conservative 0; Mismatches 48
                                                                                                  /tissue_type="head"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 CCCACCACGGATATTGACTTCTCTGCGA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 ccaaccacedrarraacricitrores 406
                           organism="Mus musculus"
                                           | type="mRNA"
| xref="taxon:10090"
                                                                                     clone="3110083012"
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            source
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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/dev stage="Post nata! day 5 to 13"
/dev stage="Post nata! day 5 to 13"
/clone lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-nata! (P) day 5; 72
from Pot 6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fastrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
Gigapack III Gold Cloning kit (catalog # 23721), both
from Strategene (La Johla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho 1 site. First strand synthesis was
primed with the linker- primer and transcribtuse
Moloney murine leukemia virus reverse transcriptuse
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pft DNA polymerase, ligated with
ECOR I adapters in the presence of ligase and digested
with Xho I. The CDNA was sequentially size fractionally ligated
columns to enrich for cDNA was then directionally ligated to
the Uni-Zap XR vector, which had been predigested with
ECOR I and Xho I. The phagemid was petimated to be 11,100,000
respectively. The cDNA was then directionally ligated to
the bhage all brant was sequentially as adone
respectively. The phagemid full interference
respectively. Strategene 'B Strategene's Brander of the phage of the phage of the phage of the phage of the phage of the phage of the phage of the pha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research,
Contact: Kachar, B.

Contact: Kachar, B.

Structural Cell Biology
National Institute of Deafness and other Communication Disorders
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Ferl: 301-402-1369
Email: kacharb@nidcd.nih.gov
Plate: 42 row: g column: 03
Plate: 42 row: g column: 03
Seq primer: MI3RPI reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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'sex="male and female"
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'strain="BALB/c"
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409 bp mRNA linear EST 19-JUN-2002 gi73g09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi73g09 5', mRNA sequence. BQ566932 BQ566932.1 GI:21470249
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/dev stage="Post natal day 5 to 13"
/dev stage="Post natal day 6 Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
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Sciurognathi, Muridae, Murinae, Mus.
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genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
78 c 131 g 120 t
                                                                                                                                                                                                                     CATGGAATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTC
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                                                                                                                                                                             Gaps
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0
                                                                                                                                  Length 474;
                                                                                                                                                                             49; Indels
                                                                                                                                  DB 13;
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Plate: 73 row: g column: 09
Seg primer: M13RP1 reverse primer (ABI).
                                                                                                                                  Score 250.6; DB 1
Pred. No. 3.1e-63;
0; Mismatches 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 CCCACCACGGATATTGACTTCTTCTGCGA 329
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 409)
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/strain="BALB/c"
                                                                                                                                  ch 75.9%;
al Similarity 85.1%;
280; Conservative 1
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Mus musculus
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                                                                                                                                         Query Match
Best Local S:
Matches 280;
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BQ566932
LOCUS
DEFINITION
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TITLE
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KEYWORDS
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epitnellum was carerully dissected out of the modifications. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptuse (MMLV-RT) and S-methyl dCTP. The second strand was synthesized with DNA polymerase and RNAse H. Complementary DNA was blunt ended with Pfu DNA polymerase and digested with Scor I adapters in the presence of ligase and digested with a contrach for conva spin-100 (Clontech, Palo, CA) and Clontech Chroma Spin-100 (Clontech, Palo, A) columns to enrich for conva Spin-100 (Clontech, Palo, A) columns to enrich for conva Spin-100 (Clontech, Palo, A) columns to enrich for conva Spin-100 (Clontech, Palo, A) and 1000 by respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with Gigapak III Gold and, upon titration on XLI Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference resistance halper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the resue plasmid DNA from the phages. Upon plating of the resue plasmid DNA from the phages. Upon plating Off Carlery (Malolal CDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA slones were generated with the 5' end of the cDNA clones were generated with the strength Highove terminator Recurse primar (GAGGAAACACCTATCACC) arrendth Biodye terminary Recurse primar (GAGGAAACACCTATCA strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on My Terrad thermal cyclers (My Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified." 119 200 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P9; 20 from P10; 14 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modicius. 140 CTATACTATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCAT 141 CTATACTATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCAT CATGGAATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGC-AGATGAGTGAGTGTGT Gaps 1; Score 238.6; DB 13; Length 409; Pred. No. 1e-59; 0; Mismatches 49; Indels 1: Query Match 72.3%; Best Local Similarity 84.8%; Matches 279; Conservative 102 H 81 9

120 TAACGTTAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGC 179

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8 윱 ò

BASE COUNT ORIGIN

201 CGATGTCAAGAAAGGCCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGGGC

a à

g ò

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/clone="glasdous"
/sex="male="glasdous"
/dev_stage="Post natal day 5 to 13"
/clonella="Mouse Organ of Corti cDNA pBluescript; The
/clonella="Mouse Organ of Corti; Vector: pBluescript; The
organ of Corti; Oco was fine dissected from a total of 386
Oc as follows: 102 samples from post-natal (PD) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
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capsule of the cochlea was chipped away, stria vascularis
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Total RNA was extracted using the micro Fasttrack kit
(catalog # K1593-02; Invitrogen, Carlabad, CA), according
to manufacturer's instructions. Extratagene) and Uni-Zap XR
vector kit (catalog # 23721), Stratagene) and Uni-Zap XR
vector kit (catalog # 23721), Stratagene) and Uni-Zap XR
digapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Britefly: 15 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker- primer and transcribtase
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
                                                                                                                                                                                                                                                                                                                                                                                                                       604 bp mRNA linear EST 19-JUN-2002 gi88d08.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA EQCENA 2698433
                             261 TGGAGAGTTTTGGGCTGGCAGTGTTATGGTGACCACCAGGATGAGATGAGAATTGTAGG 320
                                                                                                                                                         EST analysis of gene expression in the mouse Organ of Corti at the
                                                                                                                     TIATITICCCCAGGAACTIGGICAAGGAACAGCGIGIGIACCAGGAAGCIACCAAGGAAGT 299
TGGAGAATTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGAGATGGGAGTCGTGGG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 604)
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Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
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Plate: 88 row: d column: 08
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                              381 CCCAACCACGGCTATTGACTTCTTCTGG 409
                                                                                                                                                                                                                                                 300 TCCCACCACGGATATTGACTTCTTCTGCG 328
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clone="gi88d08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ567343.1 GI:21470660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301-402-1599
Fax: 301-402-1765
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Unpublished
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DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with EcoR with Xno I. The CDNA was sequentially size fractionated over pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for CDNAs greater than 400bp and 1000 bp, respectively. The CDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak II Gold and, upon tirrarion on XLI Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96 (TM) plasmid purification kit (Invitrogen, Carlabad, CA) as instructed by the manufacturer. ESTS from the 5' end of the CDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATACAC) and 25%
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAGAAGTTGTGTGCGGATGAGGAGTGTGTCTATACTATTTCTCTGGCAAGAGCACAGAA
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AUTHORS TITLE JOURNAL

FEATURES

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let from FL2 and 44 Incer Milling animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Tocalog # KLS9-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR digapack III Gold Cloning kit (catalog # 237212), both from Stratagene (La Jolla, CA) uSA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an XnO I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney muritine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Ptu DNA polymerase, igated with Econ Murit he become the paramed size septentially size fractionated over Pharmacia size septentially size fractionated over Pharmacia in the presence of ligase and digasted with Xno I. The cDNA was sequentially size fractionated over Pharmacia size septentially size fractionated over Pharmacia Size Septent (Pharmacia, Duppala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNA sys reater than 400bp and 1000 by the DNA was blund from the phages. Upon plating of the phage library was estimated to be 11,100, or resoundinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted resouce plasmid DNA from the phages. Upon plating of the phage library was estimated culture with the Concerbed (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer with the cunding one concerbed (TM) plasmid purin
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/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti, Vector: pBluescript, The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5, 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrach thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Poster
                              gene expression in the mouse Organ of Corti at the
                                                                                                                                            Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
S04249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1765
Pax: 301-402-1765
                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: 37 row: b column: 12
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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/clone="gi37b12"
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                                                                                                                                                                                                                                                                                                                                                                                                                     Email: kacharb@nidcd.nih.gov
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/strain="BALB/c"
                              EST analysis of gonset of hearing
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                                                                                                                  Unpublished
Kachar, B.
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Link Will Mission Sciurognath; Wertebrata; Buteleostomi;
Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Set (bazaki,Y.) Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.,
'Yagi,K., Tomanu,Y., Hasegawa,Y., Nogami,A., Schonbach,C.'
Cojobori,T. Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
Duackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,J.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., S., Gasserland,T., Gariboldi,M., Gissi,C., Godzik,A.,
Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M.,
King,B.L., Konagaya,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M.,
King,B.L., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Oshido,T., Pavan,W., Serpele,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D.,
Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Rangisawa,M., Shimada,K., Sultana,R., Schneider,C., Semple,C., Wang,Y.,
Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Xono,H., Kono,H., Nakamura
,M., Sakazume,N., Sato,K., Shiraki,T., Nakai,J., Aizawa,K.,
,M., Sakazume,N., Sato,K., Shiraki,T., Nakawai,J., Aizawa,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 bp mRNA linear BST 10-DBC-2002 EV232622 RIKEN full-length enriched, adult inner ear Mus musculus BY232622 BY232622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATITICCCCAGGAACTIGGICAAGGACAGCGIGIGIAACCAGGAAGCTACCAAGGAAGIT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 GATGTCAAAAAAGGGCAGCAAATCTATGTTTACTCCAAGCTGGTAACAAAAAAGGAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                           cargocoratriariocaraaacrircricraaaaarroriococaraaggagrorio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AACGTTAAAAAGGGCAGCAGATCTTGTGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 GGAAAGTTTTGGGCTGGCAGTGTTTATGGGGACCACCAGGATGAAATGGGAATTGTAGGT
                                                                                                                                                                                                                                                                                                                                                                                     1 CATGGAATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCT
                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                               71.6%; Score 236.2; DB 13; Length 490; 82.4%; Pred. No. 5.7e-59; Live 0; Mismatches 58; Indels 0;
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Mus musculus
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                                                                                                                                                                                                                                                                                                    Similarity
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Best Local 8
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BY232622
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376 GAAAATTTTGGGCTGGCAGTGTTTATGGAGATGACCACAGGATGAGATGGGAACCGGGG 435
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/db_xref="taxon:9615"
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BU748241.1 GI:23700286
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Canis familiaris
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Best Local Similarity 86.29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Genome Sequences Mamm. Genome. 12, 671-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraties for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedias real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Genome Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Laboratory in Riken Genomic Science Laboratory in Riken Genomic Science Laboratory in Riken Genomic Science Laboratory in Riken Genomic Science Laboratory in Riken Genomic Science Laboratory in Riken Genomic Science Laboratory in Riken Genomic Science Laboratory in Riken Genomic Science Laboratory in Riken Genomic Science Laboratory in Riken Genomic Science Laboratory in Riken Genomic Science Laboratory in Riken Genomic Science Laboratory in Riken Genomic Science Center and Genomic Science Laboratory in Riken Genomic Science Center and Genomic Science Laboratory in Riken Genomic Science Center and Genomic Science Laboratory in Riken Genomic Science Center and Genomic Science Laboratory in Riken Genomic Science Center and Genomic Science Laboratory in Riken Genomic Science Center and Genomic Science Laboratory in Riken Genomic Science Laboratory in Riken Genomic Science Center and Genomic Science Laboratory in Riken Genomic Science Center and Genomic Science Laboratory in Riken Genomic Science Center and Genomic Science Laboratory in Riken Genomic Science Center and Genomic Science Laboratory in Riken Genomic Science Center and Genomic Science Laboratory in Riken Genomic Science Laboratory in Riken Genomic Science Center and Genomic Science Laboratory in Riken Genomic Sc
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakwa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishli,Y., Itch,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,B.S., Rogers,J., Birney,B. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length colbs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.
Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NB 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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/clone lib="RIKEN full-length enriched, adult inner ear"
60 c 110 g 98 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computational Analysis of Full-Length Mouse cDNAs Compared with
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                                                                                                                                                                                                                                                                                                                                    Contact: Yoshihide Hayashizaki
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/strain="C57BL/6J"
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Best Local Similarity 85.0%;
Matches 244; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submission
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ORIGIN
                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                      MEDLINE
                                                                                                                                                                                                                                                                                                   PUBMED
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                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                    COMMENT
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Other ESTS: CH3#018 G05T3
Other ESTS: CH3#018 G05T3
Contact: George AL
Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2661
Email: al.george@vanderbilt.edu
Insert Length: 1892 Std Error: 0.00
Seq primer: TT: TAATACGACTACTATAGGG
High quality sequence stop: 559.
High quality sequence stop: 559.
                                                                                                                                                                                                                                                                                                                                                BU748241 FST 10-OCT-2002 CH3#018_G05T7 Canine heart normalized cDNA Library in pBluescript Canis familiaris cDNA clone CH3#018_G05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
240
                             316 ATGTGAAAAAGGACAGCAGATTTACGTTTACTCGAAGCTGGTAAAAGAAAATGGAGCTG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 ATACTATTTCTCTGGCCAGAGCTCAAAAAGATTACAATGCCCCAGACTGTAGGTTCATTA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 ACGTTAAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCTG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 795)

Yi, Y., Desai,R., Olarte,M., Henthorn,P. and George A.L.

Expressed sequence tags from Canine heart
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         force="Organ: heart, Vector: pBluescript; Site_1: 5' of vector NotI; Site_2: 3' of vector EcoRi; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="GH3#018 G05"
/tissue_type="heart"
/cell_type="heart"
dev_stage="mixed developmental stages (adult, 30 day day fetal)"
181 GGAGAATTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGGTCGTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 GAGAATTTTGGGCTGGCAGTGTTTATGGTGATGGCC----AGGACGAGATGGGAGTCGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Canine heart normalized cDNA Library in pBluescript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
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                                                                                                                                                                                     364
                                                                                                                                                       318 TATTTCCCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGC
                                                                                                                      241 TATTTCCCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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86.2%; Pred. No. 9.9e-48;
iive 0; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Canis familiaris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 t
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25 G G

Search completed: December 30, 2003, 06:07:15 Job time : 1098.64 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/SIDS1/gcgdata/geneseg/genesegn-embl/NA2001B.DAT:\*/SIDS1/gcgdata/geneseg/genesegn-embl/NA2002.DAT:\*/SIDS1/gcgdata/geneseg/genesegn-embl/NA2003.DAT:\*

|            | Description | Human MLP nucleoti | Human MLP nucleoti | DNA encoding novel | Human growth regul | Human angiogenesis | Human PRO9873 cDNA | cDNA encoding huma | Human EST-derived |
|------------|-------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|
| í<br>H     | TD          | AAF59079           | AAF59065           | AAS17583           | AAH26341           | ABL95740           | ABL88251           | ABK33571           | AAH98228          |
|            | . !         | 22                 | 22                 | 24                 | 22                 | 24                 | 24                 | 24                 | 22                |
| %<br>Query | rengen      | 330                | 384                | 387                | 426                | 521                | 521                | 521                | 891               |
| Query      | March       | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0             |
| į          | Score       | 330                | 330                | 330                | 330                | 330                | 330                | 330                | 330               |
| Result     |             | н                  | 7                  | m                  | 4                  | Ŋ                  | 9                  | 7                  | 00                |

WPI; 2001-159271/16.

| Human growth regul | Human MLP nucleoti | Human growth regul | Mouse MLP nucleoti | Mouse MLP nucleoti | Mouse MLP nucleoti | Rat MLP nucleotide | Rat MLP nucleotide | Rat MLP nucleotide | Rat MLP nucleotide | Recombinant human | Sequence encoding | Melanoma inhibitor | Human antisense ol | Human prostate exp | Sequence encoding | Breast cancer rela | Breast cancer rela | Sequence encoding | Amplified fragment | Human gene express | Human cDNA encodin | Human cDNA encodin | 130      | Human TANGO 130 cD | Human TANGO 130 po | Human prostate exp | Human prostate exp | Human prostate exp | Human prostate exp | Human TANGO 130 po | Human TANGO 130 po | Human protein enco | Human PRO19670 cDN | Human cDNA encodin | Human angiogenesis | Human PRO19670 cDN |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| AAH26342           | AAF59083           | AAH26343           | AAF59080           | AAF59068           | AAF59084           | AAF59099           | AAF59098           | AAF59093           | AAF59092           | AAH47783          | AAQ84050          | AAI70083           | AAD18732           | ABV59229           | AAQ84052          | ABL63602           | ABL64012           | AAQ84061          | AAQ84055           | AAZ14828           | AAS22695           | AAS22459           | ABQ79850 | AAZ51245           | ABQ79849           | ABV21035           | ABV23751           | ABV26878           | ABV29625           | ABQ79852           | ABQ79851           | AAH99775           | AAF92140           | ABS74460           | ABL95738           | ABL88249           |
| 22                 | 22                 | 22                 | 22                 | 22                 | 22                 | 22                 | 22                 | 22                 | 22                 | 22                | 16                | 22                 | 22                 | 23                 | 16                | 24                 | 24                 | 16                | 16                 | 20                 | 22                 | 22                 | 24       | 21                 | 24                 | 23                 | 23                 | 23                 | 23                 | 24                 | 24                 | 22                 | 22                 | 24                 | 24                 | 54                 |
| 891                | 923                | 1201               | 330                | 384                | 947                | 330                | 384                | 307                | 261                | 433               | 459               | 459                | 459                | 555                | 581               | 442                | 442                | 330               | 305                | 300                | 429                | 884                | 1230     | 1263               | 1263               | 4409               | 4409               | 4409               | 4409               | 5724               | 8121               | 417                | 1060               | 1060               | 1060               | 1060               |
| 100.0              | 100.0              | 100.0              | 76.4               | 76.4               | 76.4               | 75.5               | 75.5               | 65.0               | 58.7               | 19.2              | 19.2              | 19.2               | 19.2               | 19.2               | 19.2              | 18.7               | 18.7               | 17.4              | 16.4               | 16.2               | 16.2               | 16.2               | 16.2     | 16.2               | 16.2               | 16.2               | 16.2               | 16.2               | 16.2               | ٠.                 | 16.2               | •                  | •                  | 13.9               | •                  | •                  |
| 330                | 330                | 330                | 252.2              | 252.2              | 252.2              | 249                | 249                | 214.6              | 193.8              | 63.4              | 63.4              | 63.4               | 63.4               | 63.4               | 63.2              | 61.8               | 61.8               | 57.4              | 54.2               | 53.6               | 53.6               | 53.6               | 53.6     | 53.6               | 53.6               | 53.6               | 53.6               | 53.6               | 53.6               | ë.                 | ω,                 | 52                 | 46                 | 46                 | 46                 | 46                 |
| σ                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                | . 20              |                    | c 22               | 23                 | 24                |                    | c 26               | 27                | 28                 | 29                 | 30                 | 31                 | 32       | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |
|                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                   |                   |                    |                    |                    |                   |                    |                    |                   |                    |                    |                    |                    |          |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |

## ALIGNMENTS

AAF59079 standard; DNA; 330 BP.

AAF59079 RESULT 1

Yoshimura K; MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter; inhibitor; ds. Noguchi Y, Ogi K, Ohkubo S, Mogi S, Human MLP nucleotide sequence SEQ ID NO:23. 99JP-0186718. 29-JUN-2000; 2000WO-JP04278. (TAKE ) TAKEDA CHEM IND LTD (first entry) Nishi K, WO200102564-A1 Homo sapiens. 30-JUN-1999; 11-JAN-2001. 23-APR-2001 Itoh Y, N Tanaka H; AAF59079; 

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APPLICANT: STEPhan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC24
CURRENT APPLICATION NUMBER: US/10/219,063
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR APPLICATION NUMBER: 60/062287
PRIOR PLING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 TATACTATITCTCTGGCTAGTGCTCAAGATTATAATGCCCCGGACTGTAGATTCTT 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 ggagaarrirgggcrggcagrgrrrarggrgarggccaggacgagargggagrcgrgggr 331
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                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 330; DB 13; Length 521; 100.0%; Pred. No. 7.2e-100; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 CCCACCACGGATATTGACTTCTTCTGCGAG 330
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, Victoria
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR PLING DATE: 1999-08-17
PRIOR FLING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-31
PRIOR PAPLICATION NUMBER: 60/16418
PRIOR FILING DATE: 1999-11-09
PRIOR PLING DATE: 1999-11-16
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PRIOR PLING DATE: 1999-12-07
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PRIOR FILING DATE: 1999-12-07
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PRIOR PLING DATE: 1999-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 71, Application US/10219063 Publication No. US20030187202A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 330; Conservative
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181 GGAGAATTTTGGGCTGGCAGTGTTATGGTGATGGCCAGGACGACGAGATGGGAGTCGTGGGT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 TATACTATTTCTCTGGCTAGTGCTCAAGAATATAATAGCCCCGGACTGTAGATTCATT 211
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PRIOR APPLICATION NUMBER: 60/064103
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PRIOR PELING DATE: 1997-12-17
PRIOR PELING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079294
PRIOR PILING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079726
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
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APPLICANT: Baker, Luc
APPLICANT: Genoyers, Luc
APPLICANT: Geddard, Audrey
APPLICANT: Geddowski, Paul J.
APPLICANT: Gedowski, Paul J.
APPLICANT: Gridaldi, J. Christopher
APPLICANT: Gridaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wacd, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CATGGAATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AACGTTAAAAAAGGCCAGCAGCAGTATCTATGTACTCAAAGCTGGTAAAAGAAAATGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 330; DB 13; Length 521; Best Local Similarity 100.0%; Pred. No. 7.2e-100; Matches 330; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REPERENCE: P3530PIC27
CURRENT APPLICATION NUMBER: US/10/219,066
CURRENT FILING DATE: 2002-08-13
PRICA APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 71, Application US/10219066; Publication No. US20030187203A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo Sapien
US-10-219-063-71
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61 TATACTATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATT 120
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CURRENT APPLICATION NUMBER: US/10/219,067

CURRENT FILING DATE: 2002-08-14

PRIOR FILING DATE: 2002-08-14

PRIOR FILING DATE: 10/119,480

PRIOR PLICATION NUMBER: 60/059113

PRIOR PLING DATE: 1997-09-17

PRIOR PLING DATE: 1997-09-17

PRIOR PLING DATE: 1997-10-17

PRIOR PLING DATE: 1997-10-28

PRIOR FILING DATE: 1997-10-28

PRIOR PLING DATE: 1997-10-31

PRIOR PLING DATE: 1997-10-31

PRIOR PLING DATE: 1997-10-31

PRIOR PLING DATE: 1997-10-31

PRIOR PLING DATE: 1997-12-17

PRIOR PLING DATE: 1997-12-17

PRIOR PLING DATE: 1998-03-20

PRIOR PLING DATE: 1998-03-26

PRIOR PLING DATE: 1998-03-26

PRIOR PLING DATE: 1998-03-26

PRIOR PLING DATE: 1998-03-26

PRIOR PLING DATE: 1998-03-26

PRIOR PLING DATE: 1998-03-26

PRIOR PLING DATE: 1998-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.

SEO ID NO. 71

SEO ID NOS: 246
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100.0%; Score 330; D)
Best Local Similarity 100.0%; Pred. No. 7.2.
Matches 330; Conservative 0; Mismatches
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Jean-Philippe F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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CORGANISM: Homo Sapien
US-10-219-067-71
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APPLICANT:
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; Sequence 71, Application US/2030187204A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddwski, Paul J.
; APPLICANT: Goddwski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Girmaldi, J. Christopher
; APPLICANT: Smith, Victoria.
; APPLICANT: Smith, Victoria.
; APPLICANT: Smith, Victoria.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: ATTLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC51
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                             PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
PRIOR PELING DATE: 1997-10-28
PRIOR PELING DATE: 1997-10-31
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Best Local Similarity 100.
Matches 330; Conservative
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CORGANISM: Homo Sapien
US-10-219-066-71
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APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330P1G31
CURRENT APPLICATION NUMBER: US/10/219,068
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR PLICATION NUMBER: 60/069873
PRIOR PLICATION NUMBER: 60/079910
PRIOR PLICATION NUMBER: 60/079910
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
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APPLICANT: Baker, Kevin P.
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapien
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaddi, J. Christopher
APPLICANT: Garnaddi, J. Christopher
APPLICANT: Garnath, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stath, Victoria
APPLICANT: Stath, Victoria
APPLICANT: Stath, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Wood, Milliam I.
APPLICANT: Wood, Milliam I.
APPLICANT: Wood, Milliam I.
APPLICANT: Wood, Milliam I.
APPLICANTON: ACIDS ENCODING THE SAME
FILE REFERENCE: PS:30PLO40
CURRENT FILING DATE: 2002-04-03
FRIOR APPLICATION NUMBER: 06/05913
FRIOR APPLICATION NUMBER: 60/05913
FRIOR APPLICATION NUMBER: 60/05913
FRIOR APPLICATION NUMBER: 60/05387
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FRIOR APPLICATION NUMBER: 60/06387
FRIOR APPLICATION NUMBER: 60/06389
FRIOR PILING DATE: 1997-10-21
FRIOR APPLICATION NUMBER: 60/069873
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FRIOR APPLICATION NUMBER: 60/079294
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100.0%; Pred. No. 7.2e-100;
iive 0; Mismatches 0;
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US-10-219-069-71
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Best Local Similarity
Matches 330; Conserv
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APPLICANT: Goddard, Audrey
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
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APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: NUMBER: US/10/219,475
CURRENT FILING DATE: 2002-04-09
FRIOR FILING DATE: 1997-09-17
FRIOR FILING DATE: 1997-10-13
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                                        Sequence 71, Application US/10219475
Publication No. US20030187208A1
GENERAL INFORMATION:
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CORGANISM: Homo Sapien
US-10-219-475-71
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                                                                 APPLICANT: Gerritans, Mary
APPLICANT: Gerritans, Mary
APPLICANT: Gerritans, Mary
APPLICANT: Gerritans, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
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APPLICANT: Watanabe, Colin Catanabe, Colin L.
APPLICANT: Watanabe, Colin Catanabe, Colin M.
APPLICANT: Watanabe, Colin Moder, Colin M.
APPLICANT: Watanabe, Colin Moder, Colin M.
APPLICANT: Watanabe, Colin Moder, Colin M.
ANUMERS FILMS DATE: 1998-03-25
APPLICANT: Watanabe, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Colin Moder, Col
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 CCCACCACGGATATTGACTTCTTCTGCGAG 330
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APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo Sapien
US-10-219-073-71
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APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Saith, Victoria
APPLICANT: Saith, Victoria
APPLICANT: Saith, Victoria
APPLICANT: Saith, Victoria
APPLICANT: Saith, Victoria
APPLICANT: Matanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William L.
TITLE OF INVENTION: BCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3520PLC43
CURRENT APPLICATION NUMBER: US/10/219,483
CURRENT APPLICATION NUMBER: 60/0659113
PRIOR APPLICATION NUMBER: 60/0659113
PRIOR PAPLICATION NUMBER: 60/0659113
PRIOR PAPLICATION NUMBER: 60/06349
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PRILING DATE: 1997-10-31
PRIOR PRILING DATE: 1997-10-31
PRIOR PRILING DATE: 1998-03-26
PRIOR PLILNG DATE: 1998-03-26
PRIOR PLILNG DATE: 1998-03-25
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                                                            241 TATTICCCCAGGAACTIGGICAAGGAACAGCGIGIGIGIACCAGGAAGCTACCAAGGAAGIT
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SEQ ID NO 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 7.2e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                         0; Mismatches
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Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 71, Application US/10219483; Publication No. US20030187210A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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Best Local Similarity
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ORGANISM:
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APPLICANT: Gerriteen, Mary
APPLICANT: Gerriteen, Mary
APPLICANT: Gerriteen, Mary
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimald, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Maranabe, Colin L.
APPLICANT: Macanabe, Colin L.
APPLICANT: Mood, William I. 10/10/219,480
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC3B
FILE REFERENCE: P3530PLC3B
FILE REFERENCE: P3530PLC3B
FILE REFERENCE: P3530PLC3B
FILE REFERENCE: P3530PLC3B
FILE REFERENCE: P3530PLC3B
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FILE REFERENCE: P3530PLC3B
FILE REFERENCE: P3530PLC3B
FILE REFERENCE: P398-03-25
FRIOR FILING DATE: 1998-03-25
FRIOR FILING DATE: 1998-03-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGGAATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGATGAGTGTGTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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; Pred. No. 7.2e-100;
0; Mismatches 0;
                                                                                                  392 CCCACCACGGATATTGACTTCTTCTGCGAG 421
                                                            301 CCCACCACGGATATTGACTTCTTCTGCGAG 330
                                                                                                                                                                                                                                                                            Sequence 71, Application US/10219480 Publication No. US20030187209A1 GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
ilarity 100.0%;
Conservative 0,
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US-10-219-480-71
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Best Local Similarity
Matches 330; Conserv
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APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC41
CURRENT APPLICATION NUMBER: US/10/219,526
CURRENT FILING DATE: 2002-04-09
PRIOR PRIOR PILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1998-03-20
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                                                                                                                                                                                                                                                                                                                                 241 TAITTCCCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTT
                                                                                                     181 GGAGAATTTTGGGCTGGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGT
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SEQ ID NO 71
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Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Jean-Philippe F.
Watanabe, Colin L.
Nood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 71, Application US/10219526
Publication No. US20030187212A1
GRUBLAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desmoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-526-71
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APPLICANT: Goddard, Audray
APPLICANT: Goddard, Audray
APPLICANT: Goddard, Austin L.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMERANE POLYPEPTIDES AND NUCLEIC
CURRENT APPLICATION NUMBER: U6/10/219,525
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 00/06287
PRIOR APPLICATION NUMBER: 60/06387
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06387
PRIOR APPLICATION NUMBER: 60/06387
PRIOR APPLICATION NUMBER: 60/06387
PRIOR PILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/06387
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/06391
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/07928
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07928
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR PRIOR FILING DATE: 1998-03-27
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                                                                                                                                                                                                       TATTICCCCAGGAACTIGGICAAGGAACAGCGIGIGIACCAGGAAGCIACCAAGGAAGIT 300
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                                                                                                                       1 CATHURATATTATGGACCGTCTAGCATCCAAGAAGCTCTGTGCAGATGATGAGTGTGTC
                                                                                         GGAGAATTTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGT
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                                                                                                                                                                                                                                                                                                                     CCCACCACGGATATTGACTTCTTCTGCGAG 330
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Gerritsen, Mary
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ORGANISM: Homo Sapien
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US-10-219-530-71

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APPLICANT: Geldard, Addrey
APPLICANT: Geldard, Addrey
APPLICANT: Geldowski, Paul J.
APPLICANT: Geldowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: PS530PLCS4
CURRENT APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-06-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-3
PRIOR FILING DATE: 1997-10-3
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PRIOR PRILCATION NUMBER: 60/079284
PRIOR FILING DATE: 1998-03-26
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PRIOR PRILCATION NUMBER: 60/079284
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PRIOR PRILING DATE: 1998-03-26
PRIOR PLILING DATE: 1998-03-26
PRIOR PLILING DATE: 1998-03-27
PRIOR PRILING DATE: 1998-03-27
332 TATITICCCCAGGAACTIGGTCAAGGAACAGCGTGTGTGTACCAGGAAGCTACCAAGGAAGTT 391
                                                                                                                           TATACTATTTCTCTGGCTAGTGCTCAAGAATTATAATGCCCCGGACTGTAGATTCATT 120
                                                                                                                                                                                                                                                       121 AACGTTAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCT 180
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SEQ ID NO 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 71, Application US/10219530 Publication No. US20030187213A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desnoyers, Luc
Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Baker, Kevin P. APPLICANT: Desnoyers, Luc
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ORGANISM: Homo Sapien
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 TATTTCCCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTT 391
                                                                                                                                                                                                                                                                                         212 AACGTTAAAAAAGGCAGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAAGAAAATGGAGCT
                                                                                     1 CATGGAATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTC
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                                              Gaps
                                           0;
Query Match 100.0%; Score 330; DB 13; Length 521; Best Local Similarity 100.0%; Pred. No. 7.2e-100; Matches 330; Conservative 0; Mismatches 0; Indels 0.
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Job time: 271.994 secs
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Sequence Sequence

Sequence 1, Appli Sequence 1171, Ap Sequence 1093, A Sequence 191, App Sequence 94, Appl Sequence 2654, App Sequence 1103, Ap Sequence 4, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli

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COUNTRY: New .....
COUNTRY: USA
ZIP: 10022
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
FILING DATE: 20-July-1994
FILING DATE: 20-July-1994
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATPOREY/AGENT INFORMATION:
APPLICATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: 31,575
REFERENCE/DOCKET NUMBER: 31,575
TELEFRAN: (212) 888-3200
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TELEFRAN: (212) 888-330
                       US-08-868-786-1

US-09-134-01C-1171

US-09-134-01C-1171

US-08-961-57-191

US-09-453-7028-116

US-09-220-132-94

US-09-107-532A-2654

US-09-107-532A-2654

US-09-107-532A-2654

US-09-107-532A-2654

US-09-107-77-4

US-09-140-177-4

US-09-397-979-4

US-08-939-501-1

US-08-939-501-1

US-08-939-501-1

US-08-939-501-1

US-08-929-501-1
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
US-09-107-532A-3486
US-09-620-312D-161
                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/08578649; Patent No. 5770366; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
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LOCATION:
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LOCATION:
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    Sequence 899, App Sequence 1, Appli Sequence 13, Appli Sequence 17, Appl Sequence 17, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli
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Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 8, Appli
Sequence 24, Appl
Sequence 3, Appli
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Sequence 4, Appli
                                                                                                   ; Search time 26.6527 Seconds (without alignments) 5464.987 Million cell updates/sec
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Sequence 14,
Sequence 14,
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): /cgn2_6/ptodata/2/ina/RECTUS_COMB.seq:*
): /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-578-649-24

US-08-578-649-3

US-08-232-463-14

US-08-86-9870-1

US-09-285-161-4

US-09-785-15-1

US-09-775-15-2

US-09-734-674-3

US-09-734-674-3

US-09-734-674-3

US-09-103-840A-2

US-09-103-840A-2
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US-09-007-005-17
US-09-044-796-17
US-09-557-884-1
US-09-643-990A-1
US-09-653-333D-1
US-09-679-409-1
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US-08-578-649-18
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US-09-650-855-14
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                                                                                                         December 30, 2003, 01:34:27
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Maximum Match 100%
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seq length: 200000000
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9.0 319608 4

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8.9 1497 4

8.9 2718 4
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Perfect score:
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Best Local Similarity 54.3%;
Matches 175; Conservative (
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CDS
110..499
                FEATURE:
NAME/KEY:
LOCATION:
                                          FEATURE:
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LOCATION:
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                                    Score 63.4; DB 1; Length 459; Pred. No. 5e-11; 0; Mismatches 101; Indels
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                                      19.2%;
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TYPE: nucleic acid
STRANDEDNESS: single
   mat_peptide
                                                       153; Conservative
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                                        Query Match
Best Local Similarity
Matches 153; Conserval
              ; LOCATION:
US-08-578-649-1
      NAME/KEY:
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Sequence 18, Application US/08578649

Patent No. 5770366

GENERAL INFORMATION:
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INFORMATION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSES: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STREET: 805 Third Avenue
CITY: New York
STATE: New York
STATE: Pow York
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Score 63.2; DB 1;
Pred. No. 6.5e-11;
0; Mismatches 138;
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Tiajoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
FELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 TCAATGGGATTTCTACTGCCAG 499
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94 TATAATGCCCCGGACTGTAGATTCATTAACGTTAAAAAAGGGCAGCAGATCTATGTGTATC 153
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Sequence 24, Application US/08578649

Sequence 24, Application US/08578649

Patent No. 577036

GENERAL INFORMATION:

APPLICANT: Ulrich Bogdan

APPLICANT: Brighte Kaluza

TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: 1EM PS/2
OPERATION SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                NAME/KEY: misc RNA (CATION: join(1..29, 277..305) (CATION: join(1..29, 277..305) (CATHER INFORMATION: /function= "Primer" (S-08-578-649-8)
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APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
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                                                                                                                                                                         LENGTH: 305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: New York
COUNTRY: USA
ZIP: 10022
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08578649
Patent No. 5770366
CENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brightte Kaluza
TITLE OF INVENTION: MELANOWA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                            NAME/KEY: misc_RNA
LOCATION: 4..6
OTHER INFORMATION: /function= "Startcodon Met"
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue CITY: New York STATE: New York COUNTRY: USA
                                  INFORMATION FOR SEQ 10 NO: 18 SEQUENCE CHARACTERISTICS: LENGTH: 330 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA
                     (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.4
Best Local Similarity 58.5
Matches 141; Conservative
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LOCATION:
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                     TELEPHONE:
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US-08-578-649-8
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1586..1719
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2804..2914
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3232..3252
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1378..1504
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Matches 62; Conserva
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COTHER INFORMATION: /note= "N in positions 194, 369

OTHER INFORMATION: and 527 denotes an indefinite number and sequence OTHER INFORMATION: of nucleotides "
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Best Local Similarity 63.3%; Pred. No. 0.0016;
Matches 62; Conservative 0; Mismatches 36; Indels
                                                                                                                                                                                                                                                                       join(40..111, 40..166, 214..347, 393..503, 549
..569)
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Sequence 3, Application US/08578649

Batent No. 5770366

GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Brighte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSER: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
COUNTRY: USA

STATE: New York
CONDUTER: New York
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 TIAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTG 162
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                                                                         BOER 1035-PFF/ALT
                                   NAME: Andrew L. Tidjoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER
TELECOMMUNICATION INPORMATION:
TELEPHONE: (212) 838-9200
TELEPHONE: (212) 838-9200
TELEPHONE: (212) 838-9384
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (Genomic)
                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                             sig_peptide
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LOCATION:
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LOCATION:
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LOCATION:
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NAME/KEY:
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FEATURE:
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LOCATION: one-of(2216)
OTHER INFORMATION: /note= "N in position 2216
OTHER INFORMATION: denotes an indefinite number ans sequence of
OTHER INFORMATION: nucleotides"
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 29-Unly-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: DE P43 24 247.2
FILING DATE: 20-Unly-1993
ATTORNEY/AGENI INFORMATION:
NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31.575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G
APPLICANT: FALKORE, F. G
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: FOLGY & Lardner
STREET: FOLGY & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-232-463-14/c
; Sequence 14, Application US/08232463
Setent No. 5670367
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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1378..1449
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-860-820-1
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FEATURE:
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COUNTRY:
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; Sequence 1, Application US/08860820
; Patent No. 62450-1
; GENERAL INFORMATION:
    APPLICANT: Sonnewald, Uwe
    APPLICANT: Bowien, Jons
    APPLICANT: Bowien, Botho
    TITLE OF INVENTION: PROCESS AND DNA MOLECULES FOR INCREASING
    TITLE OF INVENTION: THE PHOTOSYNTHESIS RATE IN PLANTS
    NUMBER OF SEQUENCES: 2
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: FISH & NEAVE
    STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.3%; Score 34; DB 1; Length 7218; Best Local Similarity 8.1%; Pred. No. 0.6; Matches 19; Conservative 120; Mismatches 95; Indels
                        COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
COMPUTER: 1BM PC Compatible
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; CLONE: pTZgpt-F1s
US-08-232-463-14
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CONFUTER: IF THE COMPANIES PROPE CANADA CONFUTER: THE COMPUTER: THE
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FEATURE:
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                                                                                                                                                                                                                 144 CTATGTGTACTCAAAGCTGGTAAAAAAAAAGGAGCTGGAGAATTTTGGGCTGGCAGTGT 203
                                                                                                   Gaps
OTHER INFORMATION: SNF1 kinase subunit of protein kinase (LeSNF1)
                                                                                                 0
                                                        Score 33.6; DB 4; Length 1929; Pred. No. 0.44; 0; Mismatches 64; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA PAPLICATION NUMBER: US/08/286,870A FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CUSHMAN DARBY & CUSHMAN ADDRESSEE: Intellectual Property Group of ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP STREET: 1100 New York Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
TELECOMMUNICATION INFORMATION:
TELEFHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR EAG ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2159 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 05-AUG-1994
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGBNT INFORMATION:
NAME: PAUL. N KOKULIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: DC
COUNTRY: USA
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPER: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ELY, S
APPLICANT: TALICOR, RH
APPLICANT: TIPETT, JM
APPLICANT: TIPETT, JM
APPLICANT: BLENK, RG
TITLE OF INVENTION: BACTERIAL GENES
UNUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08286870A Patent No. 6063605
                                                                                                                                                                                                                                                                                                                                           1673 GGAATTTGTTAACAAG 1658
                                                                                                                                                                                                                                                                                                      204 TIATGGTGATGGCCAG 219
                                                          10.2%;
                                                                  Query Match 10.2's
Best Local Similarity 52.9'
Matches 72; Conservative
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STRANDEDNESS: double
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; LOCATION: 1...
US-08-286-870A-7
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US-08-286-870A-7/c
                  ; US-09-359-161-4
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Ratent No. 6566207

GENERAL INFORMATION:
APPLICANT: Tirrell, David A
APPLICANT: Kiick, Kristi L
TITLE OF INVENTION: Efficient Production of Engineered Proteins Containing
TITLE OF INVENTION: Efficient Production of Engineered Proteins Containing
TITLE OF INVENTION: Amino Acid Analogues
FILE REPREENCE: 30431-65031
CURRENT APPLICATION NUMBER: US/09/767,515
CURRENT FILING DATE: 2001-01-23
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APPLICANT: Tirrell, David A
APPLICANT: Tirrell, David A
TITLE OF INVENTION: Overexpression of Aminoacyl-tRNA Synthetases for
TITLE OF INVENTION: Deficient Production of Engineered Proteins Containing
TITLE OF INVENTION: Efficient Production of Engineered Proteins Containing
TITLE OF INVENTION: Amino Acid Analogues
TITLE OF INVENTION: Amino Acid Analogues
TITLE OF INVENTION: Amino Acid Analogues
CURRENT APPLICATION NUMBER: US/09/767,515
CURRENT APPLICATION NUMBER: 60/207,627
PRIOR APPLICATION NUMBER: 60/207,627
PRIOR PLING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 2.1
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                                                                                                                                                                                                                                             174 TGGAGCTGGAGAATTTTGGGCTGGCAGTGTTATGGTGATGGCCAGGACGAGATGGGAGT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 CGIGGGITATITICCCCAGGAACTIGGICAAGGAACAGCGIGIGIGIACCAGGAAGCIACCAA 293
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                                                                                                                                     Gaps
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9.9%; Score 32.8; DB 4; Length 6501;
Best Local Similarity 54.0%; Pred. No. 1.4;
Matches 67; Conservative 0; Mismatches 57; Indels 0,
Score 33.6; DB 3; Length 2159; Pred. No. 0.46; 0; Mismatches 69; Indels 0
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Patent No. 6586207
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                        Query Match
Best Local Similarity 52.1%;
Matches 75; Conservative
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US-09-767-515-2
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ORGANISM: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 CCCACCACGGATATTGA 317
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SOFTWARE: PatentIn Ver. 2.1
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US-09-103-840A-2
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION:
AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASLEGG for Windows Version 4.0
SEQ ID NO 3
LENGTH: 202001
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                                                                                                                                                                                                                                                                                                                                                                                                                                         180 TGGAGAATTTTGGGCTGGCAGTGTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGG 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.8%; Score 32.2; DB 4;
49.7%; Pred. No. 11;
iive 0; Mismatches 83;
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US-09-252-991A-889/c
; Sequence 889, Application US/09252991A
PRIOR APPLICATION NUMBER: 60/207,627 PRIOR FILING DATE: 2000-05-26 NUMBER OF SEQ ID NOS: 2 SO;TWARE: Patentin Ver. 2.1 SEQ ID NO 2 LENGTH: 6501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LCCATION: (1)...(202001)
CTHER INFORMATION: n = A,T,C or G
US-09-734-674-3
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                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 82; Conserve
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ORGANISM: Human
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US-09-734-674-3
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Best Local
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PRILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 889
LIBNGTH: 1944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 TATITICCCCAGGAACTIGGICAAGGAACAGCGIGTGIACCAGGAAGCTACCAAGGAAGIT 300
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APPLICANT: FLEISCHAAN, Robert D.
APPLICANT: FERSICHAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRANTER, John C.
TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 2436-22007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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llarity 51.8%; Pred. No. 2.3;
Conservative 0; Mismatches 66;
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9.5%; Score 31.2; Di
Best Local Similarity 47.9%; Pred. No. 62;
Matches 90; Conservative 0; Mismatches
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Search completed: December 30, 2003, 06:10:50 Job time : 36.6527 secs

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December 29, 2003, 16:03:18; Search time 11.4006 Seconds (without alignments) 927.898 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                  Run on:
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US-10-019-455A-24 590 1 HGIFMDRLASKKLCADDECV......RVYQEATKEVPTTDIDFFCE 110 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Scoring table: Sequence:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| S         | Description                | melanoma-derived q | prot   | transforming prote | gene VAV2 protein | divis  | myosin-IA - Acanth | hypothetical prote | asparagine synthas | fructose-bisphosph | Balbiani ring 1 ch | ATP-dependent RNA | AAA family ATPase | endo-1,4-beta-mann | orotate phosphorib | cell division cycl | disease resistance | quinone oxidoreduc | rubredoxin-NAD+ re | phosphoribosylamin | probable signal tr | hypothetical prote | sugar ABC transpor | protein-tyrosine k | protein-tyrosine k | Balbiani ring 2 ch | hypothetical_prote | Balbiani ring 2 ch | formate dehydrogen | glycosyltransferas |
|-----------|----------------------------|--------------------|--------|--------------------|-------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | ΩI                         | I38019             | TVHUVV | TVMSVV             | 151940            | RGBYC5 | T32734             | T48525             | C64439             | C69621             | A23516             | G96965            | C90186            | D72278             | D86758             | F90113             | T47442             | E86714             | 139521             | A64417             | S67383             | T29340             | AF2340             | S24550             | S24553             | B29662             | C64427             | 2996               | B83966             | 9725               |
|           | DB                         | 0                  | гH     | Н                  | 7                 | Н      | N                  | 0                  | ~                  | н                  | 7                  | 0                 | ~                 | 7                  | ~                  | 0                  | ~                  | ~                  | N                  | ч                  | C)                 | ~                  | ~                  | ٦                  | -                  | 7                  | N                  | 7                  | ~                  | 7                  |
|           | %<br>Query<br>Match Length | 131                | 839    | 844                | 878               | 1589   | 1215               | 308                | 541                | 671                | 383                | 585               | 769               | 699                | 209                | 295                | 1199               | 328                | 392                | 444                | . 670              | 2541               | 461                | 505                | 206                | 162                | 259                | 359                | 782                | 374                |
|           | Query<br>Match             |                    |        |                    | 13.8              |        |                    | 12.5               | 12.1               | 12.1               |                    |                   |                   | 11.9               |                    |                    |                    |                    | 11.7               |                    |                    |                    |                    |                    |                    |                    | 11.5               |                    |                    | 11.4               |
|           | Score                      | 253                | 9      | ın                 | 81.5              | 78.5   | 74.5               | 74                 | 71.5               | 71.5               | 71                 | 71                | 71                | 70.5               | 70                 | σ                  | 69.5               | 69                 | 69                 | 69                 | 69                 | 69                 | œ                  | 68.5               | æ                  | 68                 | 68                 | 68                 | 68                 | 67.5               |
|           | Result<br>No.              | :                  | 7      | ٣                  | 4                 | S      | 9                  | 7                  | æ                  | σ                  | 10                 | 11                | 12                | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 50                 | 21                 | 22                 | 23                 | 24                 | 25                 | 26                 | 27                 | 28                 | 29                 |

| probable chromomet | VHS domain contain | polygalacturonase | glutamyl-tRNA synt | L2 protein - human | L2 protein - human | probable ABC trans | hypothetical prote | orotate phosphorib | hypothetical prote | amiA protein - Str | mixed-lineage prot | Balbiani ring 1 ch | acetyltransferase | probable acetyltra |
|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| G96719<br>C75325   | T39655             | S24156            | G82104             | P2WL8              | S36483             | D70873             | T19413             | AG1303             | E81308             | S11148             | A53800             | A29662             | AG2737            | E97518             |
| 77                 | 4 7                | ~                 | 7                  | Ч                  | ~                  | N                  | N                  | 0                  | 7                  | ~                  | 7                  | 7                  | N                 | 7                  |
| 839                | 373                | 383               | 509                | 518                | 524                | 542                | 1187               | 209                | 258                | 493                | 847                | 162                | 229               | 229                |
| 11.4               | 11.4               | 11.4              | 11.4               | 11.4               | 11.4               | 11.4               | 11.4               | 11.3               | 11.3               | 11.3               | 11.3               | 11.2               | 11.2              | 11.2               |
| 67.5               | 67                 | 67                | 67                 | 67                 | 67                 | 67                 | 67                 | 66.5               | 66.5               | 66.5               | 66.5               | 99                 | 99                | 99                 |
| 30                 | 32                 | 33                | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                | 45                 |

## ALIGNMENTS

|       |       | 1                       |                            |
|-------|-------|-------------------------|----------------------------|
|       |       | MI                      |                            |
|       |       | regulatory protein MIA  |                            |
|       |       | pro                     |                            |
|       |       | tory                    |                            |
|       |       | ulai                    | a<br>a                     |
|       |       | reg                     | (ma                        |
|       |       | wth                     | Species: Homo sapiens (man |
|       |       | gro                     | gapi                       |
|       |       | nelanoma-derived growth | OMO                        |
|       |       | der                     | Ĭ.                         |
| 7     |       | ma-                     | ies                        |
| ESULT | 38019 | ano                     | ped                        |
| ES    | 38    | Ę,                      | S                          |

RESULT 1
138019
melanoma-derived growth regulatory protein MIA - human
C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 04-Mar-2000
C;Accession: 13019; &45038
R;Blesch, A.; Bosserhoff, A.K.; Apfel, R.; Behl, C.; Hessdoerfer, B.; Schmitt, A.; Jac
Cancer Res. 54, 5695-5701, 1994
A;Title: Cloning of a novel malignant melanoma-derived growth-regulatory protein, MIA
A;Reference number: 138019; MUD:95007612; PMID:7923218
A;Accession: 138019
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-131 <RES
A;Cross-references: EMBL:X75450; NID:9438057; PIDN:CAA53203.1; PID:9438058
C;Genetics:
A;Gene: mia
C;Superfamily: human melanoma-derived growth regulatory protein MIA

Gaps 5; Query Match 43.0%; Score 253.5; DB 2; Length 131; Best Local Similarity 45.4%; Pred. No. 4.2e-19; Matches 49; Conservative 21; Mismatches 33; Indels 5.

3;

63 83 5 MDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGE-F g ò

64 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110 84 WGGSVQGDYYGDLAARLGYFPSSIVREDQTLKPGKVDVKTDKWDFYCQ 131 ò d

transforming protein vav - human (fragments)

NiAlternate names: finger protein vav
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
S;Sofies: Sofies: Sofies: Sofies: Heslop, H.E.; Pulido, D.
R;Katzav, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.
A;Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene
A;Reference number: A39576; MUID:91/72176; PMID:2005887
A;Accession: B39576
A;Accession: B39576
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C. Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-bindin C; Superfamily: vav transforming protein; zinc finger C; Superfamily: vav transforming protein; zinc finger C; Superfamily: clozd homology; protein; zinc finger F; 32-102/Region: acidic F; 32-102/Region: acidic F; 336-340/Region: acidic F; 336-340/Region: clozd homology <CD24>
F; 346-493/Region: muclear location signal F; 355-56/Region: nuclear location signal F; 525-56/Region: zinc finger CCC motif F; 525-56/Region: zinc finger CCC motif F; 525-56/Region: zinc finger HCCH motif F; 555-56/Region: proline-rich F; 604-654/Domain: SH3 homology <SH3>
F; 606-609/Region: proline-rich F; 604-654/Domain: SH3 homology <SH2>
F; 788-836/Domain: SH3 homology <SH3>
F; 788-836/Domain: SH3 homology <SH3>
F; 788-836/Domain: SH3 homology <SH3>
F; 788-836/Domain: SH3 homology <SH3>
F; 788-836/Domain: SH3 homology <SH3>
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Ann. Hum. Genet. 59, 25-37, 1995

Ann. Hum. Genet. 59, 25-37, 1995

Ann. Hum. Genet. 59, 25-37, 1995

Ann. Hum. Genet. 59, 25-37, 1995

A;Title: Identification of VAV2 on 9q34 and its exclusion as the tuberous sclerosis 9

A;Reference number: 151940; MUD:95283235; PMID:7762982

A;Recession: 151940

A;Redecule type: mRNA

A;Redecule type: mRNA

A;Residues: 1-878 «RES>

A;Cross-references: GB:576992; NID:g913345; PIDN:AAB34377.1; PID:g913346

C;Genetics:
A;Gene: GDB:VAV2

A;Cross-references: GB:370880; OMIM:600428

A;Gene: GDB:VAV2

A;Cross-references: GDB:370880; OMIM:600428

A;Gene: GDB:VAV2

A;Cross-references: GDB:370880; OMIM:600428

A;Cross-references: GB:576992; NID:g913345; PIDN:AAB34377.1; PID:g913346

C;Genetics:
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A;Cross-references: GDB:370880; OMIM:600428

A;Cross-references: GDB:370880; OMIM:600428

A;Cross-references: GDB:370880; OMIM:600428

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A;Cross-references: GDB:370880; OMIM:600428

A;Cross-references: GDB:37080; OMIM:600428

A;Cross-references: GDB:37080; OMIM:600428

A;Cross-references:
A;Reference number: S23669; MUID:92228488; PMID:1565462
A;Contents: annotation; the authors note the frameshift difference with sequence in
A;Note: the complete sequence was submitted to Genbank; see S36941
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16
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C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 VYT---ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.5%; Score 85.5; DB 1; Length 844; 31.4%; Pred. No. 0.87; ive 14; Mismatches 21; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.8%; Score 81.5; DB 2; Length 878; 26.3%; Pred. No. 2.4; ive 21; Mismatches 22; Indels 1.
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862 GRIGWFPSTYVEEEGI 877
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Best Local S
Matches 22
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A;Status: not compared with conceptual translation
A;Residues: 1-844 <COP>
A;Residues: 1-844 <COP>
A;Residues: 1-844 <COP>
Mol. Cell. Biol. 11, 1912-1920, 1991
Mol. Cell. Biol. 11, 1912-1920, 1991
My Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene ad A;Fitle: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene ad A;Fitle: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene ad A;Fitle: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene ad A;Fitlesidues: 1-28, F. 330-93 <KAT>
A;Molecule type: MNA
A;Molecule type: MS9833; NID:g202343; PIDN:AAA63402.1; PID:g202344
R;Adams, J.M.
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A; Molecule type: mRNA
A; Molecule: 1-323, "DiLAVUPMORVLKYHILLOELVK', 346-347, 'QDAT', 352,'K', 354,'N', 355-453,'R', 45
A; Cross-references: EMBL:X64361; NID:955220; PIDN:CAA45713.1; PID:955221
A; Cross-references: EMBL:X64361; NID:955220; PIDN:CAA45713.1; PID:955221
A; Andams, J. M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.
Oncogene 7, 611-618, 1992
A; Title: The hematopoietically expressed vav proto-oncogene shares homology with the dbl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Contents: annotation
A; Note: in the sequence from mouse the authors find three additional nucleotides that proccurred in the published human sequences
C; Comment: In comparing these sequences with the mouse (see PIR: TVMSVV), there appear to
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A;Genes: GDB:VAV1; VAV
A;Genes: GDB:VAV1; VAV
A;Genes: GDB:VAV1; VAV
A;Genes: GDB:VAV1; VAV
A;Genes: GDB:VAV1; VAV
A;Genes: GDB:VAV1; VAV
A;Genes: GDB:VAV1; VAV
A;Genes: GDB:VAV1; VAV
C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding 1; C;Seywords: phosphoprotein; transforming protein; zinc finger
C;Seywords: phosphoprotein; transforming protein; zinc finger
F;188-452/Domain: DDC24 homology <CDC2+
F;589-542/Region: zinc finger CCC motif
F;547-560/Region: zinc finger HCCH motif
F;547-560/Region: zinc finger HCCH motif
F;589-648/Domain: SH3 homology <SH3A>
F;664-756/Domain: SH3 homology <SH3A>
F;664-756/Domain: SH3 homology <SH3A>
F;664-756/Domain: SH3 homology <SH3A>
F;783-831/Domain: SH3 homology <SH3A
                         A; Accession: S05382
A; Molecule type: mRNA
A; Residues: 62-839 < KAT2>
A; Cross-references: EMBL:X16316
A; Cross-references: EMBL:X16316
A; Cross-referencen, H.; Allen, J.; Lints, T.; Harvey, R.
Oncogene 7, 611-618, 1992
A; Title: The hematopoietically expressed vav proto-oncogene shares homology with the A; Reference number: $23669; MUID:92228488; PMID:1565462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 ASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRN
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Matches 23;
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Species: Methanococcus jannaschil

CiSpecies: Methanococcus jannaschil

CiSpecies: Methanococcus jannaschil

CiDate: 13-Sep-1996 #sequence_revision 09-Jun-2000 #text_change 19-Jul-2002

CiAccession: C64439

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake

Rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,

A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasch:

A;Reference number: A64300; MUID: 96337999; PMID: 8688087
                                                                                                                                                                                                                                                                          A;Introns: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 296/1; 340/3; 390/3; 447/3; 50
C;Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homo
F;14-674/Domain: myosin motor domain homology <MMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T48525
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancrof
submitted to the Protein Sequence Database, April 2000
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A;Cross-references: GB:U67554; GB:L77117; NID:g2826365; PIDN:AAB99117.1; PID:g1591755;
A;Note: an incorrect initiation codon was used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1215 <LEE>
A;Cross-references: EMBL:AF085185; NID:g3599477; PID:g3599478; PIDN:AAC35357.1
A;Experimental source: strain Neff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T22P22.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 VYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 KGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-308 <BEV>
A;Cross-references: EMBL:AL163814
A;Experimental source: cultivar Columbia; BAC clone T22P22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                              ;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                             12.6%; Score 74.5; D
llarity 28.6%; Pred. No. 18;
Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117/3; 135/3; 180/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: Z24490
A; Accession: T48525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYFPRNLVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 20, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                   A, Molecule type: DNA
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A; Accession: T32734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 5
A;Introns: 63/3; 1
A;Note: T22P22.50
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A; Residues: 1-1589 c-PAU>
A; Residues: 1-1589 c-PAU>
A; Residues: 1-1589 c-PAU>
A; Cross-references: ENREL:UJ7247; NID:9577216; PIDN:AAB67360.1; PID:9577222; GSPDB:GN0001
R; Camonis, J.H.; Kalekine, M.; Gondre, B.; Garreau, H.; Boy-Marcotte, E.; Jacquet, M.
B; Camonis, J.H.; Kalekine, M.; Gondre, B.; Garreau, H.; Boy-Marcotte, E.; Jacquet, M.
BMBO J. S, 375-380, 1986
A; Title: Characterization, cloning and sequence analysis of the CDC25 gene which control A; Reference number: A23444; MUID:86220116; PMID:3011405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myosin-1A - Acanthamoeba castellanii
C;Species: Acanthamoeba castellanii
C;Species: 29-oct-1999 #sequence_revision 29-Oct-1999 #text_change 08-Sep-2000
C;Accession: T32734
R;Lee, W.L.; Ostap, E.M.; Zot, H.G.; Pollard, T.D.
submitted to the EMBL Data Library, August 1998
A;Description: Hydrodynamic and ligand binding properties of Acanthamoeba myosin-IA GPA/A;Reference number: Z21216
                                     RGBYCS

Call division control protein CDC25 - yeast (Saccharomyces cerevisiae)

N;Alternate names: protein L2142.6; protein YLR310c

C;Species: Saccharomyces cerevisiae

C;Species: 31-Mar-1998 #sequence_revision 31-Mar-1993 #text_change 21-Jul-2000

C;Accession: A26596; S51442; A23444; S43051; 847990

R;Broek, D.; Toda, T.; Michaeli, T.; Levin, L.; Birchmeier, C.; Zoller, M.; Powers, S.;

A;Title: The S. cerevisiae CDC25 gene product regulates the RAS/adenylate cyclase pathwa

A;Reference number: A26596; MUID:87131091; PMID:3545497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Description: positive control of level of cellular cAMP at the stage at which the cell (A.Description: budding yeast CDC25; CDC25-type guanine nucleotide exchange activator how C.Superfamily: budding yeast CDC25; CDC25-type guanine nucleotide exchange activator how C.Superfamily: budding yeast CDC25, transmembrane protein (F.55-123/Domain: SH3 homology <SH3>
F;1301-1542/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>
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A;Title: The CDC25 "Start" gene of Saccharomyces cerevisiae: sequencing of the active
A;Reference number: S43051; MUID:88194639; PMID:3329037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 LASKKLCADDECVYTISLASAQEDYNAP-----DCRFINVKKGQQIYVYSKLVKENGAGE 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Residues: 1-15-20-39 - SRO-3-4, Residues: 1-15-39 - SRO-3-4, Residues: 1-15-39 - SRO-3-4, R. Cross-references: EMBL: M15458; NID: g171184; PIDN: AAA34478.1; PID: g171185 R; Pauley, A. Submitted to the EMBL Data Library, November 1994 A; Description: The sequence of S. cerevisiae cosmid L2142. A; Reference number: S51437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Residues: 1-496,'Y', 498-953,'LSVIMNLSR',964-1589 <CAM>
A;Cross-references: EMBL:X03579; NID:g3483; PIDN:CAA27259.1; PID:g3484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.3%; Score 78.5; DB 1; Length 1589; 25.8%; Pred. No. 9.2; tive 21; Mismatches 34; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 WWDGLVIDDSNGKVN-RGWFPQNFGRPLR 127
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A;Cross-references: SGD:S0004301; MIPS:YLR310c
A;Map position: 12R
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Gaps

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20;

37; Indels

Length 383;

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Cyaccesion: A23516
R;Hoog, C.; Bigberg, C.; Wieslander, L.
Nucleic Acids Res. 14, 703-719, 1986
Nucleic Acids Res. 14, 703-719, 1986
Nicleic Acids Res. 15, 703-719, 1986
Nicleic Acids Res. 15, 703-719, 1986
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Nicleic Acids Res. 15, 703-719, 1986
Nicleic Acids Res. 15, 703-719, 1986
Nicleic Acids Res. 15, 703
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-585 «KUR»
A; Coss-references: GB: AE001437; PIDN: AAK78754.1; PID: g15023664; GSPDB: GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 DKDCCKKNCNCDGAKF------PECEESNSKQSGMFDILAKLFKPQG-GDFEA 348
C;Species: Chironomus tentans
C;Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRIASKKICADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.0%; Score 71; DB 288.0%; Pred. No. 12; tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 273/1
C;Superfamily: unassigned Balbiani ring proteins
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nes 26; Conservative
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C;Species: Bacillus subtils
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C;Species: Bacillus subtils
C;Species: Bacillus subtils
R;Kunst. F; Ogasavara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Erington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Krogh, S.; Kumano, M.; Kurita, K.; Irapidus, A.; Bardinois, Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Irapidus, A.; Bardinois, Koetter, P.; Koningstein, G.; Rocha, E.; Roche, B.; Rose, W.; Sadaie, Y.; Sato, T.; Sachinois, A;Authors: Lanakos, T.; Rocha, E.; Roche, B.; Rose, W.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sadaie, Y.; Sato, T.; Seron, A; Settiuchi, J.; Sekweka, A.; Sato, A;Authors: Schleich, A.; Tanako, H.; Yamano, K.; Yasunoto, K.; Yasta, K.; Yoshida, K.; Tanako, H.; Yamano, K.; Yasunoto, K.; Yasta, K.; Yoshida, K.; A;Authors: Schleich, A.; Yamanoto, H.; Yamano, K.; Yasunoto, K.; Yasta, K.; Yoshida, K.; A;Authors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.; Atanakos, M.; A;Atter Rocaplete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Residues: 1-671 «KUN>
A;Residues: 1-671 «KUN>
A;Residues: 1-671 «KUN>
A;Residues: 1-671 «KUN>
A;Residues: Eferences: GB:299124; GB:ALO09126; NID:g2636442; FIDN:CAB16056.1; PID:g2636566
A;Residues: Ebp; yydE
C;Genetics:
A;Perhamonomers Residues: Catalning activition:
Catalyzes the hydrolysis of fructose-1,6-bisphosphate to fructose-6-phosp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Pathway: gluconeogenesis A; Note: requires and phosphoenolpyruvate for activation A; Note: requires manganese ion for stability and phosphatase; phosphoesterase core homology C; Superfamily: Bacillus subtilis fructose-bisphosphatase; phosphoesterase core homology C; Keywords: carbohydrate metabolism; gluconeogenesis; metalloprotein; phosphoric monoest
                                        A; Map position: REV1058315-1056681
C; Superfamily: asparagine synthase (glutamine-hydrolyzing)
C; Keywords: asparagine biosynthesis; ligase
F;2-541/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <MAT>F;2/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 IYAERLAKDINLKLRKKIISEEEYEEYVFKVAKAIDEVD-----IMKIGVGIPIYVASEM 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 FMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYS-----KLV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 YLDLIAQKYDCEEKVVTEIINLKA------ILNLPKGTEHFVSDLHGEYQAFQHV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 IFMDRLAS------KKLCADDEC-VYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fructose-bisphosphatase (EC 3.1.3.11) [validated] - Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Indels 29;
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                                                                                                                                                                                                                                                                                                  Query Match
12.1%; Score 71.5; DB 2; Length 541;
Best Local Similarity 25.7%; Pred. No. 15;
Matches 27; Conservative 22; Mismatches 33; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 ANEDGLKVV----LSGQGADEL-FGGY-----ARHERIYRERGEE 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 VKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKE
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Y 22.8%; Pred. No. 15,
''ve 21; Mismatches ''
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Best Local Similarity 22.8*
Matches 26; Conservative
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Cjaccession: C90186
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chr. Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, submittet, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
AAA family ATPase [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
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A23516 Balbiani ring 1 chain - midge (Chironomus tentans) (fragment)

RESULT 10

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Similarity
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A;Molecule type: DNA
A;Residues: 1-295 <DOU>
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Local Sim
21;
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C, Genetics:
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Matches
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A;Cross-references: GB:AE001779; GB:AE000512; NID:g4981777; PIDN:AAD36302.1; PID:g498178
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ciptate phosphoribosyltransferase (EC 2.4.2.10) [imported] - Lactococcus lactis subsp. ]
Cispedies: Lactococcus lactis subsp. Lactis
Cipate: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002
Cipate: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002
Cipate: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002
Ribolotin, A. Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: D86758
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endo-1,4-beta-mannosidase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72278
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 399, 323-329, 1999
A;Tille: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: D72278
                                                                                                                                                                                       A,Gene: SSO0421
C,Superfamily: transitional endoplasmic reticulum ATPase; FtsH/SEC18/CDC48-type ATP-bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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A.Cross-references: GB:AE005176; PID:g12724022; PIDN:AAK05166.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 LENTGEDIREDICSFILPKDGMEIKKTVEVRAGVFDYSNTFEKLSVKVEDLVFENEIEHL 452
                                                                                                  A; Cross-references: GB: AEO06641; NID: 913813572; PIDN: AAK40746.1; GSPDB: GN00155 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                         51 YTISRLGIENGDYVEIIGPSGSALAQALIGDGIADNEIRVDGYIRRSIGVGIGDEVTVKR 110
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                                                                                                                                                                                                                                                                                                                                                            49 YVYSKLVKENG------AGEFWAGSVYGDG--QDEMGVVGYFPRNL-----VKE
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Best Local Similarity 27.6%; Pred. No. 24;
Matches 32; Conservative 12; Mismatches 37; Indels 35;
                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                    12.0%; Score 71; DB 2; Length 769; 35.0%; Pred. No. 25; tive 10; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 AQV-QDATKVVLAPTQPISF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 QRVYQEATKEV--PTTDIDF 107
                                                                                                                                                                                                                                                                                          Best Local Similarity 35.0°
Matches 28; Conservative
          A; Reference number: A99139
                               A, Accession: C90186
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-769 < KUR>
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Gall division cycle 2 homolog [imported] - Guillardia theta nucleomorph C;Species: nucleomorph Guillardia theta
C;Species: nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001 C;Accession: F90113
C;Accession: F90113
R;Douglas, S; Zauner, S; Fraunholz, M; Beaton, M; Penny, S; Deng, L.T.; Wu, X.; Re Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Gene: pyrB
C;Superfamily: orotate phosphoribosyltransferase; orotate phosphoribosyltransferase hom
C;Keywords: glycosyltransferase; pentosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 LASKKI.CADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKI.VKENGA--GEFWA 65
                                                                                                                                                                                                                      25 LASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Genome: nucleomorph
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: nucleomorph
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                                                                                                      11.9%; Score 70; DB 2; Length 209; 26.9%; Pred. No. 7.7; tive 15; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 GEILFQGKSELDQL------NKIFQ--TIGTPTTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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28.0%; Pred. No. 13;
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155 ELEKANRKFADAGVKLAT 172
                                                                                                                                                                                                                                                                                                                                                  85 NLVKEORVYOEATKEVPT
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NCBI_TaxID=9606;
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Maximum Match 100%
Listing first 45 summaries
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 GenCore (c) 1993 -
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| O920r4 mus musculu Q15811 homo sapien Q12554 aspergillus O31153 vibrio chol P06419 human papil P36751 human papil Q8Y668 listexia mo Q9nhv9 drosophila Q8Rtv2 streptococc P08724 chironomus P50827 human papil O62683 canis famil |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ITM1_MOUSE<br>ITM1_HUMAN<br>PCL3_ASPNG<br>SYE_VIBCH<br>VL2_HPV17<br>PYRE_LISMO<br>VAV_DROME<br>PYRE_STRMU<br>BAR1_CHIPA<br>VL2_HPV36<br>ZO3_CANFA                                                                                 |
| аланаланана                                                                                                                                                                                                                       |
| 17114<br>1721<br>383<br>474<br>474<br>524<br>524<br>209<br>793<br>209<br>326<br>518                                                                                                                                               |
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#### ALIGNMENTS

OTON HUMAN

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TIGACT-2001 [Rel. 40, Created)

DT 16-COT-2001 [Rel. 40, Created)

DT 16-COT-2001 [Rel. 40, Created)

DT 16-COT-2001 [Rel. 40, Last sequence update)

DT 16-COT-2001 [Rel. 40, Last sequence update)

DE COTAGILIN precursor (Fibrocyte-derived protein) (Melanoma inhibitory activity like protein)

CO REATOR'S METAZOR'S (ACTOR HUMAN)

CONTRO RE POR MIAL.

BRANCHORE PROM NA.

REMEDINES-20134619, PubMed-1087378;

RA HORSILNES-20134619, PubMed-1087378;

RA HORSILNES-20134619, Mudapeth A.J., Morton C.C.;

RA BODIS C.S., Bell A.M., Hudapeth A.J., Morton C.C.;

RA HORSILNES-20134619, Mudapeth A.J., Morton C.C.;

RA HORSILNES-20134619, Mudapeth A.J., Morton C.C.;

RA HORSILNES-20134619, PubMed-10989416;

RA HORSILNES-20134619, PubMed-10989416;

RA HORSILNES-20134619, PubMed-10989416;

RA HORSILNES-20134619, PubMed-10989416;

RA HORSILNES-20106879; PubMed-10989416;

RA HORSILNES-20106879; PubMed-10989416;

RA HORSILNES-20106879; PubMed-10989416;

RA HORSILNES-20106879; PubMed-10989416;

RA HORSILNES-20106879; PubMed-10989416;

RA HORSILNES-20106879; PubMed-10989416;

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RA HORSILNES-20106879; PubMed-10989416;

RA HORSILNES-20106879; PubMed-10989416;

RA SEQUENCE FROW N.A.

REMELINES-20106879; PubMed-10989416;

RA SEQUENCE FROW N.A.

REMELINES-20106879; PubMed-10989416;

RA SEQUENCE FROW N.A.

REMELINES-20106879; PubMed-10989416;

RA HORSILNES-20106879; PubMed-10989416;

RA HORSILNES-201068

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musculus (Mouse)
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                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A., Mine S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Skice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wallis J.M., Thorpe A., Whitehead S.L., Whittaker P., Williams L., Williams E., Williams S.A., Wighers, J., Way P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers, J.,
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                                                                                                                                                           "The DNA sequence and comparative analysis of human chromosome 20.";
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09JUE3;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 40, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
Otoraplin precursor (Melanoma inhibitory activity-like protein)
OTOR OR MIAL.
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9BB52C7F5D4FB700 CRC64;
                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
-!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-!- SIMILARITY: Contains 1 SH3 domain.
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100.0%; Pred. No. 6.5e-54;
ive 0; Mismatches 0;
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BY SIMILARITY.
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AJ252326; CAC28085.1; JOINED.
AJ252327; CAC28085.1; JOINED.
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Pfam; PF000148; SH3; 1.
SMART; SM00126; SH3; 1.
PROSITE; PS50002; SH3; FALSE_NEG.
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nes 110; Conservative
                                                                                                                                                                            Nature 414:865-871(2001)
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EMBL;
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HSSP;
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EMBL;
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                 SEPTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 HGVFMDKLSSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKKGQQIYVXSKLVTENGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21100875; PubMed=11161796; Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.; Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.; "Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation."; Genomics 71:40-52(2001).
-: SIMCELGUIAR LOCATION: Secreted (Potential).
-: TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
-: SIMLIARITY: BELONGS TO THE MIA / OTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                  MEDLINE-20334619; PubMed=10873378; Resendes B.L., Weremowicz S., Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S., Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.; An novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping."; Genomics 66:242-248(2000).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SH3.
BY SIMILARITY.
BY SIMILARITY.
: 3DD47D4C77C4A7FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 547; DB 1;
Pred. No. 1.7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1888678; Otor.
GO; GO:0001502; P:cartilage condensation; IMP.
THEAPTO; IPR001452; SH3.
Pfam: PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTOR_CHICK STANDARD; PRT; 132 AA. 0918F6; 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.7e
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
OTORAPLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF23333; AAF82079.1; -.
EMBL; AJ243939; CAC27444.1; -.
HSSP; Q16674; 111J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14328 MW;
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nes 99; Conservative
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PROSITE; PS50002; SH3; 1.
Signal; SH3 domain.
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39 1
32
55 1
128 AA;
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OTOR.
                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
                                                                                                                   SEQUENCE FROM N.A.
                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                         rissum=Fetal
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Gallus

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKEN-G 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 YGVYMQKLSDKKLCADDECIYAISFGRAEDDYNAPDCRFVNLKKGELVYIYTKLVKENDD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95007612, PubMed=7923218;
Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
Schmitt A., Jachimczak P., Lottspeich F., Buettner R., Bogdahn U.;
"Cloning of a novel malignant melanoma-derived growth-regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 AGEFWAGSVYGDG-QDEMGVVGYFPRNLVKRQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 AGEFWSGSVYSDQYRDQQGLVGYFPSSLVTELTVYKDELQELPTTAVDFYCD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bosserhoff A. K., Hein R., Bogdahn U., Buettner R., astructure and promoter analysis of the gene encoding the human melanoma-inhibiting protein MIA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25440C1A3CF911AE CRC64;
-i- SUBCELLULAR LOCATION: Secreted (Potential).
-i- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-i- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.1%; Score 390; DB 1;
58.9%; Pred. No. 2.6e-33;
tive 26; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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TISSUE-Skin;
MEDLINE-22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96132947; PubMed=8550608;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein, MIA.";
Cancer Res. 54:5695-5701(1994).
                                                                                                                                                                                                                                                     EMBL; AF233519; AAF82728.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 AA; 15243 MW;
                                                                                                                                                                                                                                                                           HSSP; Q16674; 111J.
INTERPO; DROQUES; SH3.
Pfam; PP00018; SH3; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
S1gnal; SH3 domain.
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133
115
40
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TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                              3.5
3.5
5.8
5.8
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Q16674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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MIA HUMAN
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                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified morprofit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAG
  Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=20334619; PubMed=10873378;
MEDLINE=20334619; PubMed=10873378;
MEDLINE=20334619; Weremowicz S.,
Dobertson N.G., Hella A., Hudspeth A.J., Morton C.C.;
"A novel conserved cochlear gene, OTOR: identification, expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE=20334619; PubMed=10873378; Resendes B.L., Weremowicz S., Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S., Boblis C.S., Bell A.M., Hudspeth A.J., Morton C.C.; "A novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping."; Genomics 66:242-248(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 EFWAGSVYGDG-QDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 EFWAGSVYGEEYEDHMGTVGYFPRSLVSEQHVYQEANKTIPTTDIDFFCE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.9%; Score 477.5; DB 1; Length 132; 80.0%; Pred. No. 2.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Indels
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BY SIMILARITY.
9DICB07FD353CEIC CRC64;
                                                                                                                                                                                                                                 analysis, and chromosomal mapping.";
Genomics 66:242-248(2000).
-!- SUBCELLUIAR LOCATION: Secreted (Potential).
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
-!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTORAPLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 PC
132 OT
114 SF
40 BY
131 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF233518; AAF82727.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001452; SH3.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 80.0
Matches 88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 1
42 1
35 35
132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Otoraplin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; SH3 domain. SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q16674; 1I1J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8400;
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DISULFID
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zebeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Porbhyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Muzziy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mitching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.39 ANGSTROMS) OF 25-131.

MEDLINE=21244635; PubMed=11331761;
A Lougheed J.C., Holton J.M., Alber T., Bazan J.F., Handel T.M.;
Lougheed J.C., Holton J.M., Alber T., Bazan J.F., Handel T.M.;
T according the meanons inhibitory activity protein, a member of a recently identified family of secreted proteins.";
D Proc. Natl. Acad. Sci. U.S.A. 98:5515-5520(2001).
C -: FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO AS WELL AS SOME OTHER NEUROECTODERMAL TUMORS, INCLUDING GLICMAS.
C -: SUBCELLULAR LOCATION: Secreted.
C -: TISSUE SPECIFICITY: ALL MAINGNANT MELANOMA CELL LINES TESTED AND INFREQUENTLY IN CLIONA CELL LINES.
C -: PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
C -: SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
C -: SIMILARITY: Contains I SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MELANOMA DERIVED GROWTH REGULATORY PROTEIN.
SH3.
                                                                                                                                                                                                                                                     human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PTR, 138019; 138019.
PDB; 1110; 16-MAY-01.
PDB; 1HJD; 29-JAN-02.
PDB; 1KOX; 24-JUL-02.
Genew; HGNC; 70706; MIA.
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SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
Growth factor; Signal; SH3 dt
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                                                                                                                                                                                                                                                                                                                                                                  5 MDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGE-F 63
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=96216414; PubMed=8621736;
MEDLINE=96216414; DubMed=8621736;
MEDLINE=96216414; DubMed=8621736;
Dietz U.H., Sandell L.J.;
"Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and during chondrogenesis.";
J. Biol. Chem. 271:3311-3316(1996).
-!- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND MAINTENANCE.
                                                                                                                                                                                                                                                                                                                                 Gaps
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinoic acid-sensitive protein) (CD-RAP).
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                                                                                                                                                                                                                                                                                    43.0%; Score 253.5; DB 1; Length 131; 45.4%; Pred. No. 2.9e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.
-!- INDUCTION: Repressed by retinoic acid.
-!- PIW: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
-!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                 33; Indels
                                                                                                                                                                                                                                               14509 MW; 4D3BB30BD6008BDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
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HSSP; Q16674; 1I1J.
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Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
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01-NOV-1997
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Q28038;
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Pfam; PF00018; SH3; 1.

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                                                                                                                                                                                                                                                                                                                                                                                26 MPKLADRKMCADEECSHPISVAVALQDYVAPDCRFLTIHQGQVVYIFSKL---KGRGRLF 82
                                                                                                                                                                                                                                                                                                                                                 MDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGE-F
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"Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and during of a retinoic acid-sensitive mRNA expressed in cartilage and during chondrogenesis.";
J. Biol. Chem. 271:3311-3316 (1996).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                               11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 WAGSV----YGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FPB-2003 (Rel. 41, Last annotation update)
Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinoic acid-sensitive protein) (CD-RAP).
                         BY SIMILARITY.
MELANOMA DERIVED GROWTH REGULATORY
PROTEIN.
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                                                                                                                                                                                                                                             DB 1; Length 130;
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-- SUBCELLULAR LOCATION: Secreted.
-- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.
-- INDUCTION: Repressed by retinoic acid.
-- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
-- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                            28; Indels
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                    SH3.
BY SIMILARITY.
BY SIMILARITY.
; 95D153161C78E02A CRC64;
                                                                                                                                                                                                                      Score 252.5; DB 1
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factor; Signal; SH3 domain.
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MEDLINE=96216414; PubMed=8621736;
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129 BY
14353 MW;
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InterPro; IPR001452; SH3.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                        5 MDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGE-F 63
                                                                                                                                                                                                                                                                                                                                            26 MPKLADRKLCADEBCSHPISMÁVALQĎYVAPDCRFLTIYRGQVVYVFSKL---KGRGRLF 82
                                                                                                                                                                                                                                                                    Gaps
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--- SUBCELLIULAR LOCATION: Secreted.
--- TISSUB SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND INFREQUENTLY IN GLIOWA CELL LINES.
--- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
--- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
--- SIMILARITY: Contains 1 SH3 domain.
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Bosserhoff A.K., Kondo S., Moser M., Dietz U., Copeland N.G.,
Bosserhoff A.K., Sando S., Buetner R., Sandell L.J.;
"Mouse CD-RAP/MIS gene: structure, chromosomal localization, and
expression in cartilage and chondrosarcoma.";
Dev. Dyn. 208:516-525(1997).

-i- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO A
WELL AS SOME OTHER NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BALB/c;
MEDLINE=95007612; PubMed=7923218;
Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
Schmitt A., Jachimczak P., Lottspelch F., Buetrner R., Bogdahn U.;
"Cloning of a novel malignant melanoma-derived growth-regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                             POTENTIAL. MELANOMA DERIVED GROWTH REGULATORY PROTEIN. SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 061865; 009086; P97495;
01-NOV-1997 (Rel. 35, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Melanoma derived growth regulatory protein precursor (Melanoma
inhibitory activity) (Cartilage-derived retinoic acid-sensitive
protein) (CD-RAP).
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                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 130;
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                                                                                                                                BY SIMILARITY.

BY SIMILARITY.

MA -> VT (IN REF. 2).

SF99149AECF74501 CRC64;
                                                                                                                                                                                                                             42.5%; Score 250.5; DB 1
44.4%; Pred. No. 5.9e-19;
iive 23; Mismatches 32
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SMART; SM00326; SH3; 1.
PROSITE; PSS0002; SH3; FALSE NEG.
Growth factor; Signal; SH3 domain.
SIGNAL 1 22 POTEN
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Cancer Res. 54:5695-5701(1994).
                                                                                                                                                                                         130 AA; 14536 MW;
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                                                           130
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=129/Sv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIA OR CDRAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIA MOUSE
                                                                                                                                    DISULFID
                                                                                                                                                  DISULFID
                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                        CONFLICT
                                                                                                                DOMAIN
                                                                             CHAIN
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PROSITE, PSS0021, CH; 1.
PROSITE; PS00479; DAG PE_BIND_DOM_1; 1.
PROSITE; PSS0010, DAG PE_BIND_DOM_2; 1.
PROSITE; PSS0010, DH 2; 1.
PROSITE; PSS00741; DH 1; 1.
PROSITE; PSS00741; DH 1; 1.
-!- SIMILARITY: Contains 2 SH3 domains.
                                                                                                                                               MGD; MGI:1888518; Vav3.
InterPro; IPR001715; Calponin-like.
InterPro; IPR002347; CH type.
InterPro; IPR002131; DAG PE-bind.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001849; PH.
InterPro; IPR00129; RhOGEF.
                                                                                                                                                                                                                                                     Interpro; IPR001452; SH3.
Interpro; IPR003096; SM22_calponin.
                                                                                                                                                                                                                                                                            Pfam; PF00307; CH; 1.
Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF00621; PH; 1.
Pfam; PF00621; RhGEF; 1.
Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00458; SM2CALPONIN.
ProDom; PD0001527; CH type; 1.
ProDom; PD000066; SH2; 1.
SMART; SM00109; CL; 1.
SMART; SM00109; CH; 1.
                                                                                                                          EMBL; AF067816; AAF09171.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97946 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00325; RhoGEF; 1.
SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Conservative
                                                                                                                                                                                                                                        InterPro; IPR000980; SH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              672 7
788 8
847 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50001;
PROSITE; PS50002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSTYVEE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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     and for commercial
               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                    26 MPKLADWKLCADEECSHPISMAVALQDYVAPDCRFLTIYRGQVVYVFSKL---KGRGRLF 82
                                                                                               MGD; MGI:109615; Mia.
GO; GO:0007160; P:ecll-matrix adhesion; IMP.
GO; GO:0030198; P:extracellular matrix organization and bioge. . .; IMP.
InterPro; IRR001452; SH3.
PFam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=2017969; PubMed=10713454;
MEDLINE=2017969; PubMed=10713454;
MEDLINE=2017969; PubMed=10713454;
Trenkle T., McClelland M., Adlkofer K., Welsh J.;
"Major transcript variants of VAV3, a new member of the VAV family of guanine nucleotide exchange factors.";
Gene 245:139-149(2000).
TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE STARS OF THOSE GTPASES (BY SIMILARITY).

-!- ALTERNATIVE PRODUCTS:
EVent-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                  5 MDRLASKKI.CADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGE-F
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insold-20,00000-2; Sequence=Not described; SIMILARITY: Contains 1 calponin-homology (CH) domain. SIMILARITY: Contains 1 DBL-homology (DH) domain. SIMILARITY: Contains 1 PH domain. SIMILARITY: Contains 1 PH domain. SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG binding domain. 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                            5.
                                                                                                                                                                                                                 MELANOMA DERIVED GROWTH REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                   64 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPITDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 130;
                                                                                                                                                                                                                                                                                                                   39.9%; Score 235.5; DB 1; Length : 43.5%; Pred. No. 2.1e-17; cive 21; Mismatches 35; Indels
                                                                                                                                                                                                                                         SH3.
BY SIMILARITY.
BY SIMILARITY.
TL -> NS (IN REF. 1).
W; 16C957459C5BB5F9 CRC64;
     Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
  modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q9R0C8-1; Sequence=Displayed;
                                                                                                                                                                            PROSTIE: PS50002; SH3; FALSE NBG.
Growth factor; Signal; SH3 domain.
SIGNAL 1
                                                                                                                                                                                                                              PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
15-SEP-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                           14593 MW;
                                                     EMBL; X94322; CAA63983.1; -. BMBL; UB5612; AA842082.1; -. EMBL; X97965; CAA6608.1; -. HSSP; Q16674; 111J.
                                                                                                                                                                                                                                                                                                                      39.9
Best Local Similarity 43.5
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                           112
40
129
113
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                                                                                                                                                                                                                                           42
35
58
11
112
130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vav-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                           DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                CONFLICT
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Q9R0ČB;
                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAV3.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Photbol-ester binding; Zinc; SH2 domain; SH3 domain; Repeat; Guanine-nucleotide releasing factor; Alternative splicing.

DOMAIN 192 371 DH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PH.
PHORBOL-ESTER AND DAG BINDING.
SH3 1.
SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9A6B63F0D9E60F8F CRC64;
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31.3%; Pred. No. 0.21;
tive 14; Mismatches
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EMBL; AF030201; AAC25011.1;
EMBL; AF030202; AAC25011.1;
EMBL; AF030203; AAC25011.1;
                                                                                                                                                       EMBL; AF030207; AAC25011.1;
EMBL; AF030208; AAC25011.1;
EMBL; AF030209; AAC25011.1;
EMBL; AF030210; AAC25011.1;
                                                                EMBL; AF030227; AAC25011.1;
                                                                                                                                                                                                                                                EMBL; AF030214; AAC25011.1;
EMBL; AF030215; AAC25011.1;
EMBL; AF030216; AAC25011.1;
EMBL; AF030217; AAC25011.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC: 12657; VAV1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFAC; T00880;
                                                                                                                                                                                                                                     AF030213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC
MIM; 164875
                                                                                                                                                                                                                                                                                                                 EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                     EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 SH2 domain.
SIMILARITY: Contains 2 SH3 domains.
CAUTION: Ref.2 sequence differs from that shown due to frameshifts in position 322 and 355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 299-334 FROM N.A.
MEDLINE=96038895; PubMed=7478592;
RRAMOS-Morales F., Romero F., Schweighoffer F., Bismuth G., Camonis J., Tortolero M., Fischer S.;
"The proline-rich region of Vav binds to Grb2 and Grb3-3.";
Oncogene 11:1665-1669(1995).
                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-61 FROM N.A.

MEDLINE=91172176; PubMed=2005887;
Katzav S., Cleveland J.L., Haslop H.E., Pulido D.;

"Loss of the amino-terminal helix-loop-helix domain of the vav proto-
oncogene activates its transforming potential.";

Mol. Cell. Biol. 11:1912-1920(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY TO CDC24 FAMILY.
MEDILARE-3228488; PubMed=1555462;
Addams J.M., Houston H., Allen J., Lints T., Harvey R.;
"The hematopoietically expressed vav proto-oncogene shares homology with the dbl GDP-GTP exchange factor, the bor gene and a yeast gene (CDC24) involved in cytoskeletal organization.";
Oncogene 7:611-618(1992).
-!- FUNCTION: Couples tyrosine kinase signals with the activation of the Rho/Rac GTPases, thus leading to cell differentiation and/or proliferation.
                                                                                                                                                                              Denkinger D.J., Borges C.R., Shaw C.L., Cushman A.M., Kawahara R.S., "Transcriptional regulation of the vav proto-oncogene."; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Interacts with SLA (By similarity). Interacts with Grb2 and Grb3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOT IN OTHER CELL TYPES.

PTM: Phosphorylated on tyrosine residues.

MISCELLANEOUS: 'Vav' stands for the sixth letter of the Hebrew
                                                                                                      Eukaryotta, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 calponin-homology (CH) domain. SIMILARITY: Contains 1 DBL-homology (DH) domain. SIMILARITY: Contains 1 PH domain. SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG
                                                                                                                                                                                                                                          MEDLINE=90005432; PubMed=2477241;
Katzav S., Martin-Zanca D., Barbacid M.;
"vav, a novel human oncogene derived from a locus ubiquitously expressed in hematopoietic cells.";
EMBO J. 8:2283-2290(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Romero F.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                    747-74796 (Rel. 14, Created)
16-077-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
VAVI OR VAV.
            845 AA
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 299-837 FROM N.A.
                                                                                                                                                                                                                                  SEQUENCE OF 62-845 FROM N.A.
            STANDARD;
                                                                                                   Homo sapiens (Human)
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alphabet.
             VAV HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                 Romero
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO: 000370; F: transcription factor activity; TAS. GO; GO: 0007048; P: oncogenesis; TAS. GO; GO: 0007048; P: oncogenesis; TAS. InterPro; IPR001715; Calponin-11ke.

InterPro; IPR001219; Capponin-11ke.

InterPro; IPR001319; GAG PE-bind.

InterPro; IPR001319; GAG PE-bind.

InterPro; IPR001319; Rh.GEF.

InterPro; IPR001459; RH.

InterPro; IPR001459; RH.

InterPro; IPR001452; SAB3.

InterPro; IPR001452; SAB3.

InterPro; IPR001452; SAB3.

InterPro; IPR001452; SAB3.

IPEam; PF00109; PH; 1.

Pfam; PF00109; PH; 1.

Pfam; PF00109; SH2.

IPEam; PF00109; SH2.

IPEAM; PF00109; SH2.

IPEAM; PF00109; SH3; 2.
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SWART; SW0025; PH; 1.
SWART; SW00252; SH2; 1.
SWART; SW00252; SH2; 1.
SWART; SW00326; SH3; 2.
PROSITE; PSC0021; CH; 1.
PROSITE; PSC0491; DAG PE BIND DOM 1; 1.
PROSITE; PSC0401; DAG PE BIND DOM 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF030221, AAC25011.1; JOINED.
EMBL, AF030222; AAC25011.1; JOINED.
EMBL, AF030222; AAC25011.1; JOINED.
EMBL, AF030224; AAC25011.1; JOINED.
EMBL, AF030225; AAC25011.1; JOINED.
EMBL, AF030225; AAC25011.1; JOINED.
EMBL, XI6316; CAA34383.1; ALT_FRAME.
EMBL, MS9834; AAA63267.1; -...
PIR: B39576; TVHUVV.
HSSP; P29354; IGRI.
                                                                                                                                                                                                                                                                                                                                                         JOINED.
                                                                                                                                                                                                                                            EMBL, AF030204, AAC25011.1; JOINED.
EMBL, AF030205, AAC25011.1; JOINED.
EMBL, AF030206, AAC25011.1; JOINED.
EMBL, AF030207; AAC25011.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF030218; AAC25011.1; JOINED
AF0302219; AAC25011.1; JOINED
AF030220; AAC25011.1; JOINED.
AF030221; AAC25011.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRODOM; PR004527; CH type; 1.
ProDom; PD000093; SH2; 1.
SWART; SM00109; C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC25011.1; CAAC25011.1; AAC25011.1;
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MIM; 605541; -.
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VARSPLIC
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
      3;
                                                                                                                                                                                                                       26 ASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

TISSUE=Breast, and Colon carcinoma;

MEDLINE=98317122; PubMed=9705494;

MEDLINE=98371222; PubMed=9705494;

Trenkle T., Welsh J., Jung B., Mathieu-Daude F., McClelland M.;

"Non-stoichiometric reduced complexity probes for CRNA arrays.";

"Notleic Acids Res. 26:3883-3891(1998).

--- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,

TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE STATES OF THOSE GTPASES.
PROSITE; PS00741; DH 1; 1.
PROSITE; PS50003; PH DOMAIN; 1.
PROSITE; PS50001; SH72; 1.
PROSITE; PS50001; SH3; 2.
PROSITE; PS50001; SH3; 2.
Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=99455043; PubMed=10523675;
Movilla N., Bustelo X.R.;
"Biological and regulatory properties of Vav-3, a new member of the Vav family of oncoproteeins.";
Mol. Cell. Biol. 19:7870-7885(1999).
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NOSE_TaxID=9606;
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SIMILARITY: Contains 1 DBL-homology (DH) domain.
SIMILARITY: Contains 1 DBL-homology (DH) domain.
SIMILARITY: Contains 1 PH domain.
SIMILARITY: Contains 1 zinc-dependent phorbol-ester and 1 binding domain.
SIMILARITY: Contains 2 SH3 domain.
                                                                                                                                                                      14.7%; Score 86.5; DB 1; Length 845; 32.9%; Pred. No. 0.33; ive 13; Mismatches 21; Indels 1.
                                                                                           PHORBOL-ESTER AND DAG BINDING. SH3 1.
                                                                                                             765 SH2.
842 SH3.2.
264 A -> P (IN REF. 2).
718 I -> TV (IN REF. 2).
98313 MW; AC3BC9736FD2F138 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing, Named isoforms=2;
                                                                                                                                                                                                                                                                                                                    VAV3 HUMAN STANDARD; PRT; 847 AA. Q9UKM4; 095230; Q9Y5XB; 16-0CT-2001 (Rel. 40, Leated) 16-0CT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Alpha;
IsoId=Q9UKW4-1; Sequence=Displayed;
                                                                       HH.
                                                                                                                                                                                            23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS:
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                                                                          373
504
564
660
765
264
718
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402
516
617
671
782
264
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CONFLICT
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ProDom;
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                                                                                                                                                                23 ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Song J.S., Haleen-Smith H., Arudchandran R., Gomez J., Scott P.M., Mill J.F., Tan T.-H., Rivera J.;

"Tyrosine phosphorylation of Vav stimulates IL-6 production in mast cells by a Rac/G-Jun N-terminal kinase-dependent pathway.";

J. Immunol. 163:802-810(1999).

-:- FUNCTION: Couples tyrosine kinase signals with the activation of the Rho/Rac GTPases, thus leading to cell differentiation and/or proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Interacts with SLA (By similarity).

PTM: Phosphorylated on tyrosine residues.

SIMILARITY: Contains 1 calponin-homology (CH) domain.

SIMILARITY: Contains 1 DBL-homology (DH) domain.

SIMILARITY: Contains 1 PH domain.

SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG binding domain.
                                                                 11;
      DB 1; Length 847;
                                                                 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
VAVI OR VAV.
14.7%; Score 86.5; DB
31.3%; Pred. No. 0.33;
iive 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001715; Calponin-like.
InterPro; IPR001247; CH type.
InterPro; IPR001249; DAG PE-bind.
InterPro; IPR001219; GDS_CDC24.
InterPro; IPR001849; PH.
InterPro; IPR001849; RhoGEF.
InterPro; IPR001980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001965; SM22_calponin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=99323974; PubMed=10395673;
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Pfam; PF00130; DAG PE-bind;
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF; 1.
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Pfam; PF00018; SH3; 2.
PRINTS; PR00401; SH2DOMAIN.
                                                                 21; Conservative
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                                                                                                                                                                                                                                                        83 PRNLVKE 89
                                Similarity
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Best Local 9
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VAV RAT

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MEDLINE-91172176; Pubmed-2005887;
Katzav S., Cleveland J.L., Heslop H.E., Pulido D.;
"Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene activates its transforming potential.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
DOMAIN
1 119
CH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
14.5%; Score 85.5; DB 1; Length 843;
Best Local Similarity 31.4%; Pred. No. 0.42;
Matches 22; Conservative 14; Mismatches 21; Indels 13
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PHORBOL-ESTER AND DAG BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Indels
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01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                   SWART; SM00033; CH; 1.
SWART; SM00233; PH; 1.
SWART; SM00235; RhcGEF; 1.
SWART; SM00225; SH2; 1.
SWART; SM00226; SH3; 2.
PROSITE; PS50021; CH; 1.
PROSITE; PS50011; CH; 1.
PROSITE; PS50010; DAG PE BIND_DOM_1; 1.
PROSITE; PS50010; DH \(\overline{2}\); 1.
PROSITE; PS50010; DH \(\overline{2}\); 1.
PROSITE; PS50010; SH3; 1.
PROSITE; PS50001; SH3; 1.
PROSITE; PS50001; SH3; 2.
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PR00452; SH3DOMAIN.
PR00888; SM22CALPONIN.
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                                                       PD001527; CH type; 1.
PD000093; SHZ; 1.
PD000066; SH3; 1.
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                                                                                                                                            SM00109; C1; 1
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INTERACTION WITH SLA.
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VAV1 OR VAV.
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                                                  J. Exp. Med. 191:463.474(2000).
-!- FUNCTION: Couples tyrosine kinase signals with the activation of
the Rho/Rac GTPases, thus leading to cell differentiation and/or
                                                                                     Proliferation.
SUBUNIT: Interacts with SLA.
SUBUNIT: Interacts with SLA.
SUBUNIT: Interacts with SLA.
SUBUNIT: Interacts with SLA.
SISSUE SPECIFICITY: Widely expressed in hematopoietic cells but not in other cell types.
FTM: Phosphorylated on tyrosine residues (By similarity).
SIMILARITY: Contains 1 calponin-homology (CH) domain.
SIMILARITY: Contains 1 DBL-homology (DH) domain.
SIMILARITY: Contains 1 PH domain.
SIMILARITY: Contains 1 SH2 domain.
SIMILARITY: Contains 1 SH2 domain.
SIMILARITY: Contains 2 SH3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
MEDLINE=20130290; PubMed=10662792;
Sosinowski T., Pandey A., Dixit V.M., Weiss A.;
"Src-like adaptor protein (SLAP) is a negative regulator of T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50021; CH; 1.
PROSITE; PS00479; DAG PE BIND DOM 1; 1.
PROSITE; PS50010; DAG PE BIND DOM 2; 1.
PROSITE; PS50010; DH 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; TOLOGO, T.
TRANSFAC; TOLOGO, T.
MGD; MGI: 99923; Vav1.
InterPro; IPR003247; CH type.
InterPro; IPR003247; CH type.
InterPro; IPR003219; DAG PE-bind.
InterPro; IPR001301; GBC-DC24.
InterPro; IPR001301; Rb-GEF.
InterPro; IPR001489; PH.
InterPro; IPR001489; PH.
InterPro; IPR001485; SH2.
InterPro; IPR001485; SH2.
InterPro; IPR001485; SH2.
InterPro; IPR001485; SH2.
InterPro; IPR001485; SH2.
InterPro; IPR001485; SH2.
InterPro; IPR0018096; SH2.
InterPro; IPR0018096; SH2.
InterPro; IPR00180; SH2.
InterPro; IPR00180; SH2.
InterPro; IPR00180; SH2.
InterPro; IPR00180; SH2.
InterPro; IPR00185; SH3.
InterPro; IPR00185; SH3.
InterPro; IPR00185; SH3.
InterPro; IPR00185; SH3.
InterPro; IPR001827; CH type; IPPCDOM; PR000093; SH3; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00741; DH_1; 1.
PROSITE; PS50001; PH DOMAIN; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                             EMBL; X64361; CAA45713.1; -.
EMBL; MS9833; AAA63402.1; -.
PIR; A61187; TYWGVV.
PDB; 1F5X; 15-SEP-00.
PDB; 1GCP; 28-JAN-03.
PDB; 1GCP; 28-JAN-03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00109; C1; 1.
SMART; SM0033; CH; 1.
SMART; SM00233; PH; 1.
SMART; SM00225; RhoGEF; 1.
SWART; SM00252; SH2; 1.
                                        receptor signaling.
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                                                                                                                                                                                                                                                                  3,
                                                                                                                                                                                                                                                                                                                         26 ASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRN 85
                                                                                                                                                                                                                                                                  13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schuebel K.E., Bustelo X.R., Nielsen D.A., Song B.J., Barbacid M., Goldman D., Lee I.J.;
"Isolation and characterization of murine vav2, a member of the vav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
Suanine-nucleotide releasing factor; Repeat; Phosphorylation;
                                 CH.
DH.
PH.
PHORBOL-ESTER AND DAG BINDING.
SH3 1.
SH2.
                                                                                                                                                                                                                           5; DB 1; Length 845; 0.42;
                                                                                                                                                                                                                                                              21; Indels
                                                                                                                                            SH3 2.
Q -> E (IN REF. 2).
3666DCCD1C5229DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                            ; Pred. No. 0.42;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               868 AA
                                                                                                                                                                                                                           14.5%; Score 85.5; 31.4%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:102718; Vav2.
InterPro; IPR001715; Calponin-like.
InterPro; IPR002147; CH type.
InterPro; IPR002219; DAG PE-bind.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001849; PH.
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MEDLINE=96313271; PubMed=8710375;
                                                                                                                                                                   29 29 (
845 AA; 98136 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U37017; AAC52761.1; -.
HSSP; Q60631; 1GBQ.
                                                                                                                                                                                                                       Query Match
Best Local Similarity 31.4%
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                     1119
373
504
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765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                   3D-structure.
DOMAIN
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                                                                                                                                                DOMAIN
                                                                                                                                                                                       SEQUENCE
                                                   DOMAIN
DOMAIN
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VAV2_MOUSE
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TISSUE=Brain;
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     20 VYT---ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Guanine-nucleotide releasing factor; Repeat; Phosphorylation. DOMAIN 1 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.0%; Score 82.5; DB 1; Length 868; ilarity 27.6%; Pred. No. 0.88; Conservative 20; Mismatches 22; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILAKIII).
PHOSPHORYLATION (BY EGFR) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHORBOL-ESTER AND DAG BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY EGFR) (BY
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PHOSPHORYLATION (BY EGFR)
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868 AA; 99915 MW; D18581E7EEB2DBC2 CRC64;
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01-0cT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                    PRODOM; PD000066; SH3; 2.

SMART; SM00109; C1; 1.

SMART; SM00131; C4; 1.

SMART; SM00232; PH; 1.

SMART; SM00225; RhGEF; 1.

SMART; SM00225; RhGEF; 1.

SMART; SM00255; SH2; 1.

PROSITE; PS50021; CH; 1.

PROSITE; PS50011; DAG PE BIND DOM 1; 1.

PROSITE; PS50010; DAG PE BIND DOM 2; 1.

PROSITE; PS50010; DH 2; 7.

PROSITE; PS500010; DH 1; 1.

PROSITE; PS500013; PH DOMAIN; 1.

PROSITE; PS500013; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
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Interpro; IPR000219; RhoGEF.
Interpro; IPR000980; SH2.
Interpro; IPR001452; SH3.
Pfam; PF00130; CH; I.
Pfam; PF00130; DAG_PB-bind; 1.
Pfam; PF00159; PH; I.
Pfam; PF00151; RhoGEF; 1.
Pfam; PF00017; SH2; 1.
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852 GRIGWFPSTYVEEEGV 867
                                                                                                                                                             PRINTS, PRO0401, SH2DOMAIN.
PRINTS, PR00452; SH3DOMAIN.
ProDom, PD001527; CH_type; 1.
ProDom; PD000093; SH2; 1.
ProDom; PD000066; SH3; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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502
562
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ses 21; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159
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                                                                                                                                                       MEDLINE=95283235; PubMed=7762982; Henske E.P., Short M.P., Jozwiak S., Bovey C.M., Ramlakhan S., Hanske E.L., Kwiatkowski D.J.; Haines J.L., Kwiatkowski D.J.; "Identification of VAV2 on 9934 and its exclusion as the tuberous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50021; CH; 1.
PROSITE; PS00419; DGQ PE BIND_DOM_1; 1.
PROSITE; PS50081; DAG PE BIND_DOM_2; 1.
PROSITE; PS50010; DH Z; 1.
PROSITE; PS50003; PH DOWAIN; 1.
PROSITE; PS50003; PH DOWAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001715; Calponin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003247; CH type.
InterPro; IPR002219; DAG PE-bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00307; CH; 1.
Pfam; PF00130; DAG PE-bind; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00117; SH2: 1.
Pfam; PF000117; SH2: 1.
                                                                                               sclerosis gene TSC1.";
Ann. Hum. Genet. 59:25-37(1995)
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InterPro; IPR001849; PH.
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HSSP; P08631; 1BU1.
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PRINTS; PR0045; SH3DOMAIN.
ProDom; PD001527; CH_type; 1.
ProDom; PD000093; SH2; 1.
ProDom; PD00066; SH3; 2.
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InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
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SMART; SM0033; CH; 1.
SMART; SM00233; PH; 1.
SMART; SM00325; RhoGEF; 1.
SMART; SM00325; SH2; 1.
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ä;
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        Guanine-nuclectide
        releasing
        factor;
        Repeat;
        Phosphorylation.

        DOMAIN
        1
        119
        CH.
        CH.

        DOMAIN
        405
        512
        PH.
        PHORBOL-ESTER AND DAG BINDING.

        DOMAIN
        524
        572
        PHORBOL-ESTER AND DAG BINDING.

        DOMAIN
        673
        SH3
        1.

        DOMAIN
        816
        877
        SH2

        MOD_RES
        142
        PHOSPHORYLATION (BY EGFR).

        MOD_RES
        172
        PHOSPHORYLATION (BY EGFR).

                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.8%; Score 81.5; DB 1; Length 878; Best Local Similarity 26.3%; Pred. No. 1.1; Matches 20; Conservative 21; Mismatches 22; Indels 11:
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862 GRIGWFPSTYVEEEGI 877
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Search completed: December 29, 2003, 16:04:13 Job time: 4.31373 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 29, 2003, 16:03:18; Search time 16.9468 Seconds (without alignments) 1674.996 Million cell updates/sec Run on:

US-10-019-455A-24

590 1 HGIFMDRLASKKLCADDECV.....RVYQBATKEVPTTDIDFFCE 110 Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

830525 seqs, 258052604 residues Searched: 830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp\_archea:\* sp\_bacteria:\* SPTREMBL 23:\* Database:

sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_mamnal:\*
sp\_norgane:1e;\* sp\_rvirus:\* sp\_bacteriap:\* sp plant:\* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap: \*

# SUMMARIES

| Description              | Q9ji09 mesocricetu | Q8bje9 mus musculu | Q8bi84 mus musculu | Q96pc5 homo sapien | Q921x3 mus musculu | Q91zv0 mus musculu | Q90xf1 tetraodon n | Q8c899 mus musculu | Q8r076 mus musculu | Q8uux6 gallus gall | O9h0h2 homo sapien | Q8n157 homo sapien | Q96d37 homo sapien | 008526 mus musculu | Q8vdu4 mus musculu | Q8btv7 mus musculu |
|--------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| g.                       | 601160             | Q8BJE9             | Q8BI84             | Q96PC5             | Q921X3             | 0912V0             | Q90XF1             | Q8C899             | Q8R076             | QBUUX6             | Фэнон5             | Q8N157             | Q96D37             | 008526             | Q8VDU4             | Q8BTV7             |
| DB                       | 11                 | 11                 | 77                 | 4                  | 17                 | 11                 | 13                 | 11                 | 11                 | 13                 | 4                  | 4                  | 4                  | 11                 | 11                 | Ħ                  |
| Query<br>Match Length DB | 96                 | 268                | 1239               | 119                | 137                | 119                | 88                 | 68                 | 287                | 846                | 1196               | 1196               | .719               | 166                | 806                | 845                |
| Query                    | 38.4               | 36.4               | 36.4               | 31.4               | 30.7               | 29.1               | 28.6               | 16.9               | 15.0               | 15.0               | 15.0               | 15.0               | 14.7               | 14.5               | 14.5               | 14.5               |
| Score                    | 226.5              | 215                | 215                | 185.5              | 181                | 171.5              | 168.5              | 100                | 88.5               | 88.5               | 88.5               | 88.5               | 86.5               | 85.5               | 85.5               | 85.5               |
| Result<br>No.            | 1                  | 8                  | m                  | 4                  | S                  | 9                  | 7                  | œ                  | σ                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 |

| QBuuxS gallus gall Q9vma8 drosophila Q9h803 homo sapien Q8hwe6 tetraodon n Q81jf7 pseudomonas Q8k3e5 mus musculu Q8k3e5 mus musculu Q8k3e5 mus musculu Q8k3e5 qus arabidopsis Q9fx8 oryza sativ Q9fx00 oryza sativ Q9fx00 oryza sativ Q9fx01 oryza sativ Q9fx01 oryza sativ Q9fx02 oryza sativ Q9fx04 oryza sativ Q9fx04 oryza sativ Q9fx05 prachydanio Q8fx5 brachydanio Q8fx5 brachydanio Q8fx6 mrachydanio Q8fx16 methanosarc Q8597 bacillus su Q94588 arabidopsis Q25770 chironomus                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | \$9fu01 oryza sativ<br>\$97z29 sulfolobus<br>\$8r21 fusobacteri<br>\$9x0v4 thermotoga<br>\$9rik9 thermotoga<br>\$921g9 mus musculu                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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| QBUUX5 Q9VMA7 Q9VMA7 Q9VMA7 Q9HB03 Q9HB03 Q9HB03 Q9HJT7 Q9HJT7 Q9HJT7 Q9HJT9 Q9FT04 Q9FT04 Q9FT07 Q9HJT9 Q9FT07 Q9HJT9 Q9HJT9 Q9FT07 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9HJT9 Q9 | COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI<br>COPTOI |
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| 83.5<br>83.5<br>83.5<br>80.5<br>80.5<br>74.5<br>74.5<br>74.5<br>72.7<br>72.7<br>72.7<br>72.7<br>72.7<br>72.7<br>72.7<br>72                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 71<br>70.5<br>70.5<br>70.5<br>70.5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 11112222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 0 4 4 4 4 4 4 5 5 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |

### ALIGNMENTS

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SEQUENCE FROM N.A. Gueinbauer M., Anthuber M., Buettner R., Jauch K.W.; R.W.; M. M. Buettner R., Jauch K.W.; "Overexpression of MIA enhances extravasation and metastasis of A-mel3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Gaps
                                                                                 01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Melanoma inhibitory activity protein (Fragment).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query March 38.4%; Score 226.5; DB 11; Length 96; Best Local Similarity 46.4%; Pred. No. 4.4e-17; Matches 45; Conservative 18; Mismatches 29; Indels 5;
                                                                                                                                                                                                                                                                                                        melanoma cells.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; AF271494; AAF76220.1; -.
HSSP; Q16674; 111J.
InterPro; 1RR001452; SH3.
Pfam: PF00018; SH3; 1.
RMART; SM00126; SH3; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 1
96 96
96 AA; 10756 MW; B7B466C3B5S05BFB CRC64;
                                  96 AA.
                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
                                PRT;
                                  PRELIMINARY;
                                                                                                                                                                                                        NCBI_TaxID=10036;
                                                                                                                                                                                         Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                09JI09
RESULT 1
Q9JI09
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э; 8 LASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGE-FWAG 66 1 LADRKLCADQECSHPISMAVALQDYMAPDCRFLTIHRQQVVYVFSKL---KGRGRLFWGG 57 N

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8 LASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 LADLKKCGDLECEALINRVSAMRDYRGPDCRYLNFTKGEEISVYVKLAGER--EDLWAGS 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 MDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGE-F
                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                            61 GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFC 109
                                                                                      83 LELWAGSVEHS-----FGYFPKDLIKVLHKYTEEELHIPADETDFVC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 31.4%; Score 185.5; DB 4; Length 119; Best Local Similarity 40.2%; Pred. No. 1.7e-12; Matches 41; Conservative 15; Mismatches 37; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to cartilage derived retinoic acid sensitive protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.7%; Score 181; DB 11; Length 137; 55.4%; Pred. No. 6.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryo;
Bosserhoff A.K., Buetrner R.;
"Characterization of the MIA gene family.";
Submitted (UNL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR390175; AAL26990.1; -.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 VYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPITDIDFFC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC009815; AAH09815.1; -. MGD; MGI:109615; Cdrap.
InterPro; IPRO14152; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
SEQUENCE 137 AA; 15441 MW; 971415552E6FD536 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 AA; 13535 MW; AEF529762D880AC5 CRC64;
                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2003 (TrEMBLrel. 23, Last annotation update)
Melanonal inhibitory activity protein 2.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last seq 01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JUL-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00326; SH3;
SEQUENCE 119 AA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 36; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                     28
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                                                                                                                                                                                                       Q96PC5
Q96PC5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6J; TISSUE=Eye;
STRAIN=CS7BL/6J; TISSUE=Eye;
MEDLINE=22354681;
The FANTOM CONSORTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
hanalysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
BMBL; ROR94344; BAC39164.1; -.
NON TER 268 268
SEQÜENCE 268 AA; 29722 MW; 67339C562F684402 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of
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STRAIN=CSTBL/6J; TISSUE=Retina;
MEDLINE=22354683; PubMed=12466851;
The FANYOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.4%; Score 215; DB 11; Length 1239; 40.4%; Pred. No. 1.8e-14; tive 13; Mismatches 40; Indels 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.4%; Score 215; DB 11; Length 268; 40.4%; Pred. No. 2.7e-15; tive 13; Mismatches 40; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK044749; BAC32064.1; -.
SEQUENCE 1239 AA; 136350 MW; 6E16F9D42ECEFF05 CRC64;
                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Weakly similar to NPIP-like protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
protein.
                   SVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPT 102
                                         58 SVQGDYYGDLAARLGYFPSSIVREDQTLKPGKVDVKT 94
                                                                                                                                                                268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1239 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Conservative
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                                                                                                                                                              PRELIMINARY;
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Best Local Similarity
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Best Local Similarity
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                   67
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                                                                                                                                                                               Q8BJE9;
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Q8BJE9
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Q8BI84
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3 IMIARALQDYYPADCXFIPIRQGQLIYVYAML---KGRGSQFWAGSVQDSYYGQQE-ARI 58
                                            ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAG-EFWAGSVYGD--GQDEMGVV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
STRAIN=C78LL/61, TISSUE=Head;
MEDLINE=22354663; Pubmed=12466851;
The FANTOM Consortium,
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
Thalysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:563-573 (2002).
RMBL; AKO47965; BAC33202.1; -.
SRQUENCE 68 AA; 7431 MW; 3CBE75527D3CBF7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 HGVFMDRLASSKKLCADEECVCKALLTVWFSLSFYHIMGNLSGKQPDC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Length 68;
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SEQUENCE 287 AA, 32662 MW, BF2850B8F921F048 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 32.7 kDa protein.
VAV3.
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42.6%; Pred. No. 0.0019;
tive 9; Mismatches 8;
                                                                                                                                                                         GYFPRNLVKEORVYOEATKEVPTTDIDFFC 109
                                                                                                                                                                                                               |:|| ::|:|
59 GHFPSSIVEETHPLMAAQTEVKTSNWDFYC 88
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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InterPro; IPR001452; SH3.
Pfam; PF000017; SH2; 1.
ProDom; PD000093; SH2; 1.
ProDom; PD000066; SH3; 1.
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PROSITE; PS50002; SH3; 2.
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SMART; SM00326; SH3; 2.
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Best Local Simil
Matches 20;
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Q8R076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 LAHLKKGGDLECETLISRVLALRDYTGPDCRYLNFTTGEEISVYVKLGGDR--EDLWAGS 83
26 MPKLADWKLCADEBCSHPISMAVALQDYVAPDCRFLTIYRGQVVYVFSKL---KGRGRLF
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
01-MaR-2003 (TrEMBLrel. 23, Last annotation update)
Melanoma inhibitory activity protein (Fragment).
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
NCBL TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.1%; Score 171.5; DB 11; Length 119; 39.2%; Pred. No. 5.7e-11; Live 14; Mismatches 39; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo;
Bosserhoff A.K.,
Buettner R.;
Characterization of the MIA gene family.";
Submitted (UUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF390177; AAL26992.1;
InterPro: IPR001452; SH3.
SMART; SMO026; SH3; I.
SEQUENCE 119 AA; 13397 MW; 589F390C0B49DIC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Bossecthoff A.K., Buettner R.;
Characterization of the MIA gene family.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF390176; AAL26591.1;
Interpro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 VYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 AA; 10080 MW; C355C1FE04DA22EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2003 (TrEMBLrel. 23, Last annotation update)
Melanoma inhibitory activity protein 2.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                  PRT;
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Matches 39; Conservative
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40; Conserv
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                                                                                                  64 WAGSV 68
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PROSITE; PS50002; SH3; 2.
SH3 domain.
SEQUENCE 846 AA; 97815 MW; C47EE949D873821B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
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838 PSTYVEE 844
                                                                                                                                                                                                                                                                                                                83 PRNLVKE 89
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Q9H0H2
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                           11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11805146;

Inabe K., Ishiai M., Scharenberg A.M., Freshney N., Downward J., Kurosaki T., Ishiai M., Scharenberg A.M., Freshney N., Downward J., Kurosaki T., Ishiai M., Scharenberg A.M., Freshney N., Downward J., Kurosaki T., Sp. Med. 195:189-200 (2002).

I. Exp. Med. 195:189-200 (2002).

I. Exp. Med. 195:189-200 (2002).

I. Exp. Med. 195:189-200 (2002).

I. Exp. Med. 195:189-200 (2002).

I. SMILARITY: CONTAINS 1 PH DOMAIN.

EMBL; AV046915; AALO6249.1; CH LYP.

InterPro; IPRO1319; GA PE-bind.

InterPro; IPRO1319; DAG PE-bind.

InterPro; IPRO1319; DAG PE-bind.

InterPro; IPRO13096; SM22_calponin.

R InterPro; IPRO13096; SM22_calponin.

R Ffan; PF00169; PH; 1.

R Ffan; PF00169; PH; 1.

R Ffan; PF00169; PH; 1.

R Pfan; PF0017; SM2; I.

R Pfan; PF0017; SM2; I.

R Pfan; PF00190; CH; I.

R Pfan; PF00190; CH; I.

R Pfan; PF00190; CH; I.

R Pfan; PF00190; SM2; I.

R Pfan; PF00190; SM2; I.

R Pfan; PF00190; SM3; I.

R RYINTS; PR00491; SH3; I.

R RYINTS; PR00492; SH3; DOWAIN.

R RYINTS; PR00492; SH3; I.

R RYART; SW00199; CH; I.

R SWART; SW00199; CH; I.

R SWART; SW00125; CH; I.

R RART; SW00125; CH; I.

R RART; SW00125; CH; I.

R RART; SW00129; CH; I.

R RART; SW00129; CH; I.

R ROSTE; PS50021; H; I.

R ROSTE; PS50021; H; I.

R ROSTE; PS50021; II.

R RROSTE; PS50021; II.

R RART; R ROSTE; PS50021; II.

R RROSTE; PS00491; BR3; II.

R RROSTE; PS00491; BR3; II.

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R RROSTE; PS04901
                        Length 287;
                                                                           21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
GDP/GTP exchange factor VAV3.
                        Query Match 15.0%; Score 88.5; DB 11; Best Local Similarity 31.3%; Pred. No. 0.19; Matches 21; Conservative 14; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 846 AA.
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PSS0021; CH; I.
PSS00479; DAG PE BIND DOM 1; 1.
PSS0081; DAG PE BIND DOM 2; 1.
PSS0019; DH 1; I.
PSS0010; DH 2; 1.
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PS50003; PH^{DOMAIN}; 1.
PS50001; SH²; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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279 PSTYVEE 285
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NCBI_TaxID=9031;
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                                                                                                                                 23 ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Baueraachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.W., Otterwaelder B., Obermaier B., Tampe J., Heubner D., Mambutt R., Korn B., Klein M., Poustka A.;

"Towards a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs.";

Genome Res. 11:422-435(2001).

--- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

EMBL; AL136797; CAB66731.1; ---

--- SIMILARITY: CONTAINS 1 SH3.

InterPro; IPR001452; SH3.

InterPro; IPR001452; SH3.

R. Pf00400; WD40; 6.

R. Prints, PR00452; SH3DOWAIN.

R. Prodon; PD000066; SH311.
                                                                       Gaps
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Best Local Similarity 33.3%; Pred. No. 1.1;
Matches 27; Conservative 12; Mismatches 31; Indels 11; Gaps
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Homo sapiens (Human).
Eukaryota, Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Query Match 15.0%; Score 88.5; DB 13; Length 846; Best Local Similarity 32.8%; Pred. No. 0.72; Matches 22; Conservative 13; Mismatches 21; Indels 11;
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SMART; SM00320; WD40; 5.
PROSITE; PS50022; WD REPEATS 2; 4.
PROSITE; PS50294; WD REPEATS REGION; 1.
PROSITE; PS50294; WD REPEATS REGION; 1.
Hypothetical protein; Repeat; SH3 domain; WD repeat.
SEQUENCE 1196 AA; 137114 MW; E27E3FB1D7932024 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                       Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Octsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Satto K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fujil A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                     (TrEMBLrel. 22, Last sequence update) (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
                      PRT; 1196 AA
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                                                          01-0CT-2002 (TrEMBLrel. 22, Created) 01-0CT-2002 (TrEMBLrel. 22, Last seq 01-MAR-2003 (TrEMBLrel. 23, Last ann Hypothetical protein FLJ34943.
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01-DEC-2001 (TrEMBLrel. 19, Cr
01-DEC-2001 (TrEMBLrel. 19, La
01-MAR-2003 (TrEMBLrel. 23, La
Hypothetical protein.
Homo sapiens (Human).
                      PRELIMINARY;
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Matches
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DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 0000
CC MAMMAD OC MAMMAD OC MAMMAD OC MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMMAD CO MAMM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Muss.
NCBI_TaxID=10090;
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-I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

EMBL, D83266; BAA18950.1; -.
HSSP; Q60631; IGBQ.
A Strausberg R.;
L Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
C -1-SIMILARITY: CONTAINS 2 SH3 DOMAINS.
C -1-SIMILARITY: CONTAINS 1 PH DOMAIN.
R EMBL; BC013361; AAH13361.1; -.
R INTERPRO; IPR001219; DAG PE-bind.
R INTERPRO; IPR001311; GDS_CDC24.
R INTERPRO; IPR001311; GDS_CDC24.
R INTERPRO; IPR001319; PH.
DR INTERPRO; IPR00139; SH3.
DR INTERPRO; IPR001452; SH3.
DR Fam; PF00103; DAG PE-bind; 1.
DR Fam; PF00103; DAG PE-bind; 1.
DR Fam; PF001017; SH2; 1.
DR Pfam; PF001017; SH2; 1.
DR Pfam; PF001018; SH3; 2.
DR PRINTS; PR00401; SH20MAIN.
DR PRINTS; PR00402; SH2; 1.
DR PRINTS; PR000093; SH2; 1.
DR PF0DOM; PD000093; SH2; 1.
DR PF0DOM; PD000093; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.7%; Score 86.5; DB 4; Length 719; Best Local Similarity 32.9%; Pred, No. 0.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; SH3 domain.
SEQUENCE 719 AA; 83727 MW; A51B757DA543BA6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-UUL-1997 (TrEMBLrel. 04, Created)
01-UUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWART; SW00109; CI; I.
SWART; SW00109; CI; I.
SWART; SW00233; RhoGBF; I.
SWART; SW00225; SH2; I.
SWART; SW00226; SH3; Z.
SWART; SW00326; SH3; Z.
PROSITE; PS00479; DAG PE BIND DOM 1; I.
PROSITE; PS50010; DAG PE BIND DOM 1; I.
PROSITE; PS50010; DH Z; I.
PROSITE; PS50010; SH2; I.
PROSITE; PS50001; SH2; I.
PROSITE; PS50001; SH2; I.
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STRAIN=ddy; TISSUE=Testis;
MEDLINE=97190224; PubMed=9038379;
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                                                                                               Query Match 14.5%; Score 85.5; DB 11; Length 166;
Best Local Similarity 31.4%; Pred. No. 0.21;
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps
                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Mus. Mus.
                                                                                                                                                                                                                                                                             166 AA; 19434 MW; 2C3AF1FF07A5018F CRC64;
                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to vav oncogene.
                                                                                                                                                                                             806 AA
                                                                                                                                                                                              PRT;
MGD; MGI:98923; Vav.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
FEam; PF00017; SH2; 1.
Ffam; PF00018; SH3; 1.
Ffam; PF00018; SH3; 1.
ProDom; PD0000452; SH3CMAIN.
ProDom; PD000066; SH3; 1.
SMART; SM00252; SH2; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH3; 1.
                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                           86 LVKEQRVYQE 95
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                             SH3 domain.
SEQUENCE
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DR SMART; SM00126; SH3; 2.

DR PROSITE; PS5001; CH; 1.

DR PROSITE; PS5001; CH; 1.

DR PROSITE; PS5001; DAG_PE_BIND_DOM_2; 1.

DR PROSITE; PS0010; DH_2; 1.

DR PROSITE; PS0010; DH_2; 1.

DR PROSITE; PS50010; SH3; 1.

DR PROSITE; PS50010; SH3; 1.

DR PROSITE; PS50002; SH3; 2.

Query Match

Query Match

Query Match

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Query Match

AARAPDENINVKGQQIVVSKLVKENGAGEFWAGSVCDCQDEMGVVGYFPRN 85

AARAPDENINVKCQQIVVSKLVKENGAGEFWAGSVCDCQDEMGVVGYFPRN 85

DD 797 YVEED--YSE 804

Search completed: December 29, 2003, 16:06:25

Job time: 16:9468 secs
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809.506 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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                                                                                                                                                                                                                                                                            December 29, 2003, 16:03:18 ; Search time 21.5686 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result

angiogenesis PRO9873 prot PRO protein, human secret growth regul MLP protein MLP protein Human MLP protein Description Human Human Human Human Mouse Human Human Novel AAB82671 AAB69123 ABB95602 ABB84996 AAU83627 AAU09871 AAB82672 AAB69127 AAB69126 a 5553335555 Query Match Length DB 100.0 100.0 100.0 100.0 100.0 100.0 95.1 Score 590 590 590 590 590 590 547

450000

WPI; 2001-159271/16. N-PSDB; AAF59079

| Mouse MLP protein se Rat MLP protein se Rat MLP protein se Rat MLP protein se Melanoma inhibitin Human MLP archain thuman Melanoma inhibitin Human protein sequ Human TANGO 130 pr Human TANGO 130 pr Human TANGO 130 pr Human PRO polypept Human secreted/tra human secreted/tra Human secreted/tra Human secreted/tra Human secreted/tra Human secreted/tra Human secreted/tra Human secreted/tra Human secreted/tra Human secreted/tra Human secreted/tra Human secreted/tra Human secreted/tra Human secreted/tra Human secreted/tra Human PRO polypept Human secreted/tra Human PRO polypept Human secreted/tra Human PRO polypept Human secreted/tra Human PRO polypept Human PRO polypept Human PRO polypept Human secreted/tra Human PRO polypept Human secreted/tra Human PRO 130 MI Human angiogenesis |                                                             |
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| 2111<br>80128 ELLICILI 4440<br>8025 ELLICILI 4440<br>8030 C. C. C. C. C. C. C. C. C. C. C. C. C.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                             |
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| 544<br>544<br>541<br>541<br>541<br>541<br>541<br>541                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 215<br>215<br>215<br>215<br>215<br>215<br>215<br>215<br>215 |
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### ALIGNMENTS

Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K; MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter; Human MLP protein sequence SEQ ID NO:24. AAB69126 standard; Protein; 110 AA. 29-JUN-2000; 2000WO-JP04278. (TAKE ) TAKEDA CHEM IND LTD. 30-JUN-1999; 99JP-0186718. (first entry) WO200102564-A1. Homo sapiens. 11-JAN-2001. 23-APR-2001 inhibitor. Tanaka H; AAB69126; AAB69126 

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RESULT 3
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                                                                              The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiintlammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF55099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
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        Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                                                                                                                                                                                                        1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA
                                                                                                                                                                                                                                                            1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders,
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                            GEFWAGSVYGDGQDEMGVVGXFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                 61 GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth regulatory-like polypeptide; human; cartilage; melanoma; neuroectodermal tumour; glioma; cancer; therapy; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΰ
                                                                                                                                                                                                 Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Signal_peptide
24...128
/label= Mature_protein
/note= "separately claimed in Claim 10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
                                                                                                                                                                                                100.0%; Score 590; DB 22;
100.0%; Pred. No. 1.6e-68;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arterburn MC,
                                                                                                                                                                                                                                                                                                                                                                                                                       Human growth regulatory-like polypeptide.
                                                            Claim 1; Page 97-98; 111pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        AAB82671 standard; Protein; 128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ford JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-2001; 2001WO-US02455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2000; 2000US-0491404
02-MAY-2000; 2000US-0563786
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-483233/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boyle BJ,
                                                                                                                                                                                                       Best_Local_Similarity
Matches 110; Conserv
                                                                                                                                                                             110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAH26343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200155332-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-2001
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                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                             AAB82671;
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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                                                                                                                                                                                                    The present sequence is that of a novel human growth regulatory-like polypeptide (GRLP). The amino acid sequence is predicted from a novel assembled GRLP). The amino acid sequence is predicted from a convel assembled GRLP?

16372272. The protein has a mol.wt. of 14 kba unglycosylated.

16372272. The protein has a mol.wt. of 14 kba unglycosylated.

16372272. The protein has a mol.wt. of 14 kba unglycosylated.

16372272. The protein has a mol.wt. of 14 kba unglycosylated.

16372272. The protein has a mol.wt. of 14 kba unglycosylated.

16372272. The protein has a growth regulatory proteins.

16372272. The protein well-amily as growth regulatory proteins.

16372272. The protein well-amily a growth and 64*

16372272. The protein (CD-RAP, 44* identity and 64*

16372272. The protein world and polymucleotides of the invention can be used in the prophylatis, treatment (including gene therapy)

16372272. The prophylatis, treatment (including gene therapy)

16372272. The prophylatis, which include the GRLP mature protein, and alagnosis of disorders and diseases caused by, or involving, gloomas. The polypeptides, which include the GRLP mature protein, cartilage development and maintennes, inhibition of melanoma cell growth and tumours, including neuroectodermal tumours such as gloomas. The polypeptides, which include the GRLP mature protein, can be able to the differentiation activity, tissue growth activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activ
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hyperproliferative disorders, coagulation disorders, and nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA
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joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
cardiant; gene therapy; secretory cell function regulator; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 590; DB 22; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2e-
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                                                                                                                                  Claim 10; Page 116-117; 119pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sest Local Similarity
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Claim 11; Fig 360; 567pp; English.
                                                                                                                                                                                                                                  30-MAY-2001; 2001WO-US17443.
01-UJW-2001; 2001WO-US17800.
20-UJW-2001; 2001WO-US19592.
28-JJW-2001; 2001WO-US00000.
                                                                                                                 2001US-0802706.
2001US-0808689.
                                                                                                                                                                                                                        2001US-0870574.
08-NOV-2000; 2000US-0709238.
08-NOV-2000; 2000WO-US30952.
10-NOV-2000; 2000WO-US30873.
                                                                                2001US-0796498.
                                                                                           2001WO-US06520.
2001WO-US06666.
                                                                                                                                          2001US-0816744.
                                                                                                                                                                001US-0854208.
                                                                     2001US-0767609
                                                                                                                                                     2001US-0828366
                                                                                                                                                                          2001US-0854280
                                                                                                                                                                                      2001US-0866028
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nes 110; Conservative
                                                                                                                                                                                                                                                                                                                                                  GODDARD A.
GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                                                                                                                                                                                                                                                                        GERRITSEN M E.
                                                                                                                                                                                                                                                                                          GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                              WATANABE C K.
WILLIAMS P M.
                                                                                                                                                                                                                                                                                                                                                                                                                       PAONI N F.
STEPHAN J F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-171999/22.
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FERRARA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 AA;
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                                                                                                                                                                                                                                                                                                                              GERBER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WOOD W I
                                                                                                                                                                                                                                                                                                        BAKER K
                                                                                                                                                                                                                                                                                                                                                                                                           PAN J.
                                                                                 28-FEB-2001;
                                                                                                         01-MAR-2001;
                                                                                                                               14-MAR-2001;
                                                                                                                                                                10-MAY-2001;
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                                                                                                                                                      05-APR-2001;
                                                                                                                                                                                        25-MAY-2001;
                                   01-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic.
                                                                                                                                               The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory call, in function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing to retreating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                            1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA 60
                                                                                                                                                                                                                                                                                                                                         19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA 78
                                                                     Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
   Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                           61 GEFWAGSVYGDGODEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 590; DB 22; Length 128; 100.0%; Pred. No. 2e-68; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human angiogenesis related protein PRO9873 SEQ ID NO: 360.
                                                                                                                               Claim 2; Page 91-92; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB95602 standard; Protein; 128 AA
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2000WO-US20710.
2000US-222695P.
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2000US-0000000P.
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                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0
Matches 110, Conservative
                                       WPI; 2001-159271/16.
                                                                                                                                                                                                                                                            128 AA;
                                                   N-PSDB; AAF59065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200208284-A2.
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                   Tanaka H;
                                                                                                                                                                                                                                                              Sequence
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       Itoh Y.
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoardain infarention, trombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 HGIFMDRIASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA 60
Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
FF, Watanabe CK, Williams PM, Wood MI, Ye W;
                                                                                                                                                                                                                                                                                                                                                  One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
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Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
                                                     19 GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQBATKEVPTTDIDFPCE 128
                          GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE
                                                                                                                                                                                                                                                                                                                                                                                            Human PRO9873 protein sequence SEQ ID NO:360
                                                                                                                                                                                                                           ABB84996 standard; Protein; 128 AA
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2001US-0767609.
2001US-0796498.
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2000US-230978P.
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2000US-0709238.
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2001US-0808689.
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2001US-0854208.
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                                                                                                                                                                                                                                                                                                                                         16-MAY-2002 (first entry)
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08-NOV-2000;
10-NOV-2000;
01-DEC-2000;
20-DEC-2000;
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28-FEB-2001;
28-FEB-2001;
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02-AUG-2000;
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14-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                           One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
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   Ye W;
Stephan JF, Watanabe CK, Williams PM, Wood WI,
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                                                                                                                                                                                                                                                                                                                                 Claim 11; Fig 360; 565pp; English.
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25-JUL-2000; 2000US-220638P.
25-JUL-2000; 2000US-220664P.
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25-JUL-2000; 2000US-220605P.
25-JUL-2000; 2000US-220607P.
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26-JUL-2000; 2000US-220893P.
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ses 110, Conservative
                                                                            WPI; 2002-090516/12.
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                                                                                                                  N-PSDB; ABL88251
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N-PSDB; AAS17583
                                                                              WO200179454-A1
                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                     One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted protein; cytostatic; immunosuppressive; vulnerary; vaccine; antiinflammatory; neuroprotective; nephrotropic; cardiovascular; human; cancer; autoimmune disease; wound healing disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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phan JF, Watanabe CK, W
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Smith V, Stephan JF,
                                                                                                                                                                                                                                                                                                                                                          Claim 11; Figure 72; 359pp; English.
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                          2000WO-US23328.
2000US-0000000P.
                                                                                                         20-DEC-2000; 2000WO-US34956.
28-PEB-2001; 2001WO-US06520.
10-MAY-2001; 2001US-0854280.
                                                    2000WO-US30873.
                                                                 28-NOV-2000; 2000US-253646P.
01-DEC-2000; 2000WO-US32678.
                                                                              01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000US-0747259.
              2000WO-US23522
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                                                      10-NOV-2000;
                          24-AUG-2000;
15-SEP-2000;
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and to identify membrane-bound or soluble receptors. The polynucleotides may be used as diagnostic reagents, in chromosome localisation studies, and in tissue expression studies. The present sequence represents the
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haematopoietic disorder; inflammatory disorder; infertility;
neurological disease; psychiatric disease; cardiovascular disease;
respiratory disease; renal; gastrointestinal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 73-74; 92pp; English.
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24-APR-2000; 2000US-199417P.
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Matches 110; Conservative
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The present sequence is that of a novel human growth regulatory-like polypeptide (GRLP) mature protein. The sequence is predicted from a novel assembled CDNR (see AAHS643) based on Hyseq clone number 1637272. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP belongs to the same protein family as growth regulatory protein. Growth factors, human melanoma derived growth regulatory protein growth factors, human melanoma derived growth regulatory protein precursor (64% similarity and 45% identity over 111 amino acids) or melanoma inhibitory activity, cattle cartilage-derived retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid-sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid-sensitive proteins. GRLP polypeptides and polynucleotides of the invention and diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma cell growth and tumours, including neuroectodermal tumours such as growth and tumours, including neuroectodermal tumours such as growth and tumours, including neuroectodermal tumours such as growth and tumours, including neuroectodermal tumours such as cativity, hemostaptics, remunosuppressive or immunosuppressive or immunosuppressive or immunostimulant activity, activit/inhibin activity, chemostatic/chemokinetic activity, and activity, activit/inhibin activity, activity, and activity, activity, and activity, activity, and activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activity, activit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated human growth regulatory-like polypeptide useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, use in cancer diagnosis and therapy, drug screening, receptor/ligand activity, antinflammatory activity, and treatment of leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                       Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
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                                                                                                                                                                                           25-JAN-2001; 2001WO-US02455.
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Best Local Similarity 100.0
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
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                                                                                    WO200155332-A2
                                 Homo sapiens.
                                                                                                                                        02-AUG-2001
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DNAS. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory call function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAR59063 to AAR59099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
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                                                                   MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter; inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.7%; Score 547; DB 22; Length 110; 90.0%; Pred. No. 6.3e-63; Live 7; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse MLP protein sequence SEQ ID NO:12.
                                           Mouse MLP protein sequence SEQ ID NO:26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 98-99; 111pp; Japanese.
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                                                                                                                                                                                                                                                                       29-JUN-2000; 2000WO-JP04278.
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            23-APR-2001 (first entry)
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es 99; Conserva
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                                                                                                                                                                                                     MO200102564-A1.
                                                                                                                                                                                                                                                                                                        30-JUN-1999;
                                                                                                                                                                  Mus musculus.
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30-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 HGVFMDKLSSKKLCADEECVYISLARAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGA 78
                                                                                                                                                                                                   Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA
                                                                                                                                     Mogi S, Noguchi Y, Yoshimura
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                                                                                                                                                                                                                                                                                                                                                                                                 92.7%; Score 547; DB 22; Length 128; 90.0%; Pred. No. 7.8e-63; ive 7; Mismatches 4; Indels
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                                                                                                                                        Ogi K, Ohkubo S,
                                                                                                                                                                                                                                                           Claim 4; Page 93-94; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB69131 standard; Protein; 110 AA.
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                                                                         29-JUN-2000; 2000WO-JP04278.
                                                                                              99JP-0186718
                                                                                                                 (TAKE ) TAKEDA CHEM IND LTD
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                                                                                                                                                                       WPI; 2001-159271/16.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              128 AA;
                                                                                                                                        Nishi K,
                                                                                                                                                                                 N-PSDB; AAF59068.
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                                WO200102564-A1
                                                                                               30-JUN-1999;
           Mus musculus
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                                                    11-JAN-2001
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Tanaka H;
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The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antinflammatory and cardiant activities, and can be used in gene therapy and as secretory calls function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAF53063 to AAF53099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                             Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                        Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.7%; Score 541; DB 22;
89.1%; Pred. No. 3.8e-62;
iive 7; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat MLP protein sequence SEQ ID NO:47.
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 107; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB69130 standard; Protein; 128 AA.
(TAKE ) TAKEDA CHEM IND LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUN-2000; 2000WO-JP04278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0186718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TAKE ) TAKEDA CHEM IND LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-159271/16.
                                                                                                                                                    WPI; 2001-159271/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 AA;
                                                           Nishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nishi K,
                                                                                                                                                                                     N-PSDB; AAF59099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF59098,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200102564-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tanaka H;
                                                                                            Tanaka H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB69130;
                                                                                                                                                                                                                                                                                                                                                diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Itoh Y,
                                                           ttoh Y,
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DNAS. The MLP proceins and DNAS have antihilammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAS can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis.

AAF59063 to AAF5099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                          1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                             19 HGMFMDKLSSKKLCADEECVYTISLARAQEDYNAPDCRFINVKKGQQIYVYSKLVTENGA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mogi S, Noguchi Y, Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              joint
     Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
                                                                                                                                The present invention describes novel MLP proteins and their encoding
                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 GAFWAGSVYGDHQDEMGINGYFPSNLVREQRVYQEATKEIPTTDIDFFCE 128
                                                                                                                                                                                                                                                                                                                                   91.7%; Score 541; DB 22; Length 128; 89.1%; Pred. No. 4.7e-62; cive 7; Mismatches 5; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat MLP protein sequence SEQ ID NO:39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 9; Page 103; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohkubo S,
                                                                                                    Claim 6; Page 106; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB69129 standard; Protein; 87 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0186718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ogi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                         98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-159271/16.
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                        128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200102564-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tanaka H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB69129;
                                                                                                                                                                                                                                                                                                        Sequence
                                                                       diseases
                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                  function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing to recenting bone and joint diseases as well as pathologic angiogenesis. AAFS9063 to AAFS9089 and AAB69122 to AAB69132 represent sequences used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treat cancer (melanoma, glioblastoma, neuroblastoma, small cell lung cancer, neuroectodermal tumours) or as an immunosuppressant (it inhibits IL-2 or phytohaemagalutinin induced proliferation of peripheral blood lymphocytes). Antibodies raised against the protein can be used to detect cell producing the protein and also protein nurification. Probes derived from DNA encoding the protein purification. Probes derived from DNA encoding the protein or related proteins. The protein may be expressed as a fusion protein (conjugated with dihydrofolate reductase (DHFR)).
                                                                                                                                                                                                                6 DRIASKKICADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma; small cell lung cancer; neuroectodermal tumours; immunosuppressant; phytohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection;
                                                                                                                                                                                  Gaps
activities, and can be used in gene therapy and as secretory cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New melanoma inhibiting protein and related nucleic acid -
vectors, transformed cells, antibodies etc., useful for treating
tumours and as immunosuppressant e.g. by gene therapy
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This protein has melanoma-inhibiting activity and can be used
                                                                                                                                                Score 417; DB 22; Length 87; Pred. No. 3.8e-46;
                                                                                                                                                                                  Indels
                                                                                                                                                                                    5.
                                                                                 in the exemplification of the present invention.
                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                   66 GSVYGDGQDEMGVVGYFPRNLVKEQRV 92
                                                                                                                                                                                                                                                                                                       61 GSVYGDHQDEMGIVGYFPSNLVREQRV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Melanoma inhibiting protein (human).
                                                                                                                                                                                                                                                                                                                                                                                                      AAR69811 standard; Protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaluza B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 54; 85pp; German.
                                                                                                                                                  70.7%;
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N-PSDB; AAQ84050, AAQ84051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                    Query Match
Best Local Similarity 88.5
Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probe; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
                                                                                                                  87 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-1994;
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26-OCT-1995
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                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR69811;
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Gaps

131 AA;

Sequence

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The invention relates to the use of melanoma inhibiting activity (WIA) contein and/or its fragments that have anti-inflammatory effects and induction and/or its fragments that have anti-inflammatory effects and induction of systemic immune tolerance or specific T-cell tolerance to MIA antigen, for manufacturing a preparation against inflammatory diseases.

CC and for induction of systemic immune tolerance or specific T-cell tolerance in patients suffering from or susceptible to inflammatory diseases. A fragment of MIA is useful as a therapeutic substance and is useful for manufacture of pharmaceutical preparations against consecution disease, specifically theumatoid arthritis, autoimmune diseases, specifically theumatoid arthritis, autoimmune diseases like Graves' disease, juvenile arthritis, primary glomerulonephritis, polyarthritis, osteoarthritis, sindismune companies, which is systemic lupus erythematosis, inflammatory bowel disease, multiple sclerosis or diabetes. The MIA polypeptides have specific effect on the autoreactive T-cells thus leaving the other components of the immune system intact as compared to the non-specific suppressive effect of immunosystem intact as compared to the non-specific suppressive thuman MIA protein.
                                                                                                             5 MDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGE-F 63
                                                                                                                                    MIA; melanoma inhibiting activity protein; antiinflammatory; human; antiarthritic; antithreumatic; antithroid; osteopathic; nephrotropic; immunosuppressive; ophthalmological; dermatological; antidiabetic; neuroprotective; immune tolerance; T-cell tolerance.
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of melanoma inhibiting activity protein or its derivatives as immune modulatory agents for the treatment of inflammatory diseases, specifically rheumatoid arthritis
                                                                         5.
                             43.0%; Score 253.5; DB 16; Length 131; 45.4%; Pred. No. 1.3e-24; tive 21; Mismatches 33; Indels 5;
                                                                                                                                                                                                             64 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                   AAG65614 standard; Protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 34; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-2001; 2001WO-EP02991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000EP-0201063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MIA protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                         49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ALKU ) AKZO NOBEL NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-611446/70.
N-PSDB; AAH47783.
                                     Query Match
Best Local Similarity
131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200170253-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                07-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                             AAG65614;
Sequence
                                                                               Matches
                                                                                                                                                                                                                                                                                               RESULT 15
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27 MPKLADRKLCADQECSHPISMAVALQDYMAPDCRFLTIHRGQVVYVFSKL---KGRGRLF 83
                                                                                                              5 MDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGE-F 63
                                                       5.
  DB 22; Length 131;
                                                                                                                                                                                                                      64 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                      84 WGGSVQGDYYGDLAARLGYFPSSIVREDQTLKPGKVDVKTDKWDFYCQ 131
/ Match 43.0%; Score 253.5; DB 22; Length Local Similarity 45.4%; Pred. No. 1.3e-24; nes 49; Conservative 21; Mismatches 33; Indels
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_RWA PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_NBW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_NBW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US06_NBW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NBW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        724715
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
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                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                        Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|               |       |                |                       |    | COLLARIA         |                   |  |
|---------------|-------|----------------|-----------------------|----|------------------|-------------------|--|
|               |       | æ              |                       |    |                  |                   |  |
| Result<br>No. | Score | Query<br>Match | Query<br>Match Length | DB | ID               | Description       |  |
|               | 590   | 100.0          |                       | 12 | US-10-216-163-72 | Sequence 72, Appl |  |
| 7             | 590   | 100.0          |                       | 12 | US-10-218-765-72 | Sequence 72, Appl |  |
| ю             | 590   | 100.0          |                       | 12 | US-10-219-063-72 | 72,               |  |
| 4,            | 590   | 100.0          |                       | 12 | US-10-219-066-72 | 72,               |  |
| ហ             | 590   | 100.0          |                       | 12 | US-10-219-067-72 | 72,               |  |
| 9             | 590   | 100.0          |                       | 12 | US-10-219-068-72 | 72,               |  |
| 7             | 590   | 100.0          | 128                   | 12 | US-10-219-069-72 | Sequence 72, Appl |  |
| 00            | 590   | 100.0          |                       | 12 | US-10-219-073-72 | 72,               |  |
| 9             | 590   | 100.0          |                       | 12 | US-10-219-475-72 | 72,               |  |
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| 11            | 590   | 100.0          |                       | 12 | US-10-219-483-72 | 72,               |  |
| 12            | 590   | 100.0          |                       | 12 | US-10-219-525-72 | 72,               |  |
| 13            | 590   | 100.0          |                       | 12 | US-10-219-526-72 | 72,               |  |
| 14            | 590   | 100.0          |                       | 12 | US-10-219-530-72 | 72,               |  |
| 15            | 590   | 100,0          |                       | 12 | US-10-219-531-72 |                   |  |

| Appl     | Appl     | , App    |         |          |          |          |          | Appl     |            |          |         |          |         |         |          |         |          |          |         |          |         |         |          |         |         |          |         |         |         |  |
|----------|----------|----------|---------|----------|----------|----------|----------|----------|------------|----------|---------|----------|---------|---------|----------|---------|----------|----------|---------|----------|---------|---------|----------|---------|---------|----------|---------|---------|---------|--|
| 72,      | 72,      | 360      | 72,     | 72,      | 360      | 72,      | 72,      | 72,      | 72,        | 72,      | 72,     | 72,      | 72,     | 72,     | 72,      |         |          |          |         |          |         |         |          |         |         |          |         |         |         |  |
| ance     | ance     | ance     | equence | auce     | ance     | ance     | ance     | auce     | ance       | ance     | ednence | ance     | equence | equence | ance     | edneuce | ence     | ance     | equence | ance     | ence    | edneuce | ence     | equence | edneuce | ence     | equence | ednence | ednence |  |
| Sequence | Sequence | Seguence | sedne   | Seguence | Sequence | Sequence | Sequence | Seguence | Sequence   | Sequence | Sedne   | Seguence | Segue   | Sedue   | Sequence | Sedne   | Sequence | Sequence | Segue   | Sequence | Sequenc | Sedn    | Seguence | Segue   | Segui   | Sequence | Segui   | Sedn    | Segu    |  |
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|          |          |          |         |          |          |          |          |          |            |          |         |          |         |         |          |         |          |          |         |          |         |         |          |         |         |          |         |         |         |  |
| N        | 7        | 09       | 0       | 7        | 09       | 2        | 0        | 2        | 7          | 7        | -72     | 0        | 7       | N       | 0        |         | 0        | ~        | 7       | 7        | 2       | 7       | 7        | 7       | 7       | 2        |         | N       |         |  |
| 532-7    | 533-73   | ņ        | 7       | -7       | -3       | 7        | 7        | ٠,       | -7         | 14-      | 59A     | 49-      | 73-     | 83-7    | -91      | 34-7    | 003-7    | 75-7     | 464-72  | 2-99     | 79-7    | 81-7    | 1        | à       | 33-7    | 9        | S       |         | 7       |  |
|          | 19-5     | 23-0     | 30-4    | 32-2     | 23-0     | 27-8     | 30-1     | 230-3    | 18-6       | 30-41    | 216-1   | 18-8     | 27-8    | 27-8    | 19-0     | 30-4    | 19-      | 19-07    | 19      | 19       | 19-4    | м       | 30-      | 32-     | 32-     | 4        | н       | Н       | 13      |  |
| 4        | ÷        | 10-      | 10-     | 101      | 10-      | 10-      | 10-      | 10       | 10-        | 10-      | ģ       | 10       | -01     | 9       | 10-      | 9       | 10-2     | 10-2     | 10-2    | -01      | -01     | 10-2    | 10-2     | 10-2    | 10-2    | 10-2     | 10-2    | 10-2    | 10-2    |  |
| us-      | us-      | ns-      | us-     | us-      | ns-      | ns-      | ns-      | us-      | ns-        | -Sn      | ns-     | us-      | us-     | us-     | us-      | ns-     | ns-      | US-      | us-     | ns-      | us-     | Sn.     | us-      | us-     | us-     |          | us-     |         | ns-     |  |
| 12       | 12       | 12       | 12      | 12       | 12       | 15       | 15       | 15       | 15         | 15       | 15      | 15       | 15      | 15      | 12       | 15      | 12       | 15       | 15      | 15       | 15      | 12      | 15       | 15      | 15      | 15       | 15      | 15      | 12      |  |
| 128      | 128      | 128      | 128     | 128      | 128      | 128      | 128      | 128      | 128        | 128      | 128     | 128      | 128     | 128     | 128      | 128     | 128      | 128      | 128     | 128      | 128     | 128     | 128      | 128     | 128     | 128      | 128     | 128     | 128     |  |
|          |          |          |         |          |          |          |          |          |            | _        | _       |          | _       |         |          |         |          |          |         |          |         |         |          |         |         |          | 0       |         | _       |  |
|          |          |          | 0.00    | 0.00     | 0.00     | 0.00     | 0.00     | 0.00     | 0.00       | 0.00     | 00.0    | 0.00     | 100.0   | 0.00    | 0.00     | 0.00    | 0.00.    |          | 100,0   | 0.00     | 100.0   | 0.00    | 0.00.    | 0.00.   | 0.00.   | ٠,       | ٠,      | 00.0    | 00.0    |  |
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| 59       | 59       | 5        | 59      | 59       | 59       | 59       | 59       | 59       | 5          | 59       | 50      | 50       | 53      | 53      | 52       | 59      | S        | 5        | 52      | 55       | 25      | 53      | 35       | 55      | 5,0     | ŝ        | 55      | S       | Š       |  |
| ve.      | 7        | 00       | 0       | 0        | н        | S        | 6        | 24       | S          | 9        | 7       | 8        | 6       | 0       | 11       | 22      | E.       | 4        | S       | 98       | 2.3     | 88      | 68       | 9       | 11      | 2        | ñ       | 44      | 5       |  |
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## ALIGNMENTS

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BESULT 19.216-163-72

Sequence 72, Application US/10216163

Sequence 72, Application US/10216163

Sequence 72, Application US/10216163

Sequence 72, Application US/10216163

SEQUENCAL INFORMATION:
APPLICANT: Desmoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
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APPLICANT: Smith, Victoria
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APPLICANT: Watanabe, Colin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Goddard, Audrey
APPLICANT: Godwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
Remaining Prior Application data removed - See File Wrapper or PALM.
SEQ ID NO 72
LEMOTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-216-163-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
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                                                                                                                                                                                                                                                                                                                     100.0%; Score 590; DB 12; Length 128; 100.0%; Pred. No. 5e-64; o; Indels 0
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CURRENT APPLICATION NUMBER: US/10/218,765
CURRENT FILING DATE: 2002-08-12
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PRIOR APPLICATION NUMBER: 10/119,480
PRIOR PLING DATE: 2002-04-09
PRIOR PLING DATE: 1097-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-01-17
PRIOR FILING DATE: 1997-10-17
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DR APPLICATION NUMBER: 60/07928

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DR FLIING DATE: 1998-04-15

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DR FILING DATE: 1998-04-15

DR FLIING DATE: 1998-04-22

DR FLIING DATE: 1998-05-06

PRILING DATE: 1998-05-06
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Publication No. US20030187201A1
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 110; Conservative
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Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Baker, Kevin P. APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/08532
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APPLICATION NUMBER: 60/101741
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FILING DATE: 1998-09-24
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APPLICATION NUMBER: 60/101477
FILING DATE: 1998-09-23
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APPLICATION NUMBER: 60/106178
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PRIOR FILING DATE: 1398-10-28

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PRIOR PELICATION UNDERER: 60/106905

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APPLICANT: Gerdard, Paul J.
APPLICANT: Gradwaki, Paul J.
APPLICANT: Graduldi, J. Christopher
APPLICANT: Graduldi, J. Christopher
APPLICANT: Graduldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
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APPLICANTON NUMBER: 10/119,480
PRIOR PLING DATE: 2002-08-13
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/065913
PRIOR PLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06349
PRIOR FLING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-23
PRIOR APPLICATION NUMBER: 60/06979
PRIOR PLING DATE: 1998-03-20
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NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
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100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
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Matches 110; Conservative
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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; ORGANISM: Homo Sapien
US-10-219-063-72
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                                     1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA 60
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CURRENT APPLICATION NUMBER: US/10/219,066
CURRENT FILING DATE: 2002-08-13
FRIOR PEDLICATION NUMBER: 10/119,480
FRIOR FILING DATE: 2002-04-09
FRIOR FILING DATE: 1997-09-17
FRIOR APPLICATION NUMBER: 60/062287
FRIOR FILING DATE: 1997-10-17
FRIOR FILING DATE: 1997-10-17
FRIOR FILING DATE: 1997-10-31
FRIOR PELLOR POWER: 60/064103
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FRIOR PELLOR DATE: 1997-12-17
FRIOR APPLICATION NUMBER: 60/069873
FRIOR PELLOR DATE: 1997-12-17
FRIOR APPLICATION NUMBER: 60/069873
FRIOR FILING DATE: 1998-03-20
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 72, Application US/10219066 Publication No. US20030187203A1 GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Desnoyers, Luc
Gerritsen, Mary
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Best Local Similarity
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LENGTH: 128
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19 HGIF#DRIASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIIVYSKLVKENGA 78
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                                                                                                                                                                                                                                                                    APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Mood, William I.
APPLICANT: Mood, William I.
APPLICANT: Mood, William I.
APPLICANT: Mood, William I.
APPLICANT: WOOD, WILLE BERERENE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC51
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SEQ ID NO 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: P3250PLC31
CURRENT PELICATION NUMBER: US/10/219,067
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: UJ/119,480
PRIOR PELING DATE: 2002-04-09
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR PELING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063913
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR PELING DATE: 1997-10-31
PRIOR PELING DATE: 1998-03-26
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godwarki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
                                                                                                                                                                                   Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
; Sequence 12, Application US/10219067; Publication No. US20030187204A1; GENERAL INFORMATION:
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                                                                                           APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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ORGANISM: Homo Sapien
US-10-219-067-72
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US-10-219-068-72
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APPLICANT: Baker, Kevin P.
APPLICANT: Besnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Girney, Austin L.
APPLICANT: Smith, Victoria
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US-10-219-069-72
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APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE SEPREMENT E: 2002-08-13
CURRENT APPLICATION NUMBER: US/10/19, 480
PRIOR APPLICATION NUMBER: 60/659113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/66287
PRIOR APPLICATION NUMBER: 60/66287
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-18
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-12-17
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APPLICANT: Goddard, Paul J.
APPLICANT: Gramaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Mood, Milliam I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC40
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
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Gerritsen, Mary
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CRGANISM: Homo Sapien
US-10-219-068-72
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grinth, Victoria
APPLICANT: Safith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TILLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TILLE OF INVENTION: ACIDS ENCODING THE SAME
TILLE OF INVENTION: ACIDS ENCODING THE SAME
TILLE OF INVENTION: ACIDS ENCODING THE SAME
TILLE OF INVENTION NUMBER: US/10/219,073
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 60/063913
PRIOR FILING DATE: 1997-0-17
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FRICK APPLICATION NUMBER: 60/078910
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100.0%; Score 590; DB 12;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0;
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Gaps

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APPLICANT: GerTIESEN, Warry
APPLICANT: GerTIESEN, Warry
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Scephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
APPLICANTON: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT FILING DATE: 2002-08-13
FRIOR PELLING DATE: 2002-04-09
FRIOR FILING DATE: 1997-10-17
FRIOR APPLICATION NUMBER: 60/06387
FRIOR APPLICATION NUMBER: 60/06387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 590; DB 12; Length 128; 100.0%; Pred. No. 5e-64; ive 0; Mismatches 0; Indels 0
                                                                                                                                       Length 128;
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                                                                                                                               Query Match 100.0%; Score 590; DB 12; Best Local Similarity 100.0%; Pred. No. 5e-64; Matches 110; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 72, Application US/10219480
Publication No. US20030187209A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 110; Conservative
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ORGANISM: Homo Sapien
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-475-72
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APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/219,475
CURRENT PILING DATE: 2002-04-09
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PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
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Gerritsen, Mary
Goddard, Audrey
Godowski, Paul J
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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Publication No. US20030187208A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 110; Conservative
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CORGANISM: Homo Sapien
US-10-219-073-72
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APPLICANT: Gedard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Gurmed, Austin L.
APPLICANT: Stephan, Jean-Philippe F.
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APPLICANT: Watenabe, Colin L.
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                                   Query Match
100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0
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US-10-219-525-72
Sequence 72, Application US/10219525
Publication No. US20030187211A1
GENERAL INFORMATION:
                                                                                                                                                                                                                           Sequence 72, Application US/10219483
Publication No. US20030187210A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baker, Kevin P. APPLICANT: Desnoyers, Luc APPLICANT: Gerritsen, Mary APPLICANT: Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo Sapien
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APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
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APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
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APPLICANT: WWABER: 60/069973
PRIOR FILING DATE: 1999-03-12-17
PRIOR PILING DATE: 1999-03-25
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grinaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
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; ORGANISM: Homo Sapien
US-10-219-525-72
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US-10-219-526-72
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TYPE: PRT
CORGANISM: Homo Sapien
US-10-219-530-72
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US-10-219-531-72
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERBACE: P3530P1C41
CURRENT APPLICATION NUMBER: US/10/219,526
CURRENT FILING DATE: 2002-08-13
PRIOR PLING DATE: 1007-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/065913
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063849
PRIOR PILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-28
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PRIOR PLING DATE: 1997-12-17
PRIOR PLING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/06973
PRIOR APPLICATION NUMBER: 60/07994
PRIOR PILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079294
PRIOR PILING DATE: 1998-03-25
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APPLICANT: Goddard, Audrey,
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smathe, Colin L.
APPLICANT: Watanabe, Colin L.
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ALILE OF INVENTION: ACIDS ENCODING THE SAME
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Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0
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CURRENT APPLICATION NUMBER: US/10/219,530
CURRENT FILING DATE: 2002-08-14
PRIOR PELICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PLICATION NUMBER: 60/05917
PRIOR APPLICATION NUMBER: 60/05287
PRIOR FILING DATE: 1997-09-17
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Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-526-72
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US-10-219-530-72
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LINORATION:
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LINORATION:
CART. BAKET, KEVIN F.
LICANT: BAKET, KEVIN F.
LICANT: Gerritsen, Mary
PELICANT: Gerritsen, Mary
PELICANT: Gerritsen, Mary
PELICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Gerrinaldi, J. Christopher
APPLICANT: Gerrinaldi, J. Christopher
APPLICANT: Gerrinaldi, J. Christopher
APPLICANT: Gerrinaldi, J. Christopher
APPLICANT: Waterin L.
APPLICANT: Watering and TRANSREMBRANE POLYPEPTIDES
APPLICANT: Watering and TRANSREMBRANE
PELICANT: Watering and TRANSREMBRANE
FITTLE OF INVENTION: ACIDE ENCORNOR THE SAME
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PRIOR PELLICATION WUMBER: 60/059113
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PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR PLING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
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PRIOR PLING DATE: 1997-12-17
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100.0%; Score 590; DB 12; Length 3
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels
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Appl Appl Appl Appl Appl Appl Appl

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Sequence 4, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 23375, A
Sequence 194, App
Sequence 1964, A
Sequence 18644, A
Sequence 136, App
Sequence 219, App
Sequence 219, App
Sequence 210, Appl
Sequence 210, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 MDRLASKKI.CADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKI.VKENGAGE-F
                                                                                                                                                                                         Sequence
Sequence
Sequence
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45.4%; Pred. No. 3e-25;
tive 21; Mismatches 33; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08578649

Patent No. 5770366

GENERAL INPORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Raluza
TTTLE OF INVERTION: MELANOWA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
COMPESSEB: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
COUNTRY: USA
STATE: New York
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/C
                     US-08-460-327-2
US-08-460-327-4
US-08-459-871-2
US-08-459-871-4
US-08-252-911A-23375
US-09-252-911A-29546
US-09-252-991A-29546
US-09-252-991A-18644
US-08-630-915A-136
US-08-630-915A-219
US-08-630-915A-219
US-08-630-915A-219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31,275
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION POR SEQ ID NO. 2:
                                                                                                                                                                                                     US-08-316-301A-12
US-08-611-928-10
                                                                                                                                                                US-08-911-321-11
US-08-158-232-10
US-08-304-626-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 131 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 45.4%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
88033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MODECUDE IN
US-08-578-649-2
                                                                                                                                                                                                                                                                                               RESULT 1
US-08-578-649-2
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                                                                                                                                                                 1 HGIFMDRLASKKLCADDECV......RVYQEATKEVPTTDIDFFCE 110
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                 GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-08-578-649-5

US-07-346-510B-21

US-09-346-510B-24

US-09-346-510B-24

US-09-346-510B-24

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US-09-346-510B-24

US-09-134-078-61

US-09-134-078-61

US-08-630-915A-135

US-08-630-915A-135

US-08-645-957-8

US-08-459-967-8

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Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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STREET: P.O. BOX CITY: Princeton STATE: New T.
ADDRESSEE:
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27 MPKLADRKL.CADQECSHPISMAVALQDYMAPDCRFLTIHRGQVVYVFSKL---KGRGRLF 83
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                                                                                    64 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
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                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08578649

Patent No. 5770366

GENERAL INFORMATION:

APPLICANT: Ulrich Bogdan

APPLICANT: Reinhard Buttner

APPLICANT: Brighter Kaluza

APPLICANT: Brighter Kaluza

APPLICANT: Brighter Kaluza

APPLICANT: Brighter Kaluza

APPLICANT: Brighter Kaluza

APPLICANT: Brighter Kaluza

APPLICANT: Brighter Kaluza

APPLICANT: Brighter Kaluza

GOUNTES: 100 TNYTH MELANOMA-INHIBITING PROTEIN

STREET: 805 Third Avenue

COUNTRY: New York

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.2%; Score 231.5; DB 1;
43.5%; Pred. No. 2.2e-22;
tive 21; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31.575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INPORMATION:
TELEPHONE: (212) 689-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHRACATERISTICS:
LENGTH: 130 amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/07646537B
Patent No. 5348864
GENERALINFORMATION:
APPLICANT: Barbacid, Mariano
TITLE OF INVENTION: Vav Proto-Oncogene Protein
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-578-649-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-646-537B-2
                                                                                                                                                                                                                                                                                                                                 US-08-578-649-5
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26 ASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYPPRN 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/09346510B
Facent No. 6281014
GENERAL INFORMATION:
APPLICANT: Wang, Yinxiang
TITLE OF INVENTION:
TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof
FILE REFERENCE: D6221CIP
CURRENT FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 08/871,732
FRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 21
LENGTH: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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Best Local Similarity 31.4%; Pred. No. 0.032;
Matches 22; Conservative 14; Mismatches 21; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.8%; Score 81.5; DB 3; Length 54; 32.3%; Pred. No. 0.0023; cive 13; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: Domain
; OTHER INFORMATION: amino acid sequence of Vav SH3 domain
US-09-346-510B-21
                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/646,537B
FILING DATE:
Bristol-Myers Squibb Company ). Box 4000
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GAUL, Timothy J.
REFERENCE/DOCKET NUMBER: 33,111
REFERENCE/DOCKET NUMBER: DC10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 921-5901
TELEPAX: (609) 921-5901
TELEPAX: (609) 921-526
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 844 amino acids
TYPE: amino acid
                                                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                                Is Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                835 YVEED--YSE 842
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 LVKEORVYOE 95
                                                                   New Jersey
U.S.A.
                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Best Local Similarity
Matches 20; Conserv
                                                                                                          08543-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: unknown
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31 DYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLV 87
                                                                                                                                                         ; Sequence 38, Application US/08630915A
; Patent No. 6309820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-134-078-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 LSSSPSTSELTSIRPIGIVVAAYDIKKDSSSQLLSVQQGETIYILIKK----NSSG-99
                                                                                                                                                  US-09-356-952-4
; Sequence 4, Application US/09356952
; Patent No. 6117663
; Patent No. 6117663
; Patent No. 6117663
; Patent No. 6117663
; Patent No. 6117663
; APPLICANT: Boriack-Sjodin, Ann
; APPLICANT: Boriack-Sjodin, Ann
; APPLICANT: Cole, Philip
; APPLICANT: Cole, Philip
; APPLICANT: Cole, Philip
; TILLE OF INVENTION: THEREOF
; TILLE REFERENCE: Gol-1-228N
; CURRENT APPLICATION NUMBER: US/09/356,952
; CURRENT FILING DATE: 1999-07-19
; EARLIER FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 1999-07-21
; SOUTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Domain

COCATION: 2...49

OTHER INFORMATION: amino acid sequence of Vav SH3 domain at position 2

OTHER INFORMATION: through position 49 of SEQ ID No. 6281014 21

US-09-346-510B-24
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Fatent No. 6281014

GENERAL INFORMATION:

APPLICANT: 0'Brien, Timothy J.

APPLICANT: 0'Brien, Timothy J.

TITLE OF INVENTION:

FILE REFERENCE: D622LOIP

CURRENT APPLICATION NUMBER: US/09/346,510B

CURRENT FILING DATE: 1999-07-01

PRIOR APPLICATION NUMBER: 08/871,732

PRIOR APPLICATION NUMBER: 08/871,732

FILE SEQ ID NO 24

SEQ ID NO 24

SEQ ID NO 24

CHARLES APPLICATION NUMBER: D87-06-09

SEQ ID NO 24

CHARLES APPLICATION NUMBER: D87-06-09

SEQ ID NO 24

CHARLES APPLICATION NUMBER: D87-06-09

SEQ ID NO 24

CHARLES APPLICATION NUMBER: D87-06-09

SEQ ID NO 24

CHARLES APPLICATION NUMBER: D87-06-09

SEQ ID NO 24

CHARLES APPLICATION NUMBER: D87-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.3%; Score 78.5; DB 3; Length 1589; 25.8%; Pred. No. 0.63; ive 21; Mismatches 34; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.3%; Score 72.5; DB 3; Length 48; 31.6%; Pred. No. 0.029; tive 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 WWDGLVIDDSNGKVN-RGWFPQNFGRPLR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 FWAGSVYGDGQDEMGVVGYFPRNLVKEQR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 31.6'
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: unknown
                                 83
                                                                         51
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US-09-346-510B-24
                              3--B
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LENGTH: 1589
                                 88
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310 AAKPVVSGEEIAQVIA----SYTATGPEQLTLAPGOLI-----LIRKKNPGGWWEGEL 358
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                                                                                                                                                                                                                         APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFWAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES. Dana M.
APPLICANT: FOWLKES. Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYBEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
|-----VILNKKGQQGWRGEIYGR-----VGWFPANYV 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Lealie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 YGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 QARĞKKRQ--IĞWFPANYVK---LLSPGTSKITPTE 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 61, Application US/09134078
; Patent No. 636884
; GENERAL INFORMATION:
APPLICANT: Bylina, Edward J.
TITLE OF INVENTION: GLYCOSIDASE ENZYMES;
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.2%; Score 72; Best Local Similarity 22.9%; Pred. No. (Matches 22; Conservative 19; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 Avenue of the Americas CITY: New York
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Sequence 115, Application US/08630915A

Sequence 115, Application US/08630915A

Patent No. 6309820

GENERAL INFORMATION:

APPLICANT: BORKES, Andrew B.

APPLICANT: FOWLKES, Dana M.

APPLICANT: FOWLKES, Dana M.

APPLICANT: APPLICANT: ACCOUNTEL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

TITLE OF INVENTION: USING SAME

NUMBER OF SEQUENCES: 227

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404 LFNTGEDIREDTCSFILPKDGMEIKKTVEVRAGVFDYSNTFEKLSVKVEDLVFENEIEHL 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 LASAQEDYNAPDCRFINVKKGQQI-----YVYSK-----LVKENGAGEF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :|| :|| ::|| 464 GYG-IYGFDLDTTRIPDGEHEMFLEGHFQGKTVYCDSIKAKVVNEA-RYVLAEEVDF 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
11.9%; Score 70.5; DB 4; Length 680;
Best Local Similarity 27.6%; Pred. No. 2.1;
Matches 32; Conservative 12; Mismatches 37; Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 WAGSVYG------DGQDEMGVVGYFPRNLVKEQ----RVYQEATKEVPTTDIDF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/94,026
FILING DATE: 10-0CT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38.347
REFERENCE/DOCKET NUMBER: 0910/024002
TELEFORM SES 88.677-1456
TELEFORM SES 1886/677-1456
TELEFORM SES 1886/677-1456
TELEFORM CATALON SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 680 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Alinear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 1101-
TELECHOWICATION INFORMATION:
TELEPHONE: (212) 790-90901
TELEFRAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 869-8
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-08-630-915A-135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --LVKENGAGEF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 WAGSVYG------DGQDEMGVVGYFPRNLVKEQ---RVYQEATKEVPTTDIDF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.9%; Score 70.5; DB 4; Length 663; 27.6%; Pred. No. 2.1; trive 12; Mismatches 37; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/09134078

Patent No. 6368844

GENERAL INFORMATION:
APPLICANT: Bylinn:
TITLE OF INVENTION: GLYCOSIDASE ENZYMES

CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich Lip
STREET: 4365 Executive Drive, Suite 1600

CITY: San Diego
                                                                                                                                                        COMPUTER READABLE FORM:

CMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFFWARE: FASEEM for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
                                    ADDRESSEE: Gray Cary Ware & Freidenrich LLP STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 13-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 LASAQEDYNAPDCRFINVKKGQQI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
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INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein FRAGMENT TYPE: internal
            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                     San Diego
CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: STATE:
                                                                                                              STATE:
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CTHER INFORMATION: SEQUENCY
CTHER INFORMATION: SEQUENCY
CTHER INFORMATION: From GE
PUBLICATION INFORMATION:
CATHORS: Alloing, et al.
COLUME: A ALLOING, et al.
PAGES: 633-644
PAGES: 633-644
US-08-245-511-48
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.5%
The Conservative 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 133521
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 642 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 201 343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                    Query Match 11.3%; Score 66.5; DB 4; Length 62; Best Local Similarity 26.6%; Pred. No. 0.25; Matches 17; Conservative 11; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/245,511

FILING DATE: 18-MAY-1994

CLASSIFICATION NUMBER: US/08/15,511

FILING DATE: 01-SEP-1994

ATORNEY/AGENT INFORMATION:

NAME: Jackson Baq. David

TELEPHONE: 201 487-5800

TELEPHONE: 201 487-5800

TELEPHONE: 201 487-5800

TELEPHONE: 201 487-5800

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ORGANISM: Streptococcus pneumoniae
IMMEDIATE SOURCE:
CLONE: amiA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-245-511-48
; Sequence 48, Application US/08245511
; Partent No. 5928900
; GENERAL INFORMATION:
     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                                                                                    TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 NYVK 60
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                                                              LENGTH:
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| OTHER INFORMATION: NOTE: the reference contains a corner information in the control that control information in the control that control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control information in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the cont
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Sequence 8, Application US/08434255

Patent No. 5621089

GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Dambmann, Claus
APPLICANT: Asalyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5621089 disk of No. 5621089 th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
                                                                                                                                                                                                                      190 AMYDYAANNEDELSFSKGOLINVANK-----DDPDWWQGEI-----NGVTGLFPSNYV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 TISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGY 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 TVAVLDSGVDYNHPDLARKVIKGYDFIDRDNNPMDLNGHGTHVAGTVAADTNNGIGVAGM 93
                                                                                                                                                                          28 AQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLV
                                                                                                                        24; Indels 24; Gaps
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                                                                      Query Match
11.2%; Score 66; DB 4; Length 248;
Best Local Similarity 30.4%; Pred. No. 2;
Matches 24; Conservative 7; Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopyy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          88 KEQRVYQEATKEVPTTDID 106
                                                                                                                                                                                                                                                                                                                            ----MTTDSD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AGTIS Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 212-867-0123
212-878-9655
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
; MOLECULE TYPE: peptide US-08-630-915A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-434-255-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                            238 K
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US-08-459-967-8
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          ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
IMMEDIATE SOURCE:
CLONE: amiA
CLONE: amiA
FEATURE:
OTHER INFORMATION: the reference contains a sequence error; the
OTHER INFORMATION: correct sequence shown below is obtained from GENBANK
PUBLICATION INFORMATION:
AUTHORS: Alloing, et al.
JOURNAL: Mol. Microbiol.
VOLUME: 4
PAGES: 633-644
DATE: 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 EKVATKKALLINKDFRQALNFALDRSAYSAQ----INGKDGAALAVRNLFVKPDFVSAGEK 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 -----GAGEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 TFGDLVAAQLPAYGDEWKGVNLADGQD----GLF--NADKAKAEFRKAKKALEADGVQF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 27
CORRESPONDENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 DRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKEN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 11.3%; Score 66.5; DB 2; Length 642; Best Local Similarity 22.5%; Pred. No. 6.5; Matches 27; Conservative 20; Mismatches 44; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTONEY/AGENT INPORMATION:
NAME: MISTOCK: S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELEPROMINICATION INFORMATION:
TELEPROMINICATION INFORMATION:
TELEPROMINICATION INFORMATION:
TELEFRAME (212) 790-9090
TELEFRAME (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-08-630-915A-40
; Sequence 40, Application US/08630915A
; Datent No. 6309820
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acids
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                    US-08-600-993A-48
     ANTI-SENSE:
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Sequence 8, Application US/08459967
Parent No. 5622841
| GENERAL INFORMATION: ABLAP |
| APPLICANT: Slowa, Alan P. |
| APPLICANT: Output | Hella |
| APPLICANT: Output | Hella |
| APPLICANT: ABLAP |
| APPLICANT: ABLAP |
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22 TISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGY 81 82 FPRNLVKEQRV 92 gg ð ð

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Gaps 0;

94 APDTKILAVRV 104

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Search completed: December 29, 2003, 16:11:50 Job time : 8.0112 secs

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RESULT 1
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-MODEL=frame+ p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US10019455/runat_29122003_160347_240/app_query.fasta_1.1770
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-Q=/cgn2_1/USPTO_spool/US10019455/runat_seq.-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -GTRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE_pct -THR MAX=100 -THR_MIN.D - ALIGN=15 -MODE=LOCAL
-UNFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -NAXLEN=2000000000
-USER=US10019455 @CGN 1 1_6034_@runat_29122003 160347_240 -NCPU=6 -ICPU=3
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-DBV TIMEOUT=120 -WARN TIMEOUT=30 -TRREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Sequence:
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29: em_vi:*
30: em_htg.inm:*
31: em_htg.inv:*
32: em_htg.inv:*
33: em_htg.mus:*
34: em_htg.pln:*
35: em_htg.pln:*
36: em_htg.amm:*
37: em_htg.vr:*
38: em_htg.vr:*
40: em_htg.omus:*
41: em_htg.ous:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |       |                     |        |      | SUMMARIES |                    |
|---------------|-------|---------------------|--------|------|-----------|--------------------|
| Result<br>No. | Score | %<br>Query<br>Match | Length | DB   | ID        | Description        |
|               |       |                     |        |      |           | 1 1                |
| Н             | 590   | 00                  | 33     | 9    | BD01081   | 5 Novel            |
| 63            | 590   | 00                  | 33     | 9    | BD09311   | 117 Novel          |
| e             | 590   | 8                   |        | 9    | BD01080   | 3802 Novel         |
| 4             | 590   | 00                  | 38     | ø    | BD09      | 103                |
| ស             | 590   | 00                  | 25     | ω    | AX35881   | 8818 Sequen        |
| 9             | 290   | 00                  | 52     | 9    | AX36231   | 2311               |
| 7             | 290   | 00                  | 52     | φ    | AX45477   | 1774               |
| α             | 590   | 100.0               |        | 9    |           | 252 Seque          |
| 6             | 290   | 00                  |        | σ    | AF23326   | 3261 Homo          |
| 10            | 590   | 00                  |        | σ    | AF24350   | 5 Homo s           |
| 11            | 590   | 00                  |        | ø    | BD01082   | Novel              |
| 12            | 590   | 00                  |        | Q    | BD09312   | Novel              |
| 13            | 590   | 00                  | -      | σ    | HSA2425   | O)                 |
| 14            | 547   |                     |        | ø    | BD01081   | Novel              |
| 15            | ぜ     |                     |        | 9    | BD09311   | Nove               |
| 16            | 4     |                     |        | 9    | BD01080   | Novel              |
| 17            | 4     |                     | 384    | Y    | BD09310   | Novel              |
| 18            | 4     |                     | 929    | 10   | AF2435    | Mus n              |
| 19            | 4     | 92.7                | 947    | ø    | BD01082   | Novel              |
| 20            | 547   | 92.7                | 947    | Ø    | BD09312   | BD093122 Novel pol |
| 21            | 547   | 92.7                | 958    | 10   | MMU2439   | Mus n              |
| 22            | 547   |                     | 1054   | 20   | AF233333  | 133 Mus            |
| 23            | 541   |                     | 330    | ø    | BD010836  | Novel              |
| 24            | 541   |                     | 330    | 9    | BD093137  | Novel              |
| 25            | 541   |                     | 384    | 9    | BD010835  |                    |
| 26            | u ı   | •                   | 384    | 9    | BD093136  | Novel              |
| 27            | 477.5 | 80.9                | 484    | ហ    | AF233518  | Gallus             |
| 28            | 471   | •                   | 307    | 9    | BD010830  | Novel              |
| 29            | 471   |                     | 307    | φ.   | n         | Nove1              |
| 30            | 413   | -                   | 261    | 9    | BD010829  | Novel              |
| 31            | 413   |                     | 261    | 9    | BD093130  | 130 Novel          |
| 32            | 390   |                     |        | S)   | AF233519  | 3519 Rana c        |
| 33            |       |                     | _      | on I | HS705D16  |                    |
| 34            | 9     |                     | 144765 | N    | BX510362  | BX510362 Mus muscu |
|               | 3     |                     | ഹ      | ~    | AC106161  |                    |
| c 36          | 2     |                     | 442    | 9    | G         | 30                 |
|               | 24    |                     | 442    | 9    | AX331840  | 1840 Sequenc       |
| 38            | 53    |                     | 330    | 9    | A42959    | Se                 |
| 39            | 23    | -                   | 330    | 9    | AX016802  | AX016802 Sequence  |
| 40            | 23    |                     | 396    | σ    | 4         | 4 Homo sap         |
| 41            | 23    | ٠.                  | 396    | 12   | $\sim$    | 007775             |
| 42            | 253.5 | _                   | 459    | 9    |           |                    |
|               | 23    | m                   | 459    | φ    | 9         | 35 Sequenc         |
| C 44          | 23    | 43.0                | 459    | 9    | AX252508  | <b>6</b> 0         |
|               | 23    | 43.0                | 459    | 9    | 20        | AX287209 Sequence  |

ALIGNMENTS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 330)

1. (Dases 1 to 330)

1. (Dases 1 to 330)

2. Ito,Y., Nishi,K., Oği,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H.

Novel polypeptide and its DNA

1. Datent: WO 0102564-A 17 11-JJAN-2001;

TAKEDA CHEMICAL INDUSTRIES LID,YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO

OGI, SHOICHI OKUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,

HIDEYUK TANAKA

OS HOMO Sapiens (human)

PN WO 0102564-A/17

PP 11-JJAN-2000

PP 29-JUN-2000 WO 2000JP004278

PR 30-JUN-1999 JP 99P 186718

PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
C12N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A61K39/17,
2 A61K39/395,A61K49/16,A61P19/02,A61P19/08,A61K31/7088//(C12P21/
3 02,C12R1:19)
                                                            PAT 27-AUG-2002
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
a 60 c 91 g 88
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A61D19/08,
PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC
G01N33/53//
PC C12P21/08,C12N15/00,A61K37/02,C12N5/00
CC FF FF Source
FT Source
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Catarrhini; Hominidae; Homo.
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                                                                                                                          Bukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 330)
1 (to.Y. Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.
Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 17 21-MAR-2001;
PAKEDA CHEMICAL INDUSTRIES LTD
OS Homo sapiens (human)
PN JP 20101069994-A/17
PD 21-MAR-2001
PF 29-JUN-2000 JP 200195911
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               330 bp
Novel polypeptide and DNA thereof.
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                                                             BD010816.1 GI:18639189
JP 2001069994-A/17.
Homo sapiens (human)
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Yoshimura, K. and Tanaka, H.
Novel polypeptide and its DNA
Novel polypeptide and its DNA
Datent: WO 0102564-A 3 11-JAN-2001,
TAKEDA CHEMICAL INDUSTRIES LID. YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
OS HOMO Sapiens (human)
PN WO 0102564-A/3
PD 11-JAN-2001
PP 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
                                                                                                                                       PAT 27-AUG-2002
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02, C12R1:19)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
C12N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00,
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Novel polypeptide and its DNA.
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WO 0102564-A/3.
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JP 2001069994-A/3.
Homo sapiens (human)
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SM Homo sapiens (butheria; brimates; Catarrhini; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
BI (bases I to 384)
SI Lo, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Yoshimura, K. and Tanaka, H.
Datent: JP 201069994-A 3 1-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Homo sapiens (human)
PN JP 2001069994-A/3
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PP 29-JUN-2000 JP 2000195911
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AGIP19/00,AGIP19/02, PC
COTX14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC
G01N33/53//
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="taxon:9606"
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| AX362311 LOCUS LOCUS DEFINITION Sequence 71 from Patent W00208288. ACCESSION WEASTON WERSION WERSION KEYWORDS SOURCE Homo sapiens Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS Godowski, P.O., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watamabe, C.K. and Wood, W.I. TITLE Godowski, P.O., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watamabe, C.K. and Wood, W.I. TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same JOURNAL Genentech, Inc. (US) FEATURES Location/Qualifiers Location/Qualifiers  Location/Qualifiers  Ambier C.C. Advaref="Laxon:9606" Advaref="Laxon:9606" Location Area C.C. Advaref="Laxon:9606" Advaref="Laxon:9606" BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE COUNT LOS C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BASE C.C. BAS | Alignment Scores: Pred. No.: Score: Score: Score: Fercent Similarity: 100.00\$ Matches: Matches: Fercent Similarity: 100.00\$ Mismatches: Cuery Match: 6 Gaps: 0  1 HisGlyIlePheMetAspargLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal  0  1 HisGlyIlePheMetAspargLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal  2 TAYThrIleSerLeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPheile  0  2 TAYThrIleSerLeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPheile  2 TAYThrIleSerTeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPheile  2 TAYThrIleSerTeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPheile  2 TAYThrIleSerTeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPheile  2 TAYThrIleSerTeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPheile  2 TAYThrIleSerTeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPheile  2 TATACTATITCTCTGGCTAGTGCTCAAGAAGATTATAATAGCTCCTGTTGCTGTTGTTT  211                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                           | 101 ProThrThrAspIleAspPhePheCysClu 110 |
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Patent: WO 0200690-A 359 03-JAN-2002;
Genentech, Inc. (US)

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                                        Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis patent: W0 02082844 359 31-JAN-2002; Garter: W0 02082844 359 31-JAN-2002; Garter: Napoleone (US); Gerber, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard, Audrey (US); Goddwski, Paul J. (US); Garnety, Austin L. (US); Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US); Paoni, Nicholas F. (US); Espehan, Jean-Philippe F. (US); Maranabe, Colin K. (US); Williams, P. Mickey (US); Wood, William
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Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
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Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C.
Direct Submission
Submitted (09-FBB-2000) Pathology, Brigham and Women's Hospital, 75
Francis Street, Boston, MA 02115, USA
Location/Qualifiers
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Robertson, M.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C.

Anovel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping
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Cohen-Salmon,M., Frenz,D., Verpy,E., Voegeling,S. and Petit,C.
Direct Submission
Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue
du Dr. Roux, Paris 75015, France
Location/Qualifiers
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Homo sapiens (human)
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Novel polypeptide and DNA thereof.
BD010820
                                                                                                                   sapiens"
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                                                                                                 1. .865
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1. .865
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/gene="FDP"
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SAQEDYNAPOCRFINVKKGQQIYVYXENGAGEFWAGSVYGDGQDEMGVVGYFPR
NLVKEQRVYQEATKEVPTTDIPFPCE"
NLVK-17 C. 205 g 259 t
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HOMO sapiens fibrocyte-derived protein (FDP) mRNA, complete cds.
AF243505.1 GI:11991843
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 865)
Cohen-Salmon,M., Frenz,D., Liu,W., Verpy,E., Voegeling,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal
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J. Biol. Chem. 275 (51), 40036-40041 (2000)
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Matches:
Conservative:
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Indels:
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/note="similar to cdrap/mia"
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1.846
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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

To be so it of 923)

To,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H.

Novel polypeptide and its DNA

Novel polypeptide and its DNA

TAKEDA CHEMICAL INDUSTRIES LID,YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA, HIDEYUKI TANAKA

S HOmo sapiens (human)

PN WO 0102564-A/21

PP 29-JUN-2000 WO 2000JP004278

PR 30-JUN-1999 JP 99P 186718

PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI
                                                                                                                                     Hone sapiens (human)
WO 0102564-A/21
HI-JAN-2001
29-JUN-2000 WO 2000JP004278
30-JUN-1999 JP 99P 186718
YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
                                                                                                                                                                                                                                                                                         A61X39/395,A61X49/16,A61P19/02,A61P19/08,A61X31/7088//(C12P21/
02,C12R1:19)
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C12N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00,
A61K38/17,
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S Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
Novel polypeptide and DNA thereof
Novel polypeptide and DNA thereof
TAKEDA CHEMICAL INDUSTRIES LTD
TAKEDA CHEMICAL INDUSTRIES LTD
FOR HOMO Sapiens (Human)
NO JP 20010659994-A/21
PP 21-MAR-2001
PP 21-MAR-2001
PP 29-JUN-2000 JP 2000195911
PR
PI YASURAI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI
SHINICHI MOGI.
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC CLZNIS/09,A61K38/00,A61K45/00,A61F48/00,A61P19/02, PC
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CO7K14/47,CO7K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC
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_147 c 213 g 26
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Novel polypeptide and its DNA.
BD093121 GI:22638709
WO 0102564-A/21.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E. (bases 1 to 330)

I to, Y., Mishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and DNA thereof

L. Patent: JP 2001069994-A 18 21-MAR-2001;
PAKEDA CHEMICAL INDUSTRIES LTD
OS Mus sp. (mouse)
PN JP 2001069994-A/18
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGlyMetGlyValValGly 80
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PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC CIZNIS/09, A61K38/00, A61K45/00, A61K48/00, A61P19/02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 GGAGAATTTTGGGCTGGCAGTGTTTATGGCGATGGCCAGGACGAGATGGGAGTCGTGGGT
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Mismatches:
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Novel polypeptide and DNA thereof.
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JP 2001069994-A/18.
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Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation
Genomics 71 (1), 40-52 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="MIAL"
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                                             Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                         Rendrorff, N.D.

Submitted (21-MAY-1999) Rendtorff N.D., Department of Medical Submitted (21-MAY-1999) Rendtorff N.D., Department of Medical Biochemistry and Genetics, Blagdamsver, Institute of Medical Biochemistry and Genetics, Relagdamsver, Institute of Medical Biochemistry and Genetics, Revised by author 03-AUG-1999

Related sequence: AJ252334 (Mus musculus mRNA)

Related sequences: AJ252334 to AJ252327 (genomic sequence).
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Rendtorff,N.D., Frodin,M., Attie-Bitach,T., Vekemans,M. and
AJ242552.1 GI:12619172
melanoma inhibitory activity like protein; Mial gene.
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S. Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Noshi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Noshi,K., and Tanaka,H.
Novel polypeptide and its DNA
Novel polypeptide and its DNA
Lakeda CHEMICAL INDUSTRIES LID; YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI CWUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA, HIDEYUKI TANAKA
OS MUS Sp. (mouse)
PN WO 0102564-A/18
PD 11-1AN-2000
PP 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T YOUN WOUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
C C12N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC
A61K38/17,
C A61K39/395,A61K49/16,A61P19/02,A61P19/08,A61K31/7088//(C12P21/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT 27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                            GATGTCAAGAAAGGGCAGCAGATCTATGTTTACTCCCAAGCTGGTAACAGAAAACGGAGCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                  TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
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        / Corganism="Mus sp."
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Novel polypeptide and its DNA.
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1 CATGGTGTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGGGGGATGAGGAGGTGTCTC
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Copyright (c) 1993 - 2003 Compugen Ltd
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December 29, 2003, 16:23:14; Search time 1138.05 Seconds (without alignments) 2349.180 Million cell updates/sec
nucleic search, using frame_plus_p2n model
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1 HGIFMDRLASKKLCADDECV.....RVYQEATKEVPTTDIDFFCE 110 22781392 seqs, 12152238056 residues 0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Title: Perfect score: Scoring table: Sequence:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

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29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|            | cription | Q570035 gil43b | Q564607 gil9h02 | 568498 gil09c0 | Q564134 gilld0 | 0569741 g1135f0 | 02064944 g12/g0 | 563768 min6cng | 1549 PR6115 | 55637 gi42g03 | 56932 gi73g09 | 5411 gi37b12 | 57343 gi88d | 32622 BY23262 | 36443 144645 | 179 gi32a0 | 3241 CH3#01 | 54 AL925854 | 776 | 785 gill | * 5      | 202   | 965 Mus mus | 43 zt02b05. | 892 AGENC | 401     | 15936 UI-E-EJO | ሳ ሶ       | 92734 AGENCOTE |           | 57778     | 94561 AGENCOU | 91767 K-EST | 56328 602739 | 5502 6027394 | 759 AV592759 | 297 nq68g01 | 5724 154861 | 8982 UI-R-DY | 9768 UI-R- | 915 tu05e09. | F439750 nad13c1 | 647928 BB64792 |
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| SUMMARIES  | ΩI       | 3 BQ57003      | 3 BQ56460       | 3 BQ568        | 3 BQ56413      | 3 BQ56974       | DC00494         | BO56376        | RR61154     | BQ56563       | BQ56693       | BQ56541      | BQ56734     | BY23262       | BE23644      | 3 BQ56517  | 3 BU74824   | AL925854    | 9 5 | 8/8950Mg | #35555 P | BO563 | 1796        | AA282143    | BU19589   | 4 CA4   | A BM71593      | 2 BM85647 | 3 BO89273      | 3 BQ68197 | 3 BU15777 | 3 BU19456     | 2 BM79176   | 2 BG76632    | 2 BG76550    |              | AA627297    | 0 BE6657    | 3 BQ20898    | 4 CAS0976  | AI620915     | 0 BF4397        | 0 BB64792      |
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|            | Score    | マ              | 4               | 547            | 4.             | # ₹             | * 4             | 14             | . 4         | 4             | N             | 4            | 0 1         | w,            | Φ,           | 41         | ٠           | 53          | 4,6 | η α      | 7 6      | . 99  | .99         | 54.         | 54.       | 253.5   |                |           | 23             | 53.       | 53.       | 53.           | 53.         | 23           | 53           | 22           | . 7         | 52          | 25           |            | 49           | 49              | 47.            |
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BQ570035
gil43bl0.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gil43bl0.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gil43bl0 5', mRNA sequence.
BQ570035.
BQ570035.1 GI:21473352
EST.
Mus musculus (house mouse)
Mus musculus (house mouse)
Bustryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 398) ALIGNMENTS RESULT 1 BQ570035 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE

> em\_gss\_phg:\* em\_gss\_vrl:\* gss1:\*

JOURNAL

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488 bp mRNA linear BST 19-JUN-2002 gil9h02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA ELOS 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                      127 TATACTATTCTCTGGCAAGACACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 GGAGAGTTTTGGGCTGGCAGTGTTTATGGTGACACCACCAGGATGAGATGGGAATTGTAGGT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       City, CA). The frequency distribution of the library is as follows: 72 of genes have 1 copy, 14.3% 2, 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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National Institute of Deafness and other Communication Disorders
Solf4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1569
Fax: 301-402-1765
                                                                                                                                                                                                                                                                                                                                                                                     TyrThrIleSerLeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPheIle
                                                                                                                                                                                                                                                                                                                   HisGlyIlePheMetAspArgLeuAlaSerLysLeuCysAlaAspAspGluCysVal
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Mismatches:
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Plate: 19 row: h column: 02
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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241 GGAGAGTTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGAATTGTAGGT

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41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla

US-10-019-455A-24 (1-110) x BQ564607 (1-488)

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/dev stage="most am remark"
/dev stage="post matal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After Killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
                                                                                                                                                    BUJ568498 514 bp mRNA linear EST 19-JUN-2002 gil09c02.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gil09c02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institute of Deafness and other Communication Disorders 50/4219 South Drive, NIH, Bethesda, MD 20892-8027, USA Tel: 301-402-1599 Fax: 301-402-1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: kacharbenidcd.nih.gov
Plate: 109 row: c column: 02
Seg primer: M13RP1 reverse primer (ABI).
101 ProThrThrAspIleAspPhePheCysGlu 110
                                                   361 ccaaccaccararreacrrcrrcrereaa 390
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/clone="gi109c02"
/sex="male and female"
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/strain="BALB/c"
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BQ568498.1 GI:21471815
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Structural Cell Biology
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Matches: Conservative: Mismatches: Indels:

1.59e-64 547.00 96.36% 90.00% 92.71%

> Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores:

BASE COUNT ORIGIN Pred. No.:

Score:

81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100

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(catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237612), Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcribed using Moloney murine leukemia virus reverse transcribed using Moloney murine leukemia virus reverse transcribed using Moloney murine leukemia virus reverse transcribed using Moloney murine leukemia virus reverse transcribed using Moloney murine leukemia virus reverse transcribed using Moloney murine leukemia virus reverse transcribed using Moloney murine leukemia virus reverse transcribed using Moloney murine leukemia virus reverse transcribed using synthesized with DNA polymerase and RNAse H. Complementary DNA was blunt ended with PFU DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp. respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with BcoR I and XRh O I. The phagemid was packaged with Gagapak III Gold and, upon titration on XI Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants: Stratagene's Exassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the restatance helper phage (CAGGAAAGCTARAGCTARAGCC) and control of the converse of the manufacturer. ESTS from the S' end of the converse milverse MI as instructed by the manufacturer. (AMA CAGGAAGCTARAGCC) at render the strander of the converse m
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239 GGAGAGTITTGGGCTGCCAGTGTTTATGGTGACCACCAGGATGAGATTGTAGGT 298 TyrThrIleSerLeuAlaSerAlaGInGluAspTyrAsnAlaProAspCysArgPheIle 40 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal Length: Matches: Conservative: Mismatches: Indels: US-10-019-455A-24 (1-110) x BQ568498 (1-514) 1.71e-64 547.00 96.36% 90.00% 92.71% Best Local Similarity: Percent Similarity: Alignment Scores: 21 Query Match: DB: Pred. No.: ORIGIN gg ð δ d 엄 8

147

BASE COUNT

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/dev stage="host natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/clone_lib="mouse Organ of Corti; Vector: pBluescript; The
organ of Corti; Occ) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
cigapack III Gold Cloning kit (catalog # 237212), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligod(d7) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker- primer and transcribed using
Noloney mutine leukemia virus reverse transcriptase
(MMLV-RT) and 5-methyl drTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with PFU DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
                                                                                                                                                                                                                                                 534 bp mRNA linear EST 19-JUN-2002 gilld01.91 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gilld01 5', mRNA sequence. BO564134 BQ564134.1 GI:21467451
299 TATTICCCCAGCAACTIGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGAGAGATC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 534)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kacharbanided.nih.gov
Plate: 11 row. d column: 01
Seq primer: M13RP1 reverse primer (ABI).
                                                                                          101 ProThrThrAspIleAspPhePheCysGlu 110
                                                                                                                                                              359 ccaaccaccarantraacricricricaa 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="gilld01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'sex="male and female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kachar, B.
                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
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AUTHORS
TITLE
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COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                   RESULT 4
BQ564134
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and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for CDNAs greater than 400bp and 1000 bp , respectively. The CDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ulof saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTS from the 5' end of the cDNA clones were generated with the universal ML3 reverse primer (CAGGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MU Tetrad thermal cyclers (MI Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have I copy, 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTS and 20% are unidentified."
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Conservative: Mismatches: Indels: Length: Matches: Gaps: 1.8e-64 547.00 96.36% 90.00% 92.71% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred. No.: ORIGIN

BASE COUNT

US-10-019-455A-24 (1-110) x BQ564134 (1-534)

81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspAgluCysVal 20 57 CATGGTGTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGCGGATGAGGAGTGTGTC 116 21 TyrThrileSerLeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPheile 40 9 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 101 ProThrThrAspIleAspPhePheCysGlu 110 357 CCAACCACGGATATTGACTTCTTCTGTGAA 386 g à ò g à g ò g à Ob ò

DEFINITION ACCESSION RESULT 5 BQ569741 VERSION KEYWORDS

gil35f01.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gil35f01.yl mus equence.
BQ569741
BQ569741.1 GI:21473058
BST.

EST analysis of gene expression in the mouse Organ of Corti at the Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1559
Fax: 301-402-1765 Email: kacharb@nidcd.nih.gov Plate: 135 row: f column: 01 Seg primer: M13RP1 reverse primer (ABI). organism="Mus musculus" /db\_xref="taxon:10090" /clone="gi135f01" Location/Qualifiers Mus musculus (house mouse) /mol\_type="mRNA" /strain="BALB/c" Eukaryota; Metazoa; Mammalia; Eutheria; (bases 1 to 560) .560 onset of hearing Unpublished Kachar, B. source SOURCE ORGANISM AUTHORS TITLE JOURNAL REFERENCE FEATURES

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BASE COUNT
                          FEATURES
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strength BigDye terminator sequencing chemistry (Applied Biosystems, Poster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have bits in GenBank, but do not have assigned function; 12% are uncharacterized EGTs and 20% are unidentified."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      608 bp mRNA linear EST 19-JUN-2002
gi27g09.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
EQ564944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 GGAGAGTTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATTGTAGGT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 TATTTCCCCAGCAACTTGGTGAAGGAGCAGCGTGTATAACCAGGAGGCCACCAAGGAGATC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 TATACTATTCTCTGGCAAGACACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 TyrThrileSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheile 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 HisGlyIlePheMetAspArgLeuAlaSerLysLeuCysAlaAspAspGluCysVal 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA Fer: 301-402-1599 Fex: 301-402-1565 Exai. 301-402-1765 Email: kacharb@nidcd.nih.gov Plate: 27 row: g column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 AsnValLysLysGlyGlnClnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly
                                                                                                                                                                                                                                                                                                                          Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1-560)
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Contact: Kachar,B.
Structural Cell Biology
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EST.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                        Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
DB:
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DEFINITION
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KEYWORDS
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library construction were carried out with the Uni-Zap XR glgapack III Catalog # 237211, Stratagene) and Uni-Zap XR glgapack III Catalog # 237211, Stratagene) and Uni-Zap XR glgapack III Catalog # 237211, Stratagene) and Uni-Zap XR glgapack III Catalog Glob Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 up mRNA was primed by the contains an XNo I site. First strand synthesis was primed with the linker- primer and transcribed using knoloney mutine leukemia virus reverse transcribed using sprimed with the linker- primer and transcribed using knoloney mutine leukemia virus reverse transcribed using sprimed with the linker- primer and transcribed using knoloney mutine leukemia virus reverse transcribed using sprimed with the Daylymerase and RNase H. Complementary DNA was blunt ended with PRO plymerase and RNase H. Complementary BCOR I adapters in the presence of ligase and digested with ECOR I adapters in the presence of ligase and digested with ECOR I adapters in the presence of ligase and digested virus respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with ECOM INION OF CAP COLOUMNS to enrich for CDNAS greater than 400bp and 1000 bp. respectively. The phagemid was packaged with digapak III Gold and, upon titration on XII Blue WRF. Calls. the vector which had been predigested with the restablance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the commin 95 werl of prowth plate. Plasmid DNA was purified from 200 ul of saturated outlure with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer ESTS from the 5' end of the CDNA clones were generated with the 5' end of the CDNA clones were generated anily sequencers using poots polymer (Applied Biosystems, Roster Cliv, CA). The frequency distribution of the CDNA carlsbad, CA) as instructed by the manufacturer of the DNA clones h
                                                                                                                                                                                                                                                                                                                                                              /dev stage= and remain |
/dev stage= and remain |
/dev stage= and remain |
/done lib= Mouse Organ of Corti cDNA pBluescript. |
/done lib= Mouse Organ of Corti cDNA pBluescript. The
/done corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from Pof; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fastrack kit
(catalog # K1993-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                608
Seq primer: M13RP1 reverse primer (ABI).
                                                                                                                            'organism="Mus musculus"
                                                                                                                                                                                                                                                   db_xref="taxon:10090"
clone="gi27g09"
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                                            ocation/Qualifiers
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Pred. No.:
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/strain=bandyc:
/clone="gil08g04"
/clone="gil08g04"
/sex="male and female"
/sex="male and female"
/dev stage="bost nata"
/clone lib="Mouse Organ of Corti; Vector: pBluescript"
/note="Corgan: Organ of Corti; Vector: pBluescript; The
/note="Corgan: Oct as fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P0; 60 from P7; 46 from P0; 18 from P0; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     630 bp mRNA linear EST 19-JUN-2002 gil08g04.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA BQ568471
                                                                                                                                                                                                                                                                                                                                                                              Kachar, B.
EST analysis of gene expression in the mouse Organ of Corti at the
                                                                                                                                                                                     67 CATGGTGTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGGGGGATGAGGAGTGTGTC 126
                                                                                                                                                                                                                                                                                    247 GGAGAGTTTTGGGCTGGCAGTGTTTATGGTGACACCACGAGGATGGGAATTGTAGGT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 TyrPheProArgAsnLeuVallysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 TATTTCCCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 630)
                                                                                                                                                               1 HisGlyIlePheMetAspArgLeuAlaSerLySLysLeuCysAlaAspAspGluCysVal 20
                                                                                                                                                                                                                                                    21 TyrThrileSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheile 40
                                                                                                                                                                                                                                                                                                                                                       41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
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V 400
Conservative:
Mismatches:
Indels:
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Fax: 301-402-1765
Email: kacharbenided.nih.gov
Plate: 108 row: g column: 04
Seg primer: M13RP1 reverse primer (ABI).
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/mol_type="mRNA"
/strain="BALB/c"
                                                                        Gaps:
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Structural Cell Biology
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US-10-019-455A-24 (1-110) x BQ568471 (1-630)

Conservative: Mismatches: Indels: Matches:

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was removed and opened in Leibowitz medium. The bony capaule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory population of the cochlea was chipped away. Stria vascularis and spiral ligament were removed and the sensory fortal RNA was extracted using the micro Fastrack kit related to the modicious of the manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237612), buth from Stratagene [La Jolla, CA UGA), according to manufacturer's instructions. Briefly: 1.5 up manufacturer's instructions. Briefly: 1.5 up manufacturer's instructions. Briefly: 1.5 up manufacturer's instructions. Briefly: 1.5 up manufacturer's instructions. Briefly: 1.5 up manufacturer's instructions. Briefly: 1.5 up manufacturer's instructions. Briefly: 1.5 up manufacturer's instructions. Briefly: 1.5 up manufacturer's instructions. Briefly: 1.5 up manufacturer's instructions. Briefly: 1.5 up manufacturer's instructions. Briefly: 1.5 up manufacturer's instructions. Briefly: 1.5 up manufacturer's instructions. Briefly: 1.5 up manufacturer's instructions. Briefly: 1.5 up manufacturer's briefly: 1.5 up manufacturer's instruction with Rougested with Brong with Rno I. The playment as sequentially size and digested with Brong and 1000 columns to enrich for conva sequentially size and digested with Sun and Contech Chroma Spin-1000 (Citontech, Papa Albo, 1000 citontech Chroma Spin-1000 (Citontech, Papa Albo, 1000 citontech Chroma Spin-1000 (Citontech, Papa Albo, 1000 citontech, Brong Albo, 1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 citontech Chroma Spin-1000 cito

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Bynchesized with DAM polymerase, incomparation by was blunt ended with Pfu DNA polymerase, ingated with Brown in day of the content and incompared over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin.1000 (Clontech, Palo Alto, CA) columns to enrich for CDNA greater than 400bp and 1000 bp , respectively. The CDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with Gigapak III Gold and, upon titration on XLI Blue MRF, cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert9(TW) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (GAGGAAACAGCTAAGAC) Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Terrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POS5 polymer (Applied Biosystems, Poster City, CA).

City, CA). The frequency distribution of the library is as follows: 72 of genes have I copy; 14.3% 2; 12% 310; 1.4% 11-50 and 0.18 51-50. As to gene function, 23% have micharacterized ESTs and 20% are unidentified."

By a micharacterized ESTs and 20% are unidentified."
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// Crganism="Mus musculus"
// Mol_type="mRNA"
// Strain="Bablo"
// Ab xacf="taxon:10090"
// Ab xacf="taxon:10090"
// Clone="gi06c09"
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// Corti (OC) was fine forti; Vector: pBluescript: The organ of Corti (OC) was fine fore periods a total of 386 oc as follows: 102 samples from post-natal (P) day 5; 72 from PD: 6 from PD: 4 from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD: Aff from PD:
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                        61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
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Structural Cell Biology
Mational Institute of Deafness and other Communication Disorders
Notional Institute of Deafness and other Communication Disorders
Notional Institute of Deafness and other Communication Disorders
Notional Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
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Kachar, B.

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BQ563768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
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Mismatches:
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Plate: 42 row: g column: 03
Seg primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                               Length:
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                              US-10-019-455A-24 (1-110) x BB611549 (1-696)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ565637.1 GI:21468954
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                                                                                                                                                                                                                                                   547.00
96.36%
90.00%
92.71%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 301-402-1599
Fax: 301-402-1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            onset of hearing
Unpublished
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                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                           Query Match:
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                                                                                                                                        BASE COUNT
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BQ565637
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Nonno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Shibata,K., Itoh,M., Carninci,P., Sugahara, Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y.

Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 696)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
D., Shibata,K., Shinagawa,A., Shiraki,T., Soqabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
W. Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapped discovery of new
genes. Genome Res. 10 (10), 1617-1630 (200)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
T-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
T-181-81-45-503-922
Fax: 81-45-503-9216
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BB611549 RIKEN full-length enriched, 13 days embryo head Mus musculus cDNA clone 3110083012 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                  RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
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/dev_stage="13 days_embryo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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Location/Qualifiers
                                                                                                                       Mus musculus (house mouse)
                                                                        BB611549.1 GI:15393547
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                                                                                                                                                  Mus musculus
                                                                                                                                                ORGANISM
            DEFINITION
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JOURNAL
                                                         ACCESSION
                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                     REFERENCE
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                                                                                                                              SOURCE
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EST 19-JUN-2002
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442g03.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone g142g03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 TATTICCCCAGCAACTIGGTGAAGGAGCAGCGGGTATACCAGGAGGCCACCAAGGAGTC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 CATGGTGTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTGTC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 GATGTCAAGAAAGGGCAGCAGTTCTTTTACTCCAAGCTGGTAACAGAAAACGGAGCT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST analysis of gene expression in the mouse Organ of Corti at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 TyrThrIleSerLeuAlaSerAlaGluAspTyrAsnAlaProAspCysArgPheIle
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1 HisGlyIlePheMetAspArgleuAlaSerLysLysLysLeuCysAlaAspAspGluCysVal 20

US-10-019-455A-24 (1-110) x BQ565637 (1-474)

21 TyrThrIleSerLeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPheIle

9

40

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library construction were carried out with the Uni-Zap XR octor kit (catalog # 23721, Stratagene) and Uni-Zap XR digapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manifacturer's instructions Briefly: 15 up mRNA was manifacturer's instructions Briefly: 15.0 up mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an XND I site: First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (WMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with PK pNA polymerase, ilgated with EcoR I adapters in the presence of ligase and digested with XND I. The CDNA was sequentially size fractionated over Pharmacia Size Septo0 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for CDNA spreater than 4000b and 1000 bp. respectively. The CDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and XiD I. The phagemid was packaged with diapapak III Gold and, upon titration on XiL Blue NRF cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference helper phage (catalogue # 211203) was adopted to resume plasmid DNA from the phages. Upon plating of the resumed library, individual cDNA clones were selected and grown in 96-well, 2 and growth plate. Plasmid DNA was purified from 200 ul of seturated culture with the Concert96 (TW) plasmid purification kit (Invitrogen, Carlebad, CA) as instructed by the manifacturer. Est form the 5 end of the CDNA clones were generated with the 5 end of the CDNA clones were generated with the 5 end of the CDNA clones were generated with the 5 end of the CDNA clones were generated with Waltham WA), and analyzed on 3700 automated ca
                                                                                                                /dev stage="Post natal day 5 to 13"
/dev stage="Post natal day 5 to 13"
/clone lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After Xilling animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
(catalog # K1593-OC; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
'db xref="taxon:10090"
                                              clone="gi42g03"
'sex="male and female"
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409 bp mRNA linear EST 19-JUN-2002 g173905.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA EQUEGE6932

DEFINITION

BQ566932

ACCESSION

VERSION KEYWORDS

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 409)

Kachar, B. onset of

AUTHORS TITLE

REFERENCE

hearing

Unpublished

JOURNAL

COMMENT

Mus musculus (house mouse)

Mus musculus

ORGANISM

BQ566932.1 GI:21470249

EST analysis of gene expression in the mouse Organ of Corti at the

Contact: Kachar, B. Structural Cell Biology National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Plate: 73 row: g column: 09 Seg primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

FEATURES

Tel: 301-402-1599 Fax: 301-402-1765 Email: kacharb@nidcd.nih.gov

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61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80

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/dev_stage="Post natal day 5 to 13"
/dowslib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti, Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
oC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After Killing animals by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit
                            organism="Mus musculus"
                                                                                                                                                                                                                               'sex="male and female"
                                                                                                                                            'db_xref="taxon:10090"
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                                                                                                           'strain="BALB/c"
                                                                                                                                                                                              /clone="gi73g09"
.. .409
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Conservative: Mismatches: Indels:

Best Local Similarity: Query Match: DB: Percent Similarity:

Length: Matches:

7.38e-64 542.00 95.45% 89.09% 91.86%

Alignment Scores: No.:

BASE COUNT ORIGIN g Ś

(catalog # K1593-02; Invitrogen, Carlebad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 23721, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Volla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney mutine leukemia virus reverse transcribates (MMLV-RT) and 5-methyl GCTP. The second synthesis was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Stor I. The CDNA was sequentially size fractionated over Pharmacia Size Seph400 (Clontech, Ppla Alto, CA) columns to enrich for CDNAs greater than 400b and 1000 by respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with digapak III Gold and upon titration on XID Blue MRF. cells, the yield of the phage library was estimated to be 11,00,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 21203) was adopted to resure plasmid DNA from the phages. Upon plating of the resure plasmid DNA from the phages. Upon plating of the created library individual cDNA clones were selected and grown in 96-well, 2 ml growth plate, Plasmid DNA were generated with the Concert96(TW) plasmid purification kit (Invitrogen, with the S end of the cDNA clones were generated with the universal MN1 reverse primer (GAGGAAAGGCTPARGACTPARGACC) as instructed by the manufacturer. ESTS from the S end of the conservent without parties of the phage in the prese generated with the universal MN1 reverse primer (GAGGAAAGGCTPARGACTPARGACC) and 25% and 25% and 25% and 25% and 25% and 25% and strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on My Tetrad thermal cycles (WM sesearch, Maltham, MA), and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have a copy; 14.3% 2; 12% 3-10; 1.4% 11.50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

Conservative: Mismatches: Matches: Length: Indels: 4.5e-61 521.00 94.55% 88.18% 88.31% Best Local Similarity: Query Match: Percent Similarity: Alignment Scores: Pred. No.: ORIGIN

BASE COUNT

201 CGATGTCAAGAAGGGCAGCAGATCTATGTTTACTCCAAGCTGGTAACAGAAAACGGAGC 260 141 CTATACTATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCCAGACTGTAGGTTCAT 200 9 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAla-AspAspGluCysVa 20 20 lTyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIl 40 eAsnValLysLysGlyGlnGlnTleTyrValTyrSerLysLeuValLysGluAsnGlyAl US-10-019-455A-24 (1-110) x BQ566932 (1-409) 40 g 8 g ઠે a

/Bright = Table | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Strain | Str library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR digapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer primer and synthesis was primed with the linker- primer and transcribtase with the linker- primer and transcribtase woloney murine leukemia virus reverse transcriptase with healthy dcrp. The second strand was when healthy dcrp. The second strand was when healthy dcrp. The second strand was 490 bp mRNA linear EST 19-JUN-2002 gi37b12.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi37b12 5', mRNA sequence. Synthesized with DNA polymerase and RNase H. Complementary but was blunt ended with Pfu DNA polymerase, ligated with DNA was blunt ended with Pfu DNA polymerase, ligated with Ecox I adapters in the presence of ligase and digested with Xho I. The CDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) 80 yTyrpheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVa 100 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 490) EST analysis of gene expression in the mouse Organ of Corti at the Structural Cell Biology National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA Tel: 301-402-1599 Email: kacharbenided.nih.gov Plate: 37 row: b column: 12 Seg primer: M13RP1 reverse primer (ABI). 100 lProThrThrAspileAspPhePheCys 109 381 cccaaccacacacrarraacricricia 408 /organism="Mus musculus" Location/Qualifiers Mus musculus (house mouse) 'mol\_type="mRNA" 'strain="BALB/c" BQ565411.1 GI:21468728 Contact: Kachar, B. .490 onset of hearing Unpublished Kachar, B. source DEFINITION ORGANISM ACCESSION JOURNAL REFERENCE KEYWORDS BQ565411 FEATURES TITLE /ERSION

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source
                 SOURCE
                                                                                                                                      AUTHORS TITLE
                                                                                                                                                                                                       JOURNAL
                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
columns to enrich for CDNAs greater than 400bp and 1000 by
respectively. The CDNA was then directionally ligated to
the Uni-ZAP XR vector, which had been predigested with
ECOR I and Xho I. The phagemid was packaged with Gigapak
III Gold and, upon titration on Xil Blue MRF cells, the
yield of the phage library was estimated to be 11.00,000
recombinants. Stratagene's ExAssist Interference
resistance helper phage (catalogue # 211203) was adopted
to rescue plasmid DNA from the phages. Upon plating of the
rescued library, individual cDNA clones were selected and
grown in 96-well, 2 ml growth plate. Plasmid DNA was
purified from 200 ul of saturated culture with the
concert96(TM) plasmid purification kit (Invitrogen,
carlsbad, CA) as instructed by the manufacturer. ESTF from
the 5' end of the CDNA clones were generated with the
universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25%
strength BigDye terminator sequencing chemistry (Applied
Blosystems, Foster City, CA). Sequencing reactions were
performed on MJ Tetrad thermal cyclers (MV Research,
Waltham, MA), and analyzed on 3700 automated capillary
sequencers using POS5 polymer (Applied Blosystems, Foster
City, CA). The frequency distribution of the library is
as follows: 72% of genes have I copy, 14.3% of
genes have hits in GenBank and have know function, 23%
have hits in GenBank. 1 the here
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g188d08.71 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA EQS67343.1 G1:21470660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 TAIACTAITTCTCTGGCAAGAGCACAGGAAATTACAATGCCCCAAACTGTAGGTTCATC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||||||||
TATTICCCACCACCAGGTGAAGGAGCAGGTGTATACCAGGAGGCCACCAAGGAGAIC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 TyrThrileSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPhelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 AsnVallysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAACCACGGATATTGACTTCTTCTGGGAA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
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515.00
94.55%
85.45%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . No. .
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ठ g ò g ò 셤 ò <del>Q</del> ð 윱 ઠે ACCESSION VERSION KEYWORDS

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/Gloue="glaboud"
// Gloue="glaboud"
// Gloue=lib="Mouse Organ of Corti CDNA pBluescript"
// Gloue=lib="Mouse Organ of Corti CDNA pBluescript; The
// Gloue=lib="Mouse Organ of Corti; Vector: pBluescript; The
// Gloue=lib="Mouse Organ of Corti; Vector: pBluescript; The
// Gram of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from ps: 18 from ps; 20 from pl);
// If from Pt: 66 from ps: After killing animals by
cervical dislocation followed by decapitation, the bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fastkrack kit
(catalog # Ki59:02: Invitrogen, Carlabad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out of the Uni-Zap XR
vector kit (catalog # 237611, Stratagene) and Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
vector kit (catalog # 237612), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis wis
primed with the linker- primer and transcribed using
Moloney murine leukemia virus reverse transcribed with
Moloney murine leukemia virus reverse transcribed with
EcoR I adapters in the presence of ligase and digested
vir Xho I. The CDNA was sequentially size fractionated
over Pharmacia Size Septo0 (Pharmacia, Uppsala, Sweden)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
columns to enrich for cDNA was requentially size fractionally ligated the biage library was setimated to be 11,100, on
respectively. The CDNA was restimated to be 11,100, on
recombinants. Stratagene's Exabasist Interference
over pharmacia size Septon (Pashasist Interference
over paramacia size Septon (Pashasist Interference
over paramacia size Septon (Pashasist Interference
over paramacia size Septon (Pashasist Interference)
rescombinants when 
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                                                                                                                                                                                                                                                               EST analysis of gene expression in the mouse Organ of Corti at the
Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                          onset of hearing
Outpublished
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1765
Fax: 301-402-1765
Email: kacharb@midcd.nih.gov
Plate: 88 row: d column: 08
Seq primer: M1871 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="qi88d08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .604
                                                                                                                                                                                                         Kachar, B.
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strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function, 23% have bits in GenBank, but do not have assigned function; 12% are uncharacterized EGTs and 20% are unidentified."
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Conservative: Mismatches: Length: Matches: Indels: Gaps: 3.08e-58 502.00 96.00% 92.00% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: BASE COUNT No.: ORIGIN

US-10-019-455A-24 (1-110) x BQ567343 (1-604)

| δ  | 11  | 11 LysLysLeuCysAlaAspAspGluCysValTyrThrIleSerLeuAlaSerAlaGlnGlu 30   |
|----|-----|----------------------------------------------------------------------|
| QQ | Ħ   | AAGAAGTTGTGTGCGGATGAGGAGGTGTGTCTATACTATTTCTCTGGCAAGAGCACAGGAAA 60    |
| Qy | 31  | 31 AspTyrAsnAlaProAspCysArgPhelleAsnValLysLysGlyGlnGlnIleTyrVal 50   |
| qq | 61  | GATTACAATGCCCCAGACTGTAGGTTCATCGATGTCAAGAAAGGGCAGCAGATCTATGTT 120     |
| ò  | 51  | 51 TyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrpAlaGlySerValTyrGly 70   |
| qq | 121 | TACTCCAAGCTGGTAACAGAAAACGGAGCTGGTTTTTGGGCTGGCATGTTTATGGT 180         |
| Qy | 71  | 71 AspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsnLeuValLySGluGln 90   |
| qq | 181 | 181 GACCACCAGGATGAGATGAGAATTGTAGGTTATTTCCCCAGCAACTTGGTGAAGGAGCAG 240 |
| δδ | 91  | 91 ArgValTyrGlnGluAlaThrLysGluValProThrThrAsplleAspPhePheCysGlu 110  |
| qa | 241 | CGTGTATACCAGGAGGCCACCAAGGAGATCCCCAACGGATATTGACTTCTTCTGTGAA 300       |
|    |     |                                                                      |

BY232622 BY232622 RIKEN full-length enriched, adult inner ear Mus musculus CDNA clone F930026J20 5', mRNA sequence. Mus musculus (house mouse) BY232622.1 GI:26413732 Mus musculus DEFINITION ORGANISM RESULT 14 BY232622 ACCESSION VERSION KEYWORDS REFERENCE

EST 10-DEC-2002

Cokazaki Y. Furuno, M. Kasukawa, T., Adachi, J., Bono, H. Kondo, S., Nikaido, I., Osato, M., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojòbori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Baisel, K. W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F. Forrest, A., Frazer, K.S., Gaasterland, T. A., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gaustincich, S., Hirokawa, M., Jackson, I.J., Kang, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Magashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Petrossky, W., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.G., Red, J.J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

Conservative: Mismatches:

2.22e-52 457.00 94.79% 88.54%

Best Local Similarity:

Query Match:

Percent Similarity:

Alignment Scores:

No.:

Indels:

US-10-019-455A-24 (1-110) x BY232622 (1-365)

Length: Matches:

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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIFEA integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Butsison of Experimental Animal Research in Riken contributed to
,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale, R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Wathanabe,Y., Walls,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Alzawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,M., Sasaki,K., Ich,M., Xagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,Y., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
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URL:http://genome.gac.riken.go.jp,
URL:http://genome.gac.riken.go.jp/
Alaxwa,K., Akimura,T., Arakning,P., Fukuda,S., Hirozane
A.T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
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Tissues were provided by Kirk W. Beisel (Boys Town National Tissues were provided by Kirk W. Beisel (Boys Town No. 1002) whose Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
T-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, B., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
and -minmatch 12 options.
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Bos taurus (cow)

Bos taurus (cow)

Bos taurus,

Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.
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      20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="pooled"
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Library made from pooled tissue from day 20 and day 40
TyrThrileSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheile
                                                                                                                     41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla
                                                                                                                                                                                GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly
                                                                                                                                                                                                                                                               TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAla 96
                                                                                                                                                                                                                                                                                                                               BE236443 527 bp mRNA linear 144645 MARC 4BOV Bos taurus cDNA 5', mRNA sequence. BE236443
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Blate: 54 row: C column: 18
Seq primer: ATTAGGTGACACATATAG.
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Alignment Scores: Pred. No.:

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                                                                                                                                                  1 HisGlyllePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 GlyTyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGlu
                                                                                                                                                                                                                              TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle
                                                                                                                                                                                                                                                                                                                                              209 AACGTTAAAAAGGACAGGATCTATGTTTACTCAAAGCTG-----
                                                                                                                                                                                                                                                                                                                                                                                  61 GlyGluPheTrpAlaGlySerValTyrGlyAsp---GlyGlnAspGluMetGlyValVal
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Mismatches:
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81.08%
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74.92%
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Best Local Similarity:
Query Match:
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Compugen Ltd.
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
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December 29, 2003, 16:10:49; Search time 132.647 Seconds (without alignments) 2238.558 Million cell updates/sec
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OM protein - nucleic search, using frame_plus_p2n model
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Maximum DB seq length: 200000000
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

| No.   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   National Process   Natio   |               |       | •}•            |        |      | SUMMARIES  |                    |
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| 2         590         100.0         384         22         AAM56341         Human MLP mocle           4         590         100.0         426         22         AAM56341         Human mand mode of mode           5         590         100.0         521         24         ABL68251         Human mand mode of mode           6         590         100.0         521         24         ABL68251         Human mand mode of mode           7         590         100.0         521         24         ABL68251         CDNA           10         590         100.0         931         22         AAH56342         Human mode           11         590         100.0         921         22         AAH56342         Human mode           11         590         100.0         921         22         AAH56342         Human mode           11         590         100.0         921         22         AAH56343         Human mode           12         547         92.7         34         22         AAF5908         Human mode           13         24         24         24         24         24         24           14         19.7         34                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |               | 590   | 00.            | 330    | , 71 | 907        | MLP                |
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| 4         590         100.0         426         22         AAH56341         Human argodyne reference           6         590         100.0         521         24         ABL55440         Human argodyne reference           7         590         100.0         521         24         ABL55440         Human argodyne reference           9         590         100.0         521         24         ABL5342         Human argodyne reference           10         590         100.0         223         2AR59083         Human argowth reference           11         590         100.0         122         AAR59083         Human argowth reference           12         547         92.7         344         22         AAF59084         Human argowth reference           13         547         92.7         346         22         AAF59089         Mouse MLP nucleon           14         547         92.7         347         22         AAF59089         Rat MLP nucleon           15         541         91.7         340         22         AAF59089         Rat MLP nucleon           16         541         91.7         340         22         AAF59089         Rat MLP nucleon <t< td=""><td>М</td><td>290</td><td>100.0</td><td></td><td></td><td>58</td><td>acoding</td></t<>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | М             | 290   | 100.0          |        |      | 58         | acoding            |
| 5         590         100.0         521         24         ABL68251         Human pR09873           7         590         100.0         521         24         ABL88251         Human pR09873           8         590         100.0         931         22         AAR53083         Human mcCoding browth received by the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of                                                                                                                                                                                                                                              | 4             | 590   | 100.0          |        |      | 34         | growth regu        |
| 6 590 100.0 521 24 ABL68251                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ഗ             | 290   | 0              | 521    |      | ABL95740   | angiogen           |
| 7 590 100.0 521 24 AAH56327 CDNA ENCASTOR THOSE OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF  | 9             | 590   | 0 (            | 521    |      | 325        | PRO9873            |
| 9         590         100.0         891         22         AAM583428         Human ESJ-Gering           10         590         100.0         891         22         AAF59083         Human Diowith region           11         590         100.0         923         22         AAF59080         Human Diowith region           13         547         92.7         336         22         AAF59080         Mouse MLP nucleor           14         547         92.7         347         22         AAF59099         Rat MLP nucleor           15         541         91.7         346         22         AAF59099         Rat MLP nucleor           16         541         91.7         346         22         AAF59099         Rat MLP nucleor           19         261         22         AAF59099         Rat MLP nucleor         Rat MLP nucleor           19         24         254.5         43.1         442         24         AAF59099           21         254.5         43.0         261         AAF59099         Rat MLP nucleor           22         254.5         43.1         442         24         AAF59099           23         254.5         43.1         442                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 7             | 590   | 000            | 521    |      | 357        | a)                 |
| 10   590   100.0   923   22   AAF59083   Human MLP nucleo   11   590   100.0   923   22   AAF59083   Human MLP nucleo   12   330   22   AAF59084   Mouse MLP nucleo   13   547   92.7   384   22   AAF59084   Mouse MLP nucleo   15   541   91.7   384   22   AAF59084   Mouse MLP nucleo   16   541   91.7   384   22   AAF59084   Mouse MLP nucleo   16   541   91.7   384   22   AAF59084   Mouse MLP nucleo   18   541   91.7   384   22   AAF59084   Rat MLP nucleo   18   541   91.7   384   22   AAF59099   Rat MLP nucleo   18   541   91.7   384   22   AAF59099   Rat MLP nucleo   18   541   91.7   384   22   AAF59099   Rat MLP nucleo   18   52   53   54   31   442   24   ABL63602   Breast cancer   18   52   53   54   31   442   24   ABL63602   Breast cancer   18   52   53   54   31   442   24   ABL63602   Breast cancer   18   52   53   54   31   442   24   ABL63602   Breast cancer   18   52   53   54   54   31   44   54   54   54   54   54   54   5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 00 (          | 060   | 9 8            | 7 5 6  |      | AAH98228   |                    |
| 10   590   100.0   923   22   AAF59183                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ο ,           | 290   | 90             | 168    |      | AAH26342   |                    |
| 11 597 100.0 1201 22 AAF59068 Mouse MLP nucleo                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 01.           | 590   | 96             | 923    |      | AAF59083   |                    |
| 12         547         92.7         330         22         AAF59080         Mouse MLP nucleo           14         547         92.7         384         22         AAF59084         Mouse MLP nucleo           15         541         91.7         310         22         AAF59089         Rat MLP nucleot           16         541         91.7         384         22         AAF59093         Rat MLP nucleot           17         40         261         22         AAF59093         Rat MLP nucleot           18         413         70.0         261         22         AAF59092         Rat MLP nucleot           20         254.5         43.1         442         24         ABL64012         Brat MLP nucleot           20         254.5         43.1         442         24         ABL64012         Brat MLP nucleot           21         253.5         43.0         459         22         ABL64012         Brat MLP nucleot           22         253.5         43.0         459         26         ABC64012         Brat MLP nucleot           23         253.5         43.0         459         26         ABC64012         Brat MLP nucleot           24         43.0 <td>1</td> <td>280</td> <td>8</td> <td></td> <td></td> <td>AAH26343</td> <td></td>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 1             | 280   | 8              |        |      | AAH26343   |                    |
| 13         547         92.7         384         22         AAFFS9068         Mouse MLP nucleon           16         541         91.7         384         22         AAFFS9084         Mouse MLP nucleon           16         541         91.7         384         22         AAFFS9088         Rat MLP nucleon           16         541         91.7         384         22         AAFFS9083         Rat MLP nucleon           19         413         70.0         261         22         AAFFS9083         Rat MLP nucleon           19         413         70.0         261         22         AAFS9092         Rat MLP nucleon           19         254.5         43.1         442         24         ABBC3302         Breast cancer rocal           20         253.5         43.0         459         16         AAQ84061         Sequence encodi           21         253.5         43.0         459         16         AAQ84061         Sequence encodi           22         253.5         43.0         459         16         AAQ84061         Melanoma inhibi           24         253.5         43.0         459         26         AAAD18732         Human prostate <t< td=""><td>12</td><td>547</td><td>92.7</td><td></td><td></td><td>AAF59080</td><td></td></t<>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 12            | 547   | 92.7           |        |      | AAF59080   |                    |
| 14         547         22         AAF59084         Mouse MLP nucleout           16         541         91.7         330         22         AAF59099         Rat MLP nucleout           17         384         22         AAF59099         Rat MLP nucleout           17         41         79.8         307         22         AAF59093         Rat MLP nucleout           19         413         70.0         261         22         AAF59093         Rat MLP nucleout           19         254.5         43.1         442         24         ABL64012         Breast cancer r           20         254.5         43.1         442         24         ABL64012         Breast cancer r           21         253.5         43.0         459         12         AAL70083         Melance encodi           22         253.5         43.0         459         22         AAD10832         Human prostate           24         253.5         43.0         459         22         AAD10833         Human prostate           25         253.5         43.0         459         2AAD19832         Human protein r           25         253.5         38.4         417         22         AAD99                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 13            | 547   | 92.7           |        |      | AAF59068   | MLP                |
| 5 541   91.7   330   22   AAF59099   Rat MLP nucleot   14                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 14            | 547   | 92.7           |        |      | AAF59084   |                    |
| 16   541   91.7   384   22   AAF59098   Rat MLP nucleot   18   413   70.0   261   22   AAF59092   Rat MLP nucleot   18   413   70.0   261   22   AAF59092   Rat MLP nucleot   19   254.5   43.1   442   24   ABL646012   Breast cancer   20   253.5   43.0   459   16   AA084061   Sequence encodi   22   253.5   43.0   459   16   AA084061   Sequence encodi   23   253.5   43.0   459   22   AA170083   Human antisense   25   253.5   43.0   459   22   AA170083   Human prostate   25   253.5   43.0   459   22   AA170083   Human prostate   25   253.5   43.0   459   22   AA447783   Sequence encodi   23   226.5   38.4   417   22   AA447783   Sequence encodi   24   23   226.5   38.2   23   24   24   24   24   24   24   2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 15            | 541   | 91.7           |        |      | AAF59099   | MLP                |
| 17         471         79.8         307         22         AAF599093         Rat MLP nucleot           19         254.5         43.1         442         24         ABE63602         Breast Cancer r           20         254.5         43.1         442         24         ABE64012         Breast Cancer r           21         253.5         43.0         459         16         AA084050         Becamber encoding           22         253.5         43.0         459         22         AA170083         Melanome inhibi           24         253.5         43.0         459         22         AAD18732         Human antisense           25         253.5         43.0         459         22         AAD18733         Human antisense           26         251.5         44.0         58         23         AAD18733         Human antisense           26         251.5         44.0         417         22         AAD19775         Human antisense           27         23.5         38.2         AA17         22         AA084052         Sequence encodin           28         251.5         44.0         AAD187783         Recombinan antisense         AC086060           28                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 16            | 541   | 91.7           |        |      | AAF59098   | MLP                |
| 18         413         70.0         261         22         ABL63602         Rat MLP nucleot           20         254.5         43.1         442         24         ABL63602         Breast cancer r           20         254.5         43.1         442         24         ABL64012         Breast cancer r           21         253.5         43.0         459         16         AA084050         Bequence encodi           22         253.5         43.0         459         16         AA010083         Human antisense           24         253.5         43.0         459         22         AAD18732         Human proceencodi           24         253.5         43.0         459         22         AAD18732         Human proceencodi           25         253.5         440         23         AAH47783         Sequence encodi           26         251.5         38.4         41         22         AAH99775         Human procent           29         226.5         38.2         1263         21         AA251245         Human TANGO 130           30         225.5         38.2         4409         23         ABV26499         Human TANGO 130           31                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 17            | 471   | 79.8           |        |      | AAF59093   | MLP                |
| 19 254.5 43.1 442 24 ABL633602 Breast cancer r 20 254.5 43.0 442 24 ABL643602 Breast cancer r 21 253.5 43.0 459 16 AAQ84061 Sequence encodi 22 253.5 43.0 459 16 AAQ84061 Sequence encodi 23 253.5 43.0 459 22 AAJ10833 Melanoma inhibit 24 253.5 43.0 459 22 AAJ10833 Human antisense encodi 25 253.5 43.0 459 22 AAJ18732 Human prostate 26 251.5 42.6 43.0 555 23 AA447783 Sequence encodi 27 231.5 39.2 581 16 AAQ84052 Human prostate encodi 28 226.5 38.4 417 22 AA447783 Sequence encodi 29 226.5 38.2 1230 24 AB079850 Human protein encodi 30 225.5 38.2 1230 24 AB079850 Human protein encodi 31 225.5 38.2 1263 21 AAZ51245 Human protein encodi 32 225.5 38.2 4409 23 ABV28649 Human protein encodi 32 225.5 38.2 4409 23 ABV28649 Human protein encodi 38 225.5 38.2 4409 23 ABV28648 Human protein encodi 38 225.5 38.2 4409 23 ABV28648 Human protein encodi 38 225.5 38.2 4409 23 ABV28648 Human protein encodi 38 225.5 38.2 4409 23 ABV28648 Human protein encodi 38 225.5 38.2 4409 23 ABV28648 Human protein encodi 38 225.5 38.2 4409 23 ABV28648 Human protein encodi 38 225.5 38.2 4409 23 ABV28648 Human protein encodi 38 225.5 38.2 4409 23 ABV28648 Human protein encodi 38 225.5 38.2 4409 23 ABV28648 Human protein encodi 38 225.5 38.2 4409 23 ABV28648 Human protein encodi 38 225.2 38.2 4409 23 ABV28648 Human protein encodi 38 225.2 38.2 4409 23 ABV28648 Human protein encodi 38 225.2 38.2 4409 23 ABV28648 Human protein encodi 38 225.2 38.2 4409 23 ABV28648 Human protein encodi 38 2037 25 ABX89848 Human protein encodi 38 2037 25 ABX89848 Human protein 42 217 36.8 2037 25 ABX89839 Human protein 43 217 36.8 2037 25 ABX89839 Human protein 44 217 36.8 2037 25 ABX89839 Human protein 45 217 36.8 2037 25 ABX89839 Human protein 45 217 36.8 2037 25 ABX89839 Human protein 45 217 36.8 2037 25 ABX89839 Human protein 45 217 36.8 2037 25 ABX898339 Human protein 45 217 36.8 2037 25 ABX898339 Human protein 45 217 36.8 2037 25 ABX898339 Human protein 45 217 36.8 2037 25 ABX898339 Human protein 45 217 36.8 2037 25 ABX898339 Human protein 45 217 36.8 2037 25 ABX89 | 18            | 413   | 70.0           |        |      | AAF59092   | P nucleotid        |
| 20 254.5 43.1 442 24 ABL64012 Breast cancer r 253.5 43.0 330 16 AAQ84050 Sequence encodid 22 253.5 43.0 459 16 AAQ84050 Melanome inhibit 24 253.5 43.0 459 22 AAJ10083 Melanome inhibit 24 253.5 43.0 459 22 AAJ10083 Human antisense 25 253.5 43.0 555 22 AAJ1083 Human antisense 26 251.5 42.6 43.3 22 AAJ17083 Recombinant human 22 251.5 42.6 43.3 22 AAJ19775 Human protein encodid 28 226.5 38.4 417 22 AAJ19775 Human protein encodid 39 225.5 38.2 1230 24 ABQ79849 Human TANGO 130 31 225.5 38.2 4409 23 ABV29675 Human TANGO 130 32 225.5 38.2 4409 23 ABV28678 Human prostate 36 225.5 38.2 4409 23 ABV28678 Human prostate 36 225.5 38.2 4409 23 ABV28678 Human prostate 37 225.5 38.2 4409 23 ABV28678 Human prostate 38 225.5 38.2 4409 23 ABV28678 Human prostate 38 225.5 38.2 4409 23 ABV28678 Human prostate 39 225.5 38.2 4409 23 ABV28678 Human prostate 39 225.5 38.2 4409 23 ABV28678 Human prostate 39 225.5 38.2 4409 23 ABV28678 Human prostate 38 225.5 38.2 4409 23 ABV28678 Human prostate 39 225.5 38.2 4409 23 ABV28678 Human prostate 39 225.5 38.2 4409 23 ABV28678 Human prostate 40 217 36.8 2037 25 AASS6520 Human prostate 36 225.5 38.2 225.5 38.2 4409 23 ABV28648 Human prostate 38 225.5 38.2 4409 23 ABV28639 Human prostate 38 2037 25 AASS6520 Human prostate 39 217 36.8 2037 25 AASS69950 Human problem secreted/4 217 36.8 2037 25 ABX89848 Human problem secreted/4 217 36.8 2037 25 ABX89839 Human problem oolynman secreted/4 217 36.8 2037 25 ABX898039 Human problem oolynman problem 217 36.8 2037 25 ABX898039 Human problem 2004yn 36.8 2037 25 ABX898039 Human problem 2004yn 36.9 2037 25 ABX898039 Human problem 2004yn 36.9 2037 25 ABX898039 Human problem 2004yn 36.9 2037 25 ABX898039 Human problem 2004yn 36.9 2037 25 ABX898039 Human problem 2004yn 36.9 2037 25 ABX898039 Human problem 2004yn 36.9 2037 25 ABX898039 Human problem 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn 2004yn | Н             | 254.5 | 43.1           |        |      | ABL63602   |                    |
| 21 253.5 43.0 330 16 AAQ0840661 Sequence encodi. 2 2 253.5 43.0 459 16 AAQ084065 Sequence encodi. 2 2 253.5 43.0 459 22 AAJ17083 Human antisense encodi. 2 253.5 43.0 459 22 AAJ18732 Human antisense encodi. 2 253.5 43.0 459 22 AAJ18732 Human antisense encodi. 2 251.5 42.6 433 22 AAV18733 Recombinant human prostate 2 251.5 39.2 AAV187783 Sequence encodi. 2 225.5 38.4 417 22 AAA99775 Human protein encodi. 3 225.5 38.2 1263 24 AAQ34050 Human TANGO 130 31 225.5 38.2 4409 23 ABV23751 Human prostate 3 225.5 38.2 4409 23 ABV23751 Human prostate 4 409 23 ABV23751 Human prostate 4 409 23 ABV23751 Human prostate 4 409 23 ABV2625 Human prostate 4 409 23 ABV2625 Human prostate 4 4 2 25.5 38.2 4409 23 ABV2625 Human prostate 4 4 2 217 36.8 2037 25 AAS46220 Human protein 8 225.5 38.2 4409 23 ABV2625 Human prostate 4 4 2 217 36.8 2037 25 AAS46220 Human protein 8 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 0             | 254.5 | 43.1           |        |      | ABL64012   | Breast cancer rela |
| 22 253.5 43.0 459 16 AAQ084050 Sequence encoding a constraint of 459 22 AAJ084050 Sequence encoding a constraint of 459 22 AAJ0833 Melanoma inhibits a constraint of 459 22 AAJ083229 Human prostate becombinant hum constraint of 231.5 43.0 459 22 AAAH47783 Recombinant hum constraint of 231.5 38.4 417 22 AAAH47783 Sequence encoding a constraint of 231.5 38.4 417 22 AAAH99775 Human protein of 225.5 38.2 1230 24 ABQ79850 Human converse of 231 225.5 38.2 1263 21 AAZ21245 Human protein of 225.5 38.2 1263 21 AAZ31245 Human protein of 225.5 38.2 4409 23 ABV28678 Human protein of 225.5 38.2 4409 23 ABV28678 Human protein of 225.5 38.2 4409 23 ABV28678 Human protein of 225.5 38.2 4409 23 ABV28678 Human protein of 225.5 38.2 4409 23 ABV28678 Human protein of 225.5 38.2 4409 23 ABV28678 Human protein of 225.5 38.2 4409 23 ABV28678 Human protein of 225.5 38.2 4409 23 ABV28678 Human protein of 40 217 36.8 2037 25 AAS4620 Human converted of 225.5 38.2 225.5 38.2 4409 23 ABV28648 Human converted of 225.5 38.2 225.5 38.2 4409 23 ABV28648 Human protein of 42 225.5 4409 23 ABV28648 Human protein of 42 225.5 4409 23 ABV28648 Human protein of 42 225.5 4409 23 ABV28648 Human protein of 42 225.5 ABV28648 Human protein of 42 225.5 ABV28648 Human protein of 42 225.5 ABV28648 Human protein of 42 225.5 ABV28683 Human protein of 42 225.5 ABV286823 Human protein of 42 225.5 ABV28823 Human protein of 43 217 36.8 2037 25 ABV286823 Human protein of 43 217 36.8 2037 25 ABV28823 Human protein of 45 217 36.8 2037 25 ABV28823 Human protein of 45 217 36.8 2037 25 ABV28823 Human protein of 45 217 36.8 2037 25 ABV28823 Human protein of 45 217 36.8 2037 25 ABV28823 Human protein of 45 217 36.8 2037 25 ABV28823 Human protein of 45 217 36.8 2037 25 ABV28823 Human protein of 45 217 36.8 2037 25 ABV28823 Human protein of 45 217 36.8 2037 25 ABV28823 Human protein of 45 217 36.8 2037 25 ABV28823 Human protein of 45 217 36.8 2037 25 ABV28823 Human protein of 45 217 36.8 2037 25 ABV28823 Human Protein of 45 217 36.8 2037 25 ABV28823 Human Protein of 45 217 3 | 21            | 253.5 | 43.0           |        |      | AAQ84061   |                    |
| 23 253.5 43.0 459 22 AAD170083 Melanoma inhibit 24 253.5 43.0 459 22 AAD170083 Human antisense 25 253.5 43.0 555 22 AAD170083 Human prostate 25 253.5 43.0 555 22 AAD170229 Human prostate 26 251.5 42.6 433 22 AAD17022 Human prostate accombinant hum 27 231.5 39.2 84.17 22 AAD24052 Human protein celected 29 225.5 38.2 1230 24 AAD27955 Human cDNA encode 30 225.5 38.2 1263 24 AAD79849 Human TANGO 130 31 225.5 38.2 1263 24 AAD79849 Human TANGO 130 32 225.5 38.2 4409 23 ABV28678 Human prostate 34 225.5 38.2 4409 23 ABV28678 Human prostate 35 225.5 38.2 4409 23 ABV28678 Human prostate 35 225.5 38.2 4409 23 ABV28678 Human prostate 36 225.5 38.2 4409 23 ABV28678 Human prostate 36 225.5 38.2 4409 23 ABV28678 Human prostate 36 225.5 38.2 4409 23 ABV28678 Human prostate 36 225.5 38.2 4409 23 ABV28678 Human prostate 36 225.5 38.2 4409 23 ABV28678 Human prostate 36 225.5 38.2 4409 23 ABV28678 Human prostate 40 217 36.8 2037 25 AAS4620 Human protoin accented 41 217 36.8 2037 25 ABV2848 Human protoin accented 42 217 36.8 2037 25 ABV28639 Human protoin Auman secreted 43 217 36.8 2037 25 ABV28039 Human protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman protoin Auman Protoin Auman Protoin Auman Protoin Auman Protoin Auman Protoin Auman Protoin Auman Protoin Auman Protoin Auman Protoin Auman Protoin Auman Protoin Auman Protoin Auman Protoin Auman Auman Auman Auman Auman Auman Auman Auman Auman Auman Auman Auman Auman Auman | 22            | 253.5 | 43.0           |        |      | AAQ84050   |                    |
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| 225.5 38.4 417 22 AAM99475 Human protein edge discording a 225.5 38.4 417 22 AAM99775 Human protein e a 225.5 38.2 1230 24 AB079850 Human TANGO 130 1 225.5 38.2 1263 24 AB079849 Human TANGO 130 2 225.5 38.2 1263 24 AB079849 Human TANGO 130 1 225.5 38.2 4409 23 ABV23625 Human prostate Human prostate 4 225.5 38.2 4409 23 ABV23625 Human prostate Human prostate 5 225.5 38.2 4409 23 ABV29625 Human prostate Human prostate 6 225.5 38.2 4409 23 ABV29625 Human prostate 6 225.5 38.2 4409 23 ABV29625 Human prostate 6 225.5 38.2 4409 23 ABV29625 Human prostate 6 225.5 38.2 4409 23 ABV29625 Human prostate 6 225.5 38.2 5037 25 AAS46220 Human DNA encod 7 225.5 38.2 2037 25 AAS49850 Human DNA encod 7 227 36.8 2037 25 ABX98950 Human PRO20180                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 56            | 251.5 | 42.6           |        |      | AAH47783   | Recombinant human  |
| 8 226.5 38.4 417 22 AAH99775 . Human protein e                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 27            | 231.5 | 39.2           |        |      | AAQ84052   |                    |
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| 2 225.5 38.2 1263 24 ABQ79849 Human TANGO 130 225.5 38.2 4409 23 ABV21035 Human prostate Human prostate 4 225.5 38.2 4409 23 ABV21035 Human prostate Human prostate 5 225.5 38.2 4409 23 ABV22678 Human prostate Human prostate 6 225.5 38.2 4409 23 ABV22678 Human prostate Human prostate 7 225.5 38.2 5724 24 ABQ79851 Human TANGO 130 8 225.5 38.2 5724 24 ABQ79851 Human TANGO 130 217 36.8 2037 25 ABX98448 Human PRO20088 12 217 36.8 2037 25 ABX98450 Novel human secreted/3 217 36.8 2037 25 ABX98950 Human properties 60/21/2 217 36.8 2037 25 ABX98950 Human properties 60/21/2 217 36.8 2037 25 ABX98950 Human properties 60/21/2 217 36.8 2037 25 ABX98950 Human properties 60/21/2 217 36.8 2037 25 ABX98950 Human properties 60/21/2 217 36.8 2037 25 ABX98923 Human propolyn                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 31            | 225.5 | 38.2           |        |      | AAZ51245   | TANGO              |
| 3         225.5         38.2         4409         23         ABV21035         Human prostate           4         225.5         38.2         4409         23         ABV23551         Human prostate           5         225.5         38.2         4409         23         ABV29625         Human prostate           7         225.5         38.2         4409         23         ABV29625         Human prostate           7         225.5         38.2         4409         23         ABV29625         Human prostate           8         225.5         38.2         4409         48079851         Human prostate           9         217         36.8         2037         22         AAS46220         Human DNA encod           0         217         36.8         2037         25         ABX98448         Human CDNA encod           1         217         36.8         2037         25         ABX98448         Human secreted           2         217         36.8         2037         25         ABX98950         Human secreted           4         217         36.8         2037         25         ABX98039         Human PRO Polyn           4         217                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 32            | 225.5 | 38.2           |        |      | ABQ79849   | TANGO              |
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| 5 225.5         38.2         4409         23 ANY26878         Human prostate           6 225.5         38.2         4409         23 ANY26825         Human prostate           7 225.5         38.2         5724         48079852         Human TANGO 130           8 225.5         38.2         5724         22 AAS46220         Human TANGO 130           9 217         36.8         2037         22 AAS46220         Human DNA encod           1 217         36.8         2037         25 AXS98448         Human PRO20088           2 217         36.8         2037         25 AXS98950         Novel human secreted/           3 217         36.8         2037         25 AXS98950         Human pRO POLyn           4 217         36.8         2037         25 AXS98823         Human PRO POLyn           5 217         36.8         2037         25 AXS78823         Human PRO POLyn                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 34            | 225.5 | 38.2           |        |      | ABV23751   | prostate           |
| 6 225.5 38.2 4409 23 ABV29625 Human prostate 7 225.5 38.2 8724 24 ABQ79852 Human TANGO 130 8 225.5 38.2 8121 24 ABQ79851 Human TANGO 130 9 217 36.8 2037 22 AAS46220 Human PRO20808 1 217 36.8 2037 25 ABX98448 Human PRO20808 1 217 36.8 2037 25 ABX9850 Novel human secreted/ 2 217 36.8 2037 25 ABX9850 Human secreted/ 4 217 36.8 2037 25 ABX98823 Human PRO Polyn 5 217 36.8 2037 25 ABX98823 Human PRO Polyn 6 217 36.8 2037 25 ABX98823 Human PRO Polyn                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 35            | 225.5 | 38.2           |        |      | ABV26878   | prostate           |
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| 8 225.5 38.2 8121 24 ABQ79851 Human TANG<br>9 217 36.8 2037 22 AAS46220 Human DNA<br>1 217 36.8 2037 25 ACA57978 Human PROZ<br>1 217 36.8 2037 25 AEX98468 Human CDNA<br>2 217 36.8 2037 25 AEX98950 Novel human 3 217 36.8 2037 25 AEX98939 Human CDNA<br>3 217 36.8 2037 25 AEX98039 Human PRO<br>4 217 36.8 2037 25 AEX98039 Human PRO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 37            | 225.5 | 38.2           |        |      | ABQ79852   | TANGO 130          |
| 9 217 36.8 2037 22 AAS46220 Human DNA 21.7 36.8 2037 25 ACA57978 Human PRO2 21.7 36.8 2037 25 ACA57978 Human CDNA 22.7 36.8 2037 25 ABX98950 Novel human 3.2 21.7 36.8 2037 25 ACA65995 Human secr. 21.7 36.8 2037 25 ACA65995 Human secr. 21.7 36.8 2037 25 ABX98039 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 Human PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HUMAN PRO 2037 25 ABX78823 HU | 38            | 225.5 | 38.2           |        |      | ABQ79851   | TANGO 130          |
| 0 217 36.8 2037 25 ACA57978 Human CDNA<br>2 217 36.8 2037 25 AEX98448 Human CDNA<br>2 217 36.8 2037 25 AEX98950 Novel human<br>3 217 36.8 2037 25 ACA05995 Human secr<br>4 217 36.8 2037 25 AEX88039 Human PRO<br>5 217 36.8 2037 25 AEX78823 Human PRO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 39            | 217   | 36.8           |        |      | AAS46220   | DNA                |
| 1 217 36.8 2037 25 ABX98448 Human CDNA 2 217 36.8 2037 25 ABX98950 Novel human 3 217 36.8 2037 25 ACA05995 Human Secretary 2 2037 25 ABX98039 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 217 36.8 2037 25 ABX78823 Human PRO pt 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 40            | 217   | 36.8           |        | N    | 7          | PRO20              |
| 2 217 36.8 2037 25 ABX98950 Novel<br>3 217 36.8 2037 25 ACA05995 Human<br>4 217 36.8 2037 25 ABX98833 Human<br>5 217 36.8 2037 25 ABX78823 Human                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 41            | 217   | 36.8           |        | 0    | 4          | _                  |
| 3 217 36.8 2037 25 ACA05995 Human<br>4 217 36.8 2037 25 ABX98039 Human<br>5 217 36.8 2037 25 ABX78823 Human                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 42            | 217   | 36.8           |        | N    | 2          | Novel human secret |
| 4 217 36.8 2037 25 ABX98039 Human PRO 5 217 36.8 2037 25 ABX78823 Human PRO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 43            | 217   | 9              |        | N    | 59         | secr               |
| 5 217 36.8 2037 25 ABX78823 Human PRO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 44            | 217   | 9              |        | (1   | 8          | PRO                |
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ALIGNMENTS

MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter; inhibitor; ds. Human MLP nucleotide sequence SEQ ID NO:23. AAF59079 standard; DNA; 330 BP. (first entry) 23-APR-2001 AAF59079; RESULT 1 AAF59079 

Homo sapiens.

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                                                                                                                                                                                                           Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TATACTATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATT
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590.00
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Best Local Similarity:
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WO200102564-A1
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81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 CATGGAATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTC 114
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                                                                          MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter; inhibitor; ds.
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Matches:
Conservative:
Mismatches:
Indels:
                                             Human MLP nucleotide sequence SEQ ID NO:4.
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P-PSDB; AAB69123.
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The invention relates to an isolated novel secreted polypeptide (I) and polymucleotide (II). (I) and (II) are useful for treating cancer, autoimmune diseases, wound healing disorder, infections, haematopoietic disorders, inflammatory disorders, infections, haematopoietic psychiatric diseases, cardiovascular diseases, respiratory diseases, creat diseases, anormalities and disorders caused by abnormal expression, production, function and/or metabolism of the genes, as vaccines for inducing immunological response in a mammal, and in screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. The polypeptides can be used as immunogens to produce antibodies immunospecific for the polypeptides, as immunogens to produce antibodies immunospecific for the polypeptides, as immunogens and diagnostic reagents, in chromosome localisation studies, and in tissue expression studies. The present sequence represents the coding sequence of novel human secreted protein #12.
295 TATTTCCCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTT 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted protein; cytostatic; immunosuppressive; vulnerary; vaccine; antiinflammatory; neuroprotective; nephrotropic; cardiovascular; human, cancer; autoimmune disease; wound healing disorder; infection; haematopoietic disorder; inflammatory disorder; infection; neurological disease; psychiatric disease; cardiovascular disease; respiratory disease; renal; gastrointestinal; ss.
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/product= "Human secreted protein"
                                                                                                                                                                 CCCACCACGGATATTGACTTCTTCTGCGAG 384
                                                                                                                          ProThrThrAspileAspPhePheCysGlu 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding novel secreted protein #12.
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                                                                                                                                                                                                                                                                                                                                                                        AAS17583 standard; cDNA; 387 BP
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24-APR-2000; 2000US-199417P.
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234
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                                                                                                                                                       115 TATACTATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATT 174
                                                                                                                                                                                                                                                                                                                                          294
                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                             21 TyrThrileSerLeualaSerAlaGlnGluāspTyrAsnālaProAspCysArgPheIle 40
                                                                                                                                                                                                                                                     41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
                                                                                                                                       1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system
                                                                                                                                                                                                                                                                                                                                                                                      295 TATITICCCCAGGAACTIGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTT
                                                                                                                                                                                                                                                                               175 AACGTTAAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCT
                                                                                                                                                                                                                                                                                                               GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly
                                                                                                                                                                                                                                                                                                                                         235 GGAGAATTITIGGGCTGCCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth regulatory-like polypeptide; human, cartilage; melanoma;
neuroectodermal tumour, glioma; cancer; gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human growth regulatory-like polypeptide clone 16372272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT,
         387
1110
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                                     Conservative:
                                                  Mismatches:
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                                                                  Indels:
                                                                                                             US-10-019-455A-24 (1-110) x AAS17583 (1-387)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH26341 standard; cDNA; 426 BP
       2.44e-75
590.00
100.00$
100.00$
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02-MAY-2000; 2000US-0563786.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483233/52.
                                                      Best Local Similarity:
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                                       Percent Similarity:
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Alignment Scores:
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                                                                    Query Match:
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antiarteriosclerotic; gene; ss.

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TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20
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The present sequence is that of Hyseq clone identification number 16372225, which was obtained from a human thymus cDNA library using standard PCR with primers specific for vector sequences flanking the inserts, sequencing by hybridisation sequence some passembly of a full-length expressed sequence tag was used in the assembly of a full-length cDNA sequence (see AAH5634) encoding a novel human growth could be some protein family as growth regulatory proteins, pelongs to the same protein family as growth regulatory proteins, growth factors, human melanoma derived growth regulatory protein precursor (64% similarity and 45% identity over 111 amino acids) or melanoma inhibitory activity, cattle cartilage-derived retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid-sensitive proteins. GTLP polypeptides and polymucleotides of the invention can be used in the prophylaxis, treatment (including gene therapy) cartilage development and maintenance, inhibition of melanoma cell growth and tumours, including neuroectodermal tumours such as glomas. The polymucleotides can also be used to design probes and primers for chromosome and gene mapping, in the recombinant production of protein, in the generation of antisense, ribozyme and peptide-nucleic acid molecules, and to produce transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla
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Mismatches:
Indels:
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Matches:
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Best Local Similarity:
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Paoni NF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillan KJ, Marsters SA, Pan J, Williams PM, Wood WI, Ye W;
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2001US-0767609.
2001US-0796498.
2001WO-US06520.
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2001US-0802706.
2001US-0808689.
2001US-0816744.
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2001US-0854208.
2001US-0854280.
2001US-0866028.
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2000US-220664P.
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                                                          09-JUL-2001; 2001WO-US21735
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2001US-0870574
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                                                                                                                                                                                                                                                                                                                      GERBER H.
GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PAN J.
PAN J.
PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferrara N,
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FERRARA N.
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                            WO200208284-A2
                                                                                                                                          15-SEP-2000;
18-SEP-2000;
18-SEP-2000;
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20-DEC-2000;
22-JAN-2001;
               Homo sapiens.
                                                                                        25-JUL-2000;
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                                                                                                                                    SEP-2000;
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08-NOV-2000;
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22-MAR-2001;
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                                           31-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WILL/)
(WOOD/)
                                                                                                                                                                                                                                                                                                                                                                (GETH )
(BAKE/)
                                                                                                                                                                                                                                                                                                                                                                                                                          (HILL/)
(MARS/)
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac atherosciepty, trauma, cancer, age-related macular degeneration, atheroscieptis, hypertension, arterial restencis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 GGAGAATTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGAGTCGTGGGT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                              healing. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                               521
110
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Matches:
Conservative:
Mismatches:
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                                                                               Claim 1; Fig 359; 567pp; English.
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Best Local Similarity:
Query Match:
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Pred. No.:
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Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnezary; antiatteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; theumatoid arthritis; mycardial infarction; thromopophebitis; wound healing; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
                                                                                                                                                Human PRO9873 cDNA sequence SEQ ID NO:359.
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WO200200690-A2

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2000WO-US34956.
2001US-0767699.
2001US-076650.
2001WO-US06666.
2001US-0802706.
2001US-0802706.
2001US-0816744.
2001US-082836.
2001US-082836.
2001US-082836.
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                                                                 2000US-230978P.
2000US-0664610.
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2000WO-US32678.
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2000WO-US23328.
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                                             02-AUG-2000;
                                                   17-AUG-2000;
                                                             24-AUG-2000;
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                                                                                                 10-NOV-2000;
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                                                                                                          20-DEC-2000;
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09-MAR-2001;
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                                   25-JUL-2000;
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                               25-JUL-2000;
03-JAN-2002
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(GETH ) GENENTECH INC.

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errara N, Gerber H, Gerritsen ME, Goddard A; Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF; Watanabe CK, Williams PM, Wood WI, Ye W; Baker KP, Ferrara N, Godowski PJ, Stephan JF,

WPI; 2002-090516/12. P-PSDB; ABB84996 One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal

Claim 2; Fig 359; 565pp; English.

ABBBS5003. The PRO proteins and polymucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polymucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polymucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABLB8259 to ABLB8267 represent primers and probes used in the exemplification of the present invention. ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to

Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;

Alignment Scores:

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                                                                                                         CATGGAATATTTATGGACCGTCTACCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTC
                                                                                                                                    TyrThr11eSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPhe11e
                                                                                                                                                  AsnvalLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla
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                                                                                                                                                                                                                      GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly
                                                                                                                                                                                                                                    Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha; gene; ss.
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 Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                         ProThrThrAspleAspPhePheCysGlu 110
                                                                                                                                                                                                                                                                                                                    CCCACCACGGATATTGACTTCTTCTGCGAG 421
                                                                         (1-521)
                                                                         US-10-019-455A-24 (1-110) x ABL88251
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25-JUL-2000; 2000US-220585P.
25-JUL-2000; 2000US-220665P.
25-JUL-2000; 2000US-220664P.
25-JUL-2000; 2000US-220664P.
25-JUL-2000; 2000US-220664P.
25-JUL-2000; 2000US-220664P.
25-JUL-2000; 2000US-220666P.
26-JUL-2000; 2000US-220866P.
28-JUL-2000; 2000WO-US2322.
15-SEP-2000; 2000WO-US23328.
15-SEP-2000; 2000WO-US23328.
16-SEP-2000; 2000WO-US23328.
16-SEP-2000; 2000WO-US235678.
20-DEC-2000; 2000WO-US235678.
                                                                                                                                                                                                                                                                                                                                                                     ABK33571 standard; cDNA; 521
3.71e-75
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                     Percent Similarity:
Best Local Similarity:
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The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encoding PRO polypeptides.

Encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for treating a PRO related disorder. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in perioyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating to inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABK31356-ABK33657 represent human process.
                                                                                                                                                                                                          One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
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                                                                                                  Godowski PJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 AACGTTAAAAAAGGGCAGCAGATCTATGTGTACTCAAAGCTGGTAAAAGAAAATGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly
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                                                                                                  Goddard A, Goucard TF Watanabe CK,
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                                                                                                               Gerritsen ME, Goddard Smith V, Stephan JF,
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Matches:
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                                                                                                                                                                                                                                                                                       Claim 2; Figure 71; 359pp; English.
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20-DEC-2000; 2000MO-US34956.
28-FEB-2001; 2001MO-US06520.
10-MAY-2001; 2001US-0854280.
25-MAX-2001; 2001WO-US17092.
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C, Gurney AL,
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Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                              Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; BST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                  Chen R, Asundi V;
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Matches:
Conservative:
Mismatches:
                                                                                           Human EST-derived coding sequence SEQ ID NO: 85.
                                                                                                                                                                                                                                                                                                                                                                                               , Liu C, Zhou P, Qian XB, Wang Z,
Drmanac RA, Zhang J, Werhman T;
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          AAH98228 standard; cDNA; 891 BP.
                                                                                                                                                                                                                                                                                                  25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                         25-JAN-2001; 2001WO-US02687.
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAM23569
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                                                                                                                                                                                           Homo sapiens.
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                                                                  12-OCT-2001
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                                      AAH98228;
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TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
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61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of a novel nucleic acid that was assembled from human thymus CDNA library-derived Hyseq clone identification number 16372272 (see AAH26341). A recursive algorithm was used to extend the clone by pulling additional sequences from different databases. A full-length sequence (see AAH26343) encoding novel human growth regularory-like polypeptide (GRLP, see AAB82671) was subsequently obtained. Human GRLP belongs to the same protein family as growth regulatory proteins, prouth factors, human melanoma derived growth regulatory protein precursor (64% similarity and 45% identity over 111 amino acids) or melanoma inhibitory activity, cattle carilage-derived retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid sensitive protein (CD-RAP, 44% identity and 64% can be used in the prophylaxis; treatment (including gene therapy) and diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma celling and primers, for chromosome and gene mapping, in the recombinant and arithmers, for chromosome and gene mapping, in the recombinant and arithmers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human growth regulatory-like polypeptide partial cDNA clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           373 CCCACCACGGATATTGACTTCTTCTGCGAG 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH26342 standard; cDNA; 891 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2000; 2000US-0491404. 02-MAY-2000; 2000US-0563786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2001; 2001WO-US02455.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483233/52.
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81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
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                                                                                                                                                                                                                                                                                                                                                                                                                        TyrThr11eSerLeualaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPhe11e
                                                                                                                                                                                                                                                                                                                                                                                                                                           148 TATACTATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATT
                                                                                                                                                                                                                                                                                                                                                             HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal
                                                                                                                                                                                                                                                                                                                                                                                    88 CATGGAATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 AACGTTAAAAAAGGCAGCAGCAGATCTATGTGTACTCAAAGGGTAAAAAGAAAATGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Growth regulatory-like polypeptide; human; cartilage; melanoma;
neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
                                                                                                                                                                                        Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;
                                                                                                                                                                                                                                    923
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                            Example 1; Page 99-100; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 CCCACCACGATATTGACTTCTTCTGCGAG
                                                                                                                                                                                                                                                                                                                                 US-10-019-455A-24 (1-110) x AAF59083 (1-923)
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
Score:
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                                                                                                                                                                                                                                                                                                                                  GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGlyMwetGlyValValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPhelle
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molecules, and to produce transgenic animals.
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                                                                     891
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                         Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
                                                                   Length:
Matches:
Conservative:
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                                                                                                                                           Gaps:
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                                                                                                                                                                     US-10-019-455A-24 (1-110) x AAH26342
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acid
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                                                                                              Percent Similarity:
Best Local Similarity:
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 peptide-nucleic
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                                                       Alignment Scores:
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Tanaka H;
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Ford JE,
              25-JAN-2000; 2000US-0491404.02-MAY-2000; 2000US-0563786.
         25-JAN-2001; 2001WO-US02455.
                            Boyle BJ,
                      (HYSE-) HYSEQ INC
WO200155332-A2.
     02-AUG-2001
                              Drmanac RT;
                            Mize NK,
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WPI; 2001-483233/52. P-PSDB; AAB82671.

Liu C;

Tang YT,

Arterburn MC,

Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system disorders

Claim 1; Page 115-116; 119pp; English.

the present sequence is that of a novel nucleic acid encoding human growth regulatory-like polypeptide (GRLP, see AAB82671).
The sequence was assembled using human thymus cDNA library-derived Hyseq clone identification number 16372272 (see AAH26341) as seed, using software programs to pull additional sequences from Hyseq's proprietary database containing expressed sequences from Hyseq's and by gel sequencing using primers to extend both 5' and 3' ends. The predicted protein has a mol.wt. of 14 kDa unglycosylated. GRLP, belongs to the same protein family as growth regulatory proteins, prought factors, human melatoma derived growth regulatory proteins, prought factors, human melatoma derived growth regulatory protein precursor (64% similarity and 45% identity over 111 amino acids) con melanoma inhibitory activity, cattle cartilage-derived cretinoic acid sensitive protein (CD-RAP, 44% identity and 64% imminoterial cartilage-derived cretinoic acid sensitive protein (CD-RAP, 44% identity and 64% imminoterial and diagnosis of disorders and other retinoic acid-sensitive and diagnosis of disorders and diseases caused by, or involving, and diagnosis of disorders and diseases caused by, or involving, and diagnosis of disorders and diseases caused by, or involving, and primers, for chromosome and gene mapping, in the recombinant production of protein, in the generation of antisense, ribozyme and peptide-nucleic acid molecules, and to produce transgenic animals. They may also have cytokine and cell proliferation or animals. They may also have cytokine and cell proliferation or involvity, haematopolesis regulating activity, tissue growth activity, and trivity, inhibin activity, and memorparity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activity and activit activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, use in cancer diagnosis and therapy, drug screening, receptor/ligand activity, antiinflammatory activity, and treatment of leukaemia, nervous system disorders, arthritis and inflammation.

Sequence 1201 BP; 357 A; 188 C; 275 G; 381 T; 0 other;

| Alignment Scores:   |          |               |      |
|---------------------|----------|---------------|------|
| Pred. No.:          | 1.21e-74 | Length:       | 1201 |
| <br>                | 290.00   | Matches:      | 110  |
| Percent Similarity: | 100.00%  | Conservative: | 0    |
| Local Similarity:   | 100.00%  | Mismatches:   | 0    |
| Query Match:        | 100.00%  | Indels:       | 0    |
|                     | 22       | Gana          | c    |

DNAS. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis.

AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used

330

Length:

2.97e-69

Alignment Scores: Pred. No.:

Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other; in the exemplification of the present invention.

The present invention describes novel MLP proteins and their encoding

US-10-019-455A-24 (1-110) x AAH26343 (1-1201)

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B7 CATGGAATATTATGGACCGTCTAGCTTCCAAGAACTCTGTGCAGATGATGAGTGTGTC 146 1 HisGlyllePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20

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386
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                                                                                                                                                               TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
               147 TATACTATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCCGGACTGTAGATTCATT 206
                                                                                                                                     267 GGAGAATTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGT 326
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                                                                                                        GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                                  327 TATITCCCCAGGAACIIGGTCAAGGAACAGCGIGIGIACAGGAAGCIACCAAGGAAGII
21 TyrThrIleSerLeuAlaSerAlaGluGluAspTyrAsnAlaProAspCysArgPheIle
                                                    41 AsnValLysLysGlyGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                           MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
                                                                                                                                                                                                                     101 ProThrThrAspileAspPhePheCysGlu 110
                                                                                                                                                                                                                                             387 CCCACCACGGATATTGACTTCTTCTGCGAG 416
                                                                                                                                                                                                                                                                                                                                                                                    Mouse MLP nucleotide sequence SEQ ID NO:25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 98; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                      AAF59080 standard; DNA; 330 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-0186718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAB69127.
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